Aae38358 Conus Aae38341 Conus Aae38347 Conus Aae38348 Conus Aau10212 Snail Aae38352 Conus Aau10214 Snail Aae38357 Conus Aau10214 Snail		Aac10211 Kap Aac38553 Conus pur Aac38551 Conus pur Aac38551 Conus pur Aac38559 Conus pur Aac38559 Conus pur Aac39559 Conus pur Aac39569 Anclogue Aac3659 Gmega con Aac3659 Anclogue Aac569 Anclogue Aac569 Anclogue Aac569 Anclogue Aac569 Comega-con		AAA015126 Cone anal Abb96786 Conega-con Aa126915 Xenogas-con Aar39616 WVIIC/SNX Aar3961765 SNX-231. Aar37761 WVIIC/SNX Aaw12952 NXR-231. Aaw12957 Omega con Aaw12967 Conug gen Aaw72614 Conug gen Aaw95572 Omega-con Aaw95573 Omega-con Aaw95573 Omega-con Aaw95673 Omega-con Aaw95673 Omega-con Aay56481 Natural o Aay56481 Omega-con Aay56481 Omega-con Aay56481 Omega-con Aay56481 Omega-con Aay56481 Omega-con Aay56481 Omega-con Aay56481 Omega-con Aay51315 Amino aci Aab14377 Omega-con Aab14375 Omega-con Aab19450 Primary 8 Aab19450 Primary 8
120 100.0 27 6 AAE38 120 100.0 27 6 AAE38 120 100.0 27 6 AAE38 110 100.0 27 6 AAE38 117 97.5 27 4 AAU30 116 96.7 27 6 AAE38 116 96.7 27 4 AAU30 115 95.8 27 4 AAU30	115 95.8 27 4 115 95.0 27 4 114 95.0 27 4 114 95.0 27 6 114 95.0 27 6 112 93.3 27 4 112 93.3 27 4 112 93.3 27 4	93333333333333333333333333333333333333	77 64.2 26 2 77 64.2 26 3 77 64.2 26 3 77 64.2 26 3 77 64.2 26 3	77 64. 72 72 60. 72 73 60. 73 75 60. 74 60. 75 75 75 75 75 75 75 75 75 75 75 75 75 7
prod section of the s	ace8/8ec	·	.ed,	11 Kap 11 Kap 12 B pur 13 B pur 14 B pur 15 B pur 16 B pur 17 B pur 18 pur 19 pur 10 B pur 11 B pur 11 B pur 12 B pur 13 B pur 14 B pur 15 B pur 16 B pur 17 B pur 18 pur 19 pur 10 B pur
on 5.1.6 Compugen Ltd. Search time 125 Second (without allignments)	odn 1130 uottitu	2105692	results predicted by chance to have a results predicted by chance to have a 1 to the score of the result being printed of the total score distribution. SUMMARIES 1D	Aav16200 Snain Aau10200 Snain Aau10205 Snain Aau10207 Snain Aau10208 Snain Aau102

Snail Kappa-conotoxin PVIIA analogue R2A

(first entry)

16-JAN-2002

AAU10200;

AAU10200 standard; peptide; 27 AA.

```
AAU10200
                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a new kappa-conotoxin PVIIA which targets potassium channels and can be used to augment neurotransmitter release in pathological situations such as autoimmune disease, e.g. Alzheimer's disease, Lambert-Eaton syndrome or myasthenia gravia. This peptide together with delta-conotoxin PVIIA act synergistically to rapidly kampblize fish which are injected with the two peptides. Injection of kappa-conotoxin PVIIA alone results in different symptoms with an injected fish becoming hyperactive and then contracting and suddenly extending all major fins. This "fine-popping" occurs repeatedly resulting in a series of jerky movements, but injection of only kappa-conotoxin pVIIA does not immobilize or kill the fish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New kappa-conotoxin peptides - which target potassium channels and can be
used to augment neurotransmitter release in e.g. autoimmune diseases.
                                                                                                                                                                                                                                                         /note= "Optionally 4-trans-hydroxyproline, hydroxyproline
Abb07821 Constitut
Adi16933 Human NOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                    Kappa-conotoxin PVIIA; potassium channel; neurotransmitter release; cone snail; venom; goldfish; delta-conotoxin PVIIA; disulphide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 120; DB 2; Length 27; 63.0%; Pred. No. 0.00084; ive 10; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            Olivera BM;
                                        ALIGNMENTS
                                                                                                                                                                                                                                .. .16
'note= "disulphide bond"
                                                                                                                                                                                                                                                                                               15. .26
/note= "disulphide bond"
                                                                                                                                                                                                                                                                                     'note= "disulphide bond"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CXIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB07821
ADI16933
                                                                                                                                                                                                                    Location/Qualifiers
                                                                                        AAW35723 standard; peptide; 27 AA
                                                                                                                                                                                                                                                                                                                                                                                                                            Shon K, Grilley MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 23; 29pp; English
                                                                                                                                                                                                                                                                                                                                                                   97WO-US003483.
                                                                                                                                                                                                                                                                                                                                                                                       96US-00619936.
                                                                                                                                                                                                                                                                                                                                                                                                         (UTAH ) UNIV UTAH RES FOUND.
  വവ
                                                                                                                                                                                                                                                                  or proline"
                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 63.0 tes 17; Conservative
  2444
2444
                                                                                                                                                 Kappa-conotoxin PVIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-480162/44.
                                                                                                                                                                                                  Conus purpurascens.
 56.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 27 AA;
                                                                                                                                                                                                                      Key
Disulfide-bond
                                                                                                                                                                                                                                                                             Disulfide-bond
                                                                                                                                                                                                                                                                                               Disulfide-bond
                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                    14-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                       18-MAR-1996;
                                                                                                                               03-APR-1998
                                                                                                                                                                                                                                                                                                                                                25-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                            rerlau H,
  68
                                                                                                          AAW35723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
                                                                             RESULT 1
  100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
```

셤

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappaconotoxin PVIIA peptide.
Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; R2A.
                                                                                                                                                                                                                                                                                                            /note= "The C-terminus is either a carboxyl group or an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treating disorders associated with radical depolarization of excitable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mccabe RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Layer RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 120; DB 4;
66.7%; Pred. No. 0.00084;
ive 9; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27
                                                                                                                                                                                                                                                     'note= "Hyroxyproline"
                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU10195 standard; peptide; 27 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cornell-Bell AH, Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 27; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-SEP-2000; 2000WO-US025827.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-SEP-1999; 99US-0155135P.
20-JUL-2000; 2000US-0219438P.
                                                                                                                                                                                                                                                                                                                                           amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (COGN-) COGNETIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-648090/74.
                                                                                                                      Conus purpurascens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                               WO200121648-A1
                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-MAR-2001;
                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jones RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
```

Mccabe RT;

Layer RT,

1

```
The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conctoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                                                                                               Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappaconotoxin PVIIA peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; HIIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C-terminus is either a carboxyl group or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 120; DB 4; Length 27; 100.0%; Pred. No. 0.00084;
                                                        Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Snail Kappa-conotoxin PVIIA analogue H11A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CXIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ź
                                                                                                                                                                                                                                                   Claim 1; Page 27; 46pp; English.
                                                        Pemberton KB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pemberton KB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-SEP-1999; 99US-0155135P
20-JUL-2000; 2000US-0219438P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-SEP-2000; 2000WO-US025827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU10208 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.
                  (COGN-) COGNETIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COGN-) COGNETIX INC.
                                                                                                               WPI; 2001-648090/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conus purpurascens.
Synthetic.
                                                        Cornell-Bell AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cornell-Bell AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200121648-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-MAR-2001
                                                                          Jones RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jones RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU10208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU10208
ID AAU1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                       /notes "Others Arg, homoArg, ornithine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N-trimethyl-Lys, any synthetic basic amino acid, His or halo-His"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Other= Arg, homoArg, ornithine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N-trimethyl-Lys, any synthetic basic amino acid, His or halo-His"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Other= Arg, homoArg, ornithine, Lys, N-methyl-Lys, N,N-trimethyl-Lys, any synthetic basic amino acid, His or halo-His"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Other= Arg, homoArg, ornithine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N-trimethyl-Lys, any synthetic basic amino acid, His or halo-His"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Other= Arg, homoArg, ornithine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N-trimethyl-Lys, any synthetic basic amino acid, His or halo-His"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /notes "Others Arg, homoArg, ornithine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N-trimethyl-Lys, any synthetic basic amino acid, His or halo-His"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Other= Phe, Tyr, meta-Tyr, ortho-Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr, (D.L)-Trp, neo-Trp or (D.L)-halo-Trp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= OTHER // Inc. meta-Tyr, ortho-Tyr, nor-Tyr, /note= "Other= Phe, Tyr, meta-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-halo-Tyr, (D.L)-Trp, neo-Trp or (D.L)-halo-Trp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          占
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "The C-terminus is either a carboxyl group
                                                                                                                               Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac i cerebral ischaemia; ocular ischaemia; asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Other= Pro or Hydroxyproline'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "Other= His or halo-His"
                                                                                             Snail Kappa-conotoxin PVIIA analogue #1
                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                           'label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                           'label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     label - OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-SEP-1999; 99US-0155135P.
20-JUL-2000; 2000US-0219438P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000WO-US025827
                                                      (first entry)
                                                                                                                                                                                                              Conus purpurascens.
Synthetic.
                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200121648-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-SEP-2000;
                                                      16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-MAR-2001
                AAU10195
```

ö

Gaps

ö

Indels

an

Mccabe RT;

Layer RT,

```
activating a KATP channel by administering to an individual a kappa-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200121648-A1
                                                                                                                                                                                                                                                                                                                                                                                                                               Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                     16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                 AAU10199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jones RR;
                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                  Conus
                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                           RESULT 6
AAU10199
  셤
                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                        ö
                                                                                                       depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, sepecially cardiac ischaemia, cerebral ischaemia, ocular analogue of the invention
                           Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-
                                                                                                                                                                                                                                                                                                                                                                                                        Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; coular ischaemia; asthma; F9M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     an
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "The C-terminus is either a carboxyl group or
amide group"
                                                                                                The invention relates to treating disorders associated with radical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mccabe RT;
                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                    Length 27;
                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Layer RT,
                                                                                                                                                                                                                   ; Score 120; DB 4;
Pred. No. 0.00084;
9; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                     Snail Kappa-conotoxin PVIIA analogue F9M
                                                                                                                                                                                                                                                                   1 CXIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                            AAU10205 standard; peptide; 27 AA
                                                                            Claim 1; Page 28; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pemberton KE,
                                                                                                                                                                                                                    100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-SEP-1999; 99US-0155135P.
20-JUL-2000; 2000US-0219438P.
                                                                                                                                                                                                                           66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-SEP-2000; 2000WO-US025827
                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                               Query Match
Best Local Similarity 66.7°
Matches 18, Conservative
                                                         conotoxin PVIIA peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (COGN-) COGNETIX INC
          WPI; 2001-648090/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-648090/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cornell-Bell AH,
                                                                                                                                                                                                Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200121648-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                    16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jones RR;
                                                                                                                                                                                                                                                                                                                                                AAU10205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Conus
                                                                                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                          셤
```

```
The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with channel, especially cardiac lembrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; K19A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappaconotoxin PVIIA peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "The C-terminus is either a carboxyl group or amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mccabe RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 120; DB 4; Length 27;
Pred. No. 0.00084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Layer RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Snail Kappa-conotoxin PVIIA analogue K19A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRIXNQKCMQHLDDCCSRKCNRFNKCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CXIXNQXCXQXLDDCCSXXCNXXNXCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU10199 standard; peptide; 27 AA.
                                                     Claim 1; Page 28; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 27; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
66.7%; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-SEP-1999; 99US-0155135P.
20-JUL-2000; 2000US-0219438P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-SEP-2000; 2000WO-US025827.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 66.7
Matches 18; Conservative
conotoxin PVIIA peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (COGN-) COGNETIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-648090/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cornell-Bell AH,
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 27 AA;
```

ö

```
ö
The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; R18A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "The C-terminus is either a carboxyl group or an
                                                                                                                                                                                                                          ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mccabe RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                   Score 120; DB 4; Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Temple DL, Layer RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 0.00084;
9; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Snail Kappa-conotoxin PVIIA analogue R18A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRIXNOKCFOHLDDCCSRACNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cornell-Bell AH, Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 27; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU10196 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                   100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-SEP-2000; 2000WO-US025827.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-SEP-1999; 99US-0155135P,
20-JUL-2000; 2000US-0219438P,
                                                                                                                                                                                                                                                                                                                                                                                                                      66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           conotoxin PVIIA peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (COGN-) COGNETIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-648090/74.
                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conus purpurascens.
Synthetic.
                                                                                                                                                                                                                                                                                                                        Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200121648-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jones RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU10196;
                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
AAU10196
AAU
      888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ठ
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA, peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, sepecially cardiac ischaemia, cerebral ischaemia, coular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                                                                                                                                                                                                                                                                                                                                              Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; K25A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-conotoxin PVIIA peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "The C-terminus is either a carboxyl group or an
amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating disorders associated with radical depolarization of excitable
radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                                                                                         Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to treating disorders associated with radical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RT;
                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mccabe
                                                                                                                                      Indels
                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Layer RT,
                                                                                                           Score 120; DB 4;
Pred. No. 0.00084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Temple DL,
                                                                                                                                      9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                 Snail Kappa-conotoxin PVIIA analogue K25A.
                                                                                                                                                                   27
                                                                                                                                                                                   'note= "Hyroxyproline"
                                                                                                                                                                   1 CXIXNQXCXQXLDDCCSXXCNXXNXCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                          Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pemberton KB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 27; 46pp; English.
                                                                                                                                                                                                                                                                         AAU10202 standard; peptide; 27
                                                                                                          Query Match
Best Local Similarity 66.7%;
Matches 18; Conservative 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-SEP-1999; 99US-0155135P.
20-JUL-2000; 2000US-0219438P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-SEP-2000; 2000WO-US025827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (COGN-) COGNETIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-648090/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             purpurascens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cornell-Bell AH,
                                                                             Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200121648-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                    16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                      AAU10202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jones RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conue
                                                                                                                                                                                                                                              RESULT
      ឧដ្ឋឧដ្ឋន
                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                          ઢ
```

Ä,

Seguence 27

g

1 CXIXNOXCXQXLDDCCSXXCNXXNXCV 27

ð

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-condroxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conducting are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
                                                                                                                                                                                                                                                                         Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; R22A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappaconotoxin PVIIA peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treating disorders associated with radical depolarization of excitable
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "The C-terminus is either a carboxyl group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mccabe RT;
                               ö
Score 120; DB 4; Length 27; Pred. No. 0.00084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 27;
                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Temple DL, Layer RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 120; DB 4;
Pred. No. 0.00084;
9; Mismatches 0;
               66.7%; Pred. No. 0.00
ive 9; Mismatches
                                                                                                                                                                                                                                              Snail Kappa-conotoxin PVIIA analogue R22A.
                                                        1 CXIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                          'note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                             ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cornell-Bell AH, Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 27; 46pp; English.
                                                                                                                                                         AAU10197 standard; peptide; 27
   100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
66.7%; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-SEP-1999; 99US-0155135P.
20-JUL-2000; 2000US-0219438P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-SEP-2000; 2000WO-US025827
                                                                                                                                                                                                                                                                                                                                                                                                                                                 amide group"
                                                                                                                                                                                                                  (first entry)
          Local Similarity 66.7
nes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                analogue of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (COGN-) COGNETIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-648090/74.
                                                                                                                                                                                                                                                                                                                                   Conus purpurascens
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200121648-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 27 AA
                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-SEP-1999;
                                                                                                                                                                                                                 16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-MAR-2001
                                                                                                                                                                                      AAU10197;
 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jones RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                Best Loc
Matches
                                                                                                                                             AAU10197
                                                                                                                                                          g
                                                         δ
```

```
The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia, and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                                                                                                                                            Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; F9Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappaconotoxin PVIIA peptide.
                                                                                                                                                                                                                                                                                                                                                       or an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mccabe RT;
                                                                                                                                                                                                                                                                                                                                                 /note= "The C-terminus is either a carboxyl group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Layer RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.7%; Score 120; DB 4;
66.7%; Pred. No. 0.00084;
ttive 9; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Temple DL,
                                                                                                                                                                  Snail Kappa-conotoxin PVIIA analogue F9Y
|:||||:||:||:||CRIXNQKCFQHLDDCCSRKCNAFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CXIXNOXCXQXLDDCCSXXCNXXXXX 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                  Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cornell-Bell AH, Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 28; 46pp; English.
                                                                               AAU10206 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-SEP-1999; 99US-0155135P.
20-JUL-2000; 2000US-0219438P.
                                                                                                                                                                                                                                                                                                                                                                   amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-SEP-2000; 2000WO-US025827.
                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COGN-) COGNETIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-648090/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 18; Conserva
                                                                                                                                                                                                                                                      purpurascens.
                                                                                                                                                                                                                                                                                                                                                                                            WO200121648-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 27 AA;
                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                       16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                       29-MAR-2001
                                                                                                                                                                                                                                                                  Synthetic
                                                                                                           AAU10206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jones RR;
                                                                                                                                                                                                                                                      Conus
                                                      RESULT 10
                                                                   AAU10206
                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
```

ö

Gaps

ö

0; Indels

Conservative

18;

Best Loca Matches

Local Similarity

```
Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; F9A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappaconotoxin PVIIA peptide.
                                                                                                                                                                                                                                                                                                          /note= "The C-terminus is either a carboxyl group or an
                                                                       Snail Kappa, conotoxin PVIIA analogue P9A
                                                                                                                                                                                                                                                                        'note= "Hyroxyproline"
                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 27; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cornell-Bell AH, Pemberton KB,
                                                                                                                                                                                                                                                                                                                                                                                                                                      21-SEP-2000; 2000WO-US025827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-SEP-1999; 99US-0155135P.
20-JUL-2000; 2000US-0219438P.
                                                                                                                                                                                                                                                                                                                               amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.78;
                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 66.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (COGN-) COGNETIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-648090/74.
                                                                                                                                                                                Conus purpurascens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                 WO200121648-A1
                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                       Modified-site
                                     16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                    29-MAR-2001
AAU10201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jones RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular schaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                                                                                                                                                                  cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; R2Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       asthma comprises
                                                                                                                                                                                                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprise activating a KATP channel by administering to an individual a kappa-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to treating disorders associated with radical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mccabe RT;
                                                                                                                                                                                                                                                                                                                                                                                                  /note= "The C-terminus is either a carboxyl group
                                                                                                                                                                                                 Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 120; DB 4; Length 27; 66.7%; Pred. No. 0.00084; ive 9; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Layer RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Temple DL,
                                                                                                                                                             Snail Kappa-conotoxin PVIIA analogue R2Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CXIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CQIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                               'note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                    AAU10207 standard; peptide; 27 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 28; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-SEP-1999; 99US-0155135P.
20-JUL-2000; 2000US-0219438P.
                                                                                                                                                                                                                                                                                                                                                                                                                     amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-SEP-2000; 2000WO-US025827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

Query Match

Best Local Similarity 66.77,

Best Local 18; Conservative
                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       conotoxin PVIIA peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (COGN-) COGNETIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-648090/74.
                                                                                                                                                                                                                                                                        Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cornell-Bell AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200121648-A1
                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                        16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-MAR-2001
                                                                                                                                                                                                                                                                                           Synthetic
                                                                                      AAU10207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jones RR;
                  RESULT 11
```

Mccabe RT;

Layer RT,

Temple DL,

```
ö
The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                            Score 120; DB 4; Length 27;
Pred. No. 0.00084;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Snail Kappa-conotoxin PVIIA analogue K7A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ż
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU10204 standard, peptide, 27
                                                                                                                                                                                                                                                                                                                                                                            100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU10204;
```

AAU10201 standard; peptide; 27 AA.

RESULT 12 AAU10201 ID AAU1 XX

8 셤 Location/Qualifiers

Conus purpurascens.

Synthetic

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprishing administering to an individual a kappa-conctoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and astebma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
           Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; K7A.
                                                                                                                                                                                                                                                                                                                                                                                                                    Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappaconotoxin PVIIA peptide.
                                                                                                                                                             'note= "The C-terminus is either a carboxyl group or an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                       Mccabe RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 27;
                                                                                                                                                                                                                                                                                                                                                      Temple DL, Layer RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 120; DB 4;
Pred. No. 0.00084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CXIXNOXCXOXLDDCCSXXCNXXNXCV 27
                                                                                                                                     note= "Hyroxyproline"
                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                    Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 28; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU10218 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
66.7%; F
                                                                                                                                                                                                                                                        21-SEP-2000; 2000WO-US025827.
                                                                                                                                                                                                                                                                                   . 99US-0155135P,
                                                                                                                                                                                                                                                                                              20-JUL-2000; 2000US-0219438P
                                                                                                                                                                           amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 66.77
Best Local Similarity 67.77
                                                                                                                                                                                                                                                                                                                         (COGN-) COGNETIX INC.
                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-648090/74.
                                                                  Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                 Cornell-Bell AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 27 AA;
                                                                                                                                                                                                   WO200121648-A1
                                                                                                                     Modified-site
                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                  22-SEP-1999;
                                                                                                                                                                                                                              29-MAR-2001
                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                 Jones RR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU10218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU1021
ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
```

Purple cone snail, kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; 04A.

Snail Kappa-conotoxin PVIIA analogue 04A

(first entry)

16-JAN-2002

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprisation of excitable membrane by activating a Kappa conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active PVIIA) pettide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP. channel, especially cardiac ischaemia, cerebral ischaemia, ocular
                                                                                                                                                                                                                                                                                                                                                                                     Treating disorders associated with radical depolarization of excitable medbrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappaconotoxin PVIIA peptide.
                                                                                                  /note= "The C-terminus is either a carboxyl group or an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; R2K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                  Mccabe RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                  Layer RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 120; DB 4; 63.0%; Pred. No. 0.00084;
                                                                                                                                                                                                                                                                                                              Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Snail Kappa-conotoxin PVIIA analogue R2K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:|:|:|:|:|:|CRIANQKCFQHLDDCCSRKCNRFNKCV 27
                                                                         'note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU10203 standard; peptide; 27 AA
                                                                                                                                                                                                                                                                                                             Cornell-Bell AH, Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 28; 46pp; English.
                                                                                                                                                                                                          21-SEP-2000; 2000WO-US025827
                                                                                                                                                                                                                                      22-SEP-1999; 99US-0155135P
20-JUL-2000; 2000US-0219438P
                                                                                                                       amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 63.0°
Matches 17; Conservative
                                                                                                                                                                                                                                                                                 (COGN-) COGNETIX INC
                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-648090/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conus purpurascens
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 27 AA;
                                          Key
Modified-site
                                                                                                                                                WO200121648-A1
                                                                                    Modified-site
                                                                                                                                                                                                                                   22-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
Modified-site
                                                                                                                                                                            29-MAR-2001
                                                                                                                                                                                                                                                                                                                                Jones RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU10203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ద
```

```
The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia, anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                              'note= "The C-terminus is either a carboxyl group or an
                                                                                                                                                                                                                                                                                                                          excitable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and astima. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                       Treating disorders associated with radical depolarization of excital membrane e.g. cardiac, cerebral and ocular ischemia and asthma compiactivating a KATP channel by administering to an individual a kappa-
                                                                                                                                                                                                                                               Mccabe RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 120; DB 4; Length 27; Pred. No. 0.00084; 9; Mismatches 0; Indels
                                                                                                                                                                                                                                            Temple DL, Layer RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conus purpurascens kappa-PVIIA analogue peptide, K25A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:||||:|:||:||CSSRCNRFNKCV 27
/note= "Hyroxyproline"
27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                              Cornell-Bell AH, Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 27; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE38342 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                   22-SEP-1999; 99US-0155135P
20-JUL-2000; 2000US-0219438P
                                                                                                                                     21-SEP-2000; 2000WO-US025827
                                               amide group'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Hyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 66.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                      conotoxin PVIIA peptide.
                                                                                                                                                                                                               (COGN-) COGNETIX INC
                                                                                                                                                                                                                                                                                          WPI; 2001-648090/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003063782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 27 AA;
                                                                            WO200121648-A1
               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-NOV-2003
                                                                                                                                                                                                                                                            Jones RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE38342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
```

```
ö
                                                                                                                                                                                                                 Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                               invention relates to kappa-PVIIA-related conotoxins and their use as
                                                                                                                                                                                                                                                                                                           organ protectants. The invertion also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angine, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, escebatal ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The presensequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Length 27;
                                                                                                                                        Mcintosh JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conus purpurascens kappa-PVIIA analogue peptide, K7A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 6;
                                                                                                                                        Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.0%; Prec. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 120; 63.0%; Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CXIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:|:|:|:|:|:|CSIPADDCCSRKCNRFNACV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ż
                                                                                                                                                                                                                                                                Disclosure; Page 7; 32pp; English
                                                                                                                                        Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE38344 standard; peptide; 27
                              28-JAN-2003; 2003WO-US002384
                                                            29-JAN-2002; 2002US-0352219P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JAN-2003; 2003WO-US002384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JAN-2002; 2002US-0352219P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Hyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 63.0
Matches 17; Conservative
                                                                                           COGNETIX INC.
UNIV UTAH RES
                                                                                                                                       Pemberton-Goodman KB,
                                                                                                                                                                                      WPI; 2003-679464/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conus purpurascens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2003063782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
Modified-site
 07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-AUG-2003
                                                                                                                                                       Olivera BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE38344;
                                                                                                        (UTAH )
                                                                                           (COGN-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE38344
ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
```

ö

Olivera BM;

```
Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                        The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arthythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, ecebral ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The present adquence is Comus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protection and preservation of an organ e.g. heart of a mammal comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 120; DB 6; Length 27; 63.0%; Pred. No. 0.00084; ive 10; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mcintosh JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conus purpurascens kappa-PVIIA analogue peptide, K19A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CXIXNQXCXQXLDDCCSXXCNXXNXCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                   Disclosure; 'Page 6; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE38339 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JAN-2003; 2003WO-US002384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JAN-2002; 2002US-0352219P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (COGN-) COGNETIX INC.
(UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Query Match
Best Local Similarity 63.0%;
Best Local 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Hyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-NOV-2003. (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pemberton-Goodman KE,
                                           WPI; 2003-679464/64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-679464/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003063782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Modified-site
Olivera BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Olivera BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE38339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE38339
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                         The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arriththmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropsthy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, carebral cerebral ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, atthma and congestive heart failure. The present sequence is Conus purpurascens (purple cone smail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                      Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retlinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 120; DB 6; Length 27; 63.0%; Pred. No. 0.00084; ive 10; Mismatches 0; Indels
                                                                                   Mcintosh JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Temple DL, Mcintosh JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conus purpurascens kappa-PVIIA analogue peptide, R18A.
                                                                                   Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CXIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |:|:|:|:|:|:|CRIPNQACFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                         Disclosure; Page 7; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ą
                                                                                Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pemberton-Goodman KE, Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE38336 standard; peptide; 27
                                    FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JAN-2003; 2003WO-US002384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JAN-2002; 2002US-0352219P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (COGN-), COGNETIX INC. (UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Hyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
           (COGN-) COGNETIX INC. (UTAH ) UNIV UTAH RES
                                                                            Pemberton-Goodman KE,
                                                                                                                                               WPI; 2003-679464/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conus purpurascens
```

Sequence 27 AA;

WO2003063782-A2

07-AUG-2003

Modified-site

20-NOV-2003

AAE38336;

AAE3833

ઠ 셤

ô

Gaps

;

present

ö

Gapa

ö

IndelB

```
Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury,
organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, neptropathy, acute heart failure, peripheral circulation disturbances, hypertension, angine, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, escebal ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The presensequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                       Score 120; DB 6; Length 27; Pred. No. 0.00084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conus purpurascens kappa-PVIIA analogue peptide, R22A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jones RM, Temple DL,
                                                                                                                                                                                                                                                                                                           10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                  |:|:|:|:|:||CRIPNQKCMQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Page 6; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE38337 standard; peptide; 27
                                                                                                                                                                                                                                                                         100.0%;
63.0%; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JAN-2003; 2003WO-US002384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JAN-2002; 2002US-0352219P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Hyp
                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 63.0°
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COGNETIX INC.
UNIV UTAH RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pemberton-Goodman KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-679464/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003063782-A2
                                                                                                                                                                                                                                        Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-AUG-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Olivera BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE38337;
                                                                                                                                                                                                    peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COGN-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UTAH)
                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE38337
       ద
                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                              use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to kappa-PVIIA-related conotoxins and their use as
                                                                                                                          related conocoxins. The conocoxins can also be used for arresting, protecting and or preserving somatic cells. The invention is for the protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, peripheral circulation disturbances, hypertension, angina, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, ecrebral ischaemia, coronary artery bypass graft (ABBS) surgery, ischaemic heart disease, aathma and congestive heart failure. The present equence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                          The invention relates to kappa-PVIIA-related conotoxins and their use an organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 120; DB 6; Length 27; 63.0%; Pred. No. 0.00084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mcintosh JM
                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
       use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conus purpurascens kappa-PVIIA analogue peptide, F9M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                      10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:|:||:||:||:||CRIPNOKCFOHLDDCCSRACNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                          Disclosure; Page 7; 32pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE38345 standard; peptide; 27 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 7; 32pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JAN-2002; 2002US-0352219P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-JAN-2003; 2003WO-US002384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (COGN-) COGNETIX INC.
(UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Hyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                      17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pemberton-Goodman KE,
                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conus purpurascens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003063782-A2.
                                                                                                                                                                                                                                                                                                                                 Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-AUG-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Olivera BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE38345;
                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 20
       용
                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠ
```

Mcintosh JM;

ö

Gaps

ò

us-10-627-685a-1.rag

```
/label= Arg, Orn, Lys, His, OTHER / note= "OTHER Homo-Arg, N-methyl-Lys, N-N-trimethyl-Lys, any synthetic basic amino acid, halo-His; preferably Arg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Arg, Orn, Lys, His, OTHER
home= "OTHER = Homo-Arg, N-methyl-Lys, N-N-dimethyl-Lys,
N-N-Lrimethyl-Lys, any synthetic basic amino acid, halo
His; preferably Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Phe, Tyr, OTHER
//note= "OTHER = Meta-Tyr, ortho-Tyr, nor-Tyr, mono- halo-Tyr, di-halo-Tyr, O-Bulpho-Tyr, O-phospho-Tyr, nitro-Tyr, D or L-Trp, neo-Trp, D or L-halo-Trp or any synthetic aromatic amino acid; preferably Phe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Arg, Orn, Lys, His, OTHER /note= "OTHER = Homo-Arg, N-methyl-Lys, N-N-trimethyl-Lys, any synthetic basic amino acid, halo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Arg, Orn, Lys, His, OTHER
hone= "OTHER = Homo-Arg, N-methyl-Lys, N-N-dimethyl-Lys,
N-N-Lrimethyl-Lys, any synthetic basic amino acid, halo
-His; preferably Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Arg, Orn, Lys, His, OTHER
/note= "OTHER = Homo-Arg, N-methyl-Lys, N-N-dimethyl-Lys,
N-N-N-trimethyl-Lys, any synthetic basic amino acid, halo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Purple cone snail, kappa-PVIIA-related conotoxin, urinary incontinence, ischaemic heart disease, cerebral ischaemia, anxiety disorder; diabetes, organ protectant; arrhythmia, reperfusion injury; hypertension, angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Phe, Tyr, OTHER
/note= "OTHER = Meta-Tyr, ortho-Tyr, nor-Tyr, mono- halo-
Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr,
    sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= His, OTHER
/note= "OTHER = Halo-His; preferably His"
                                                                                                                                                                Indels
                                                                                                                       Length
                                                                                                                       .
9
                                                                                                                  Score 120; DB 6;
Pred. No. 0.00084;
                                                                                                                                                             10; Mismatches
                                                                                                                                                                                                  1 CXIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                              |:|:|:|:|:|| CAIPNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conus purpurascens kappa-PVIIA peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   His; preferably Arg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        His; preferably Arg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                         AAE38335 standard; peptide; 27 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Pro, Hyp
                                                                                                                100.08;
                                                                                                                                    63.0%;
                                                                                                                                                           17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                         Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                    Sequence 27
                                                                                                                                                                                                                                                                                                                                                                                                                                              20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                     AAE38335;
                                                                                                                Query Match
Best Local 8
                             peptide
                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                              RESULT 23
      SXXX
                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                    ö
diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral vasospasa accompanying subarachnoid haemorrhage, anxiety disorder, cerebral ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, astham and congestive heart failure. The present sequence is Conus purpurascens (purple cone smail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incortinence, reperfusion injury, peripheres, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, ecrebral ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant, arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention relates to kappa-PVIIA-related conotoxins and their use as
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                         Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mcintosh JM;
                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conus purpurascens kappa-PVIIA analogue peptide, R2A.
                                                                                                                                                                                                                       ;
9
                                                                                                                                                                                                                    k; Score 120; DB 6;
; Pred. No. 0.00084;
10; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Temple DL,
                                                                                                                                                                                                                                                                                                         1 CXIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                  |:|:||:||:||:||CRIPNQKCFQHLDDCCSRKCNAFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 7; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE38340 standard; peptide; 27
                                                                                                                                                                                                                  ch 100.0%;
1 Similarity 63.0%;
17; Conservative 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JAN-2003; 2003WO-US002384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JAN-2002; 2002US-0352219P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (COGN-) COGNETIX INC. (UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Hyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pemberton-Goodman KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-679464/64.
                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conus purpurascens
                                                                                                                                                                           Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003063782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
Modified-site
```

07-AUG-2003

Olivera BM;

The

20-NOV-2003

AAE38340

Best Loca Matches

à 엄

8\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$

/label= Hyp

```
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                       /label= Arg, Orn, Lys, His, OTHER
force= "OTHER = Homo-Arg, N-methyl-Lys, N-N-dimethyl-Lys,
N-N-N-trimethyl-Lys, any synthetic basic amino acid, halo-
His; preferably Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present
                                                                                                                                                                                                                                                                                                                                         Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral wasospes accompanying subarachnoid hasmorrhage, arristly disorder, cerebral ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic, heart disease, asthma, and congestive heart failure. The present cheart disease, asthma, and congestive heart failure. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence is Conus purpurascens (purple cone snail) kappa PVIIA peptide
D or L-Trp, neo-Trp, D or L-halo-Trp or any synthetic aromatic amino acid; preferably Phe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 120; DB 6; Length 27; 100.0%; Pred. No. 0.00084;
                                                                                                                                                                                                                                                                     Temple DL, Mcintosh JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conus purpurascens kappa-PVIIA analogue peptide, F9Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CXIXNOXCXOXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE38346 standard; peptide; 27 AA
                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 5; 32pp; English
                                                                                                                                                                                                                                                                     Jones RM,
                                                                                                                                                                    28-JAN-2003; 2003WO-US002384.
                                                                                                                                                                                                29-JAN-2002; 2002US-0352219P.
                                                                                                                                                                                                                           (COGN-) COGNETIX INC.
(UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                     Pemberton-Goodman KE,
                                                                                                                                                                                                                                                                                                                WPI; 2003-679464/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conus purpurascens.
                           Misc-difference
                                                                                                               WO2003063782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Modified-site
                                                                                                                                           07-AUG-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-NOV-2003
                                                                                                                                                                                                                                                                                   Olivera BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE38346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
```

```
The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrivthmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy; nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, cerebral ischaemic heart disease, asthma and congestive heart failure. The present sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                           Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Purple cone snail, kappa-PVIIA-related conotoxin, urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant, arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 27;
                                                                                                                                                                                                                                                Mcintosh JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conus purpurascens kappa-PVIIA analogue peptide, R2K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; DB 6;
0.00084;
                                                                                                                                                                                                                                                Pemberton-Goodman KE, Jones RM, Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 Similarity 63.0%; Pred. No. 0.00
17; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CRIPNOKCYOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 7; 32pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE38343 standard; peptide; 27 AA.
                                                                                       28-JAN-2003; 2003WO-US002384.
                                                                                                                                 29-JAN-2002; 2002US-0352219P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Hyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                              (COGN-) COGNETIX INC. (UTAH ) UNIV UTAH RES
                                                                                                                                                                                                                                                                                                                WPI; 2003-679464/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conus purpurascens
WO2003063782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003063782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-NOV-2003
                                            07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-AUG-2003
                                                                                                                                                                                                                                                                        Olivera BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE38343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE38343
```

ö

```
Conus purpurascens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003063782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-AUG-2003.
Olivera BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Olivera BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE38341;
                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 27
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                               organ protectants. The invention also relates to a method of arresting protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral exerbral schaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, and congestive heart failure. The present sequence is Conus purpurascens (purple cone smail) kappa PVIIA analogue
                                                                                                                                                                                                                                                         Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertenaion; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                The invention relates to kappa-PVIIA-related conotoxins and their use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mcintosh JM;
                                                                                                                                                           Mcintosh JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conus purpurascens kappa-PVIIA analogue peptide, Q4A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 120; DB 6;
63.0%; Pred. No. 0.00084;
iive 10; Mismatches 0;
                                                                                                                                                           Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CXIXNQXCXQXLDDCCSXXCNXXNXCV
                                                                                                                                                                                                                                                                                                                       Disclosure, Page 7; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE38358 standard; peptide; 27 AA.
                                                                                                                                                           Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pemberton-Goodman KE, Jones RM,
                 28-JAN-2003; 2003WO-US002384.
                                                       29-JAN-2002; 2002US-0352219P.
                                                                                              (COGN-) COGNETIX INC.
(UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JAN-2003; 2003WO-US002384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9-JAN-2002; 2002US-0352219P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (COGN-), COGNETIX INC. (UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 63.0
nes 17; Conservative
                                                                                                                                                         Pemberton-Goodman KE,
                                                                                                                                                                                                                     WPI; 2003-679464/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conus purpurascens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003063782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-AUG-2003
                                                                                                                                                                               Olivera BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE38358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
```

용 ò

```
organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, ischaemic heart disease, asthma and congestive heart failure. The present sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                     Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                        invention relates to kappa-PVIIA-related conotoxins and their use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protection and preservation of an organ e.g. heart of a mammal comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mcintosh JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conus purpurascens kappa-PVIIA analogue peptide, F9A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.00084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 120; 63.0%; Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                Disclosure; Page 8; 32pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE38341 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JAN-2003; 2003WO-US002384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JAN-2002; 2002US-0352219P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (COGN-) COGNETIX INC.
(UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Hyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 63.0°
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pemberton-Goodman KE,
WPI; 2003-679464/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-679464/64.
```

ö

Gaps

ö

```
The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ischaemic heart disease, cerebral ischaemia, anxiety disorder; diabetes, organ protectant, arrhythmia, reperfusion injury; hypertension; angina, retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                       sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, repertusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral vasospassm accompanying subarachnoid haemorrhage, anxiety disorder, cerebral ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The prese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
                                                                                                                                                                                                                                                                              100.0%; Score 120; DB 6; Length 27; 63.0%; Pred. No. 0.00084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mcintosh JM;
                                                                                                                                                                                                                                                                                                                 0; Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conus purpurascens kappa-PVIIA analogue peptide, H11A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Temple DL,
                                                                                                                                                                                                                                                                                                                   10; Mismatches
                                                                                                                                                                                                                                                                                                                                                       1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                          CQI PNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 7; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE38348 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JAN-2003; 2003WO-US002384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JAN-2002; 2002US-0352219P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Hyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                   17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COGNETIX INC.
UNIV UTAH RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pemberton-Goodman KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-679464/64.
                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conus purpurascens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003063782-A2
                                                                                                                                                                                                                                             Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Olivera BM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE38348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UTAH )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COGN-)
                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE38348
         셤
                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                           The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, cerebral ischaemia, coronary artery bypass graft (GABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The present sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to kappa-PVIIA-related conotoxins and their use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 120; DB 6; Length 27; 63.0%; Pred. No. 0.00084; ive 10; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mcintosh JM,
           of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conus purpurascens kappa-PVIIA analogue peptide, R2Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:|:|:|:|:|:|CRIPNOKCAQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE38347 standard; peptide; 27 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 7; 32pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JAN-2002; 2002US-0352219P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-JAN-2003; 2003WO-US002384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (COGN-) COGNETIX INC.
(UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Hyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                              17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pemberton-Goodman KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-679464/64.
                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conus purpurascens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003063782-A2
                                                                                                                                                                                                                                                                                                                                        Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-AUG-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Olivera BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE38347;
                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                              Matches
         용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CX2X474X8X411X474X4X4X6X4X114X8X4X4X4X4X6X6X
```

ઠે

```
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conocoxins are used for traating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; S17A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-
diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, cerebral ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart discase, asthma and congestive heart failure. The preser sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /notes "The C-terminus is either a carboxyl group or an
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Temple DL, Layer RT, Mccabe RT;
                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                           100.0%; Score 120; DB 6; Length 27; 63.0%; Pred. No. 0.00084; tive 10; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Snail Kappa-conotoxin PVIIA analogue S17A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CXIXNQXCXQXLDDCCSXXCNXXNXCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cornell-Bell AH, Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 28; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU10212 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-SEP-1999; 99US-0155135P.
20-JUL-2000; 2000US-0219438P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-SEP-2000; 2000WO-US025827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amide group'
                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           conotoxin PVIIA peptide.
                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (COGN-) COGNETIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-648090/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conus purpurascens.
                                                                                                                                                                                                                                                                  Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200121648-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jones RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU10212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 30
AAU10212
ID AAU10212
XX
AC AAU10
XX
DT 16-JA
DE SNAil 16
   88888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving sometic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, ischaemic heart disease, asthma and congestive heart failure. The present sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                      Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischemic heart disease; cerebral ischemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; andina; retinopathy; coronary artery bypass graft surgery; acute heart failure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a mammal comprises
ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to kappa-PVIIA-related conotoxins and their use
                                                                                                         Gaps
                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mcintosh JM;
                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      congestive heart failure; neuropathy; nephropathy; CABG
                                                                          Length
                                                                                                                                                                                                                                                                                                                                           Conus purpurascens kappa-PVIIA analogue peptide, S17A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protection and preservation of an organ e.g. heart of use of a compound binding to kappa-PVIIA-binding site.
                                                                       Score 117; DB 4;
Pred. No. 0.0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jones RM, Temple DL,
                                                                                                         10; Mismatches
                                                                                                                                        1 CXIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                          27
                                                                                                                                                        |:||||:|:|:|:||CRIXNQKCFQHLDDCCARKCNRFNKCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                 Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 7; 32pp; English.
                                                                                                                                                                                                                                                AAE38352 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JAN-2003; 2003WO-US002384.
                                                                          97.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JAN-2002; 2002US-0352219P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Hyp
                                                                                                                                                                                                                                                                                                            (first entry)
              analogue of the invention
                                                                                                         17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (COGN-) COGNETIX INC. (UTAH ) UNIV UTAH RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pemberton-Goodman XE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-679464/64.
                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conus purpurascens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2003063782-A2
                                           Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
Modified-site
                                                                                                                                                                                                                                                                                                            20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Olivera BM;
                                                                                                                                                                                                                                                                               AAE38352;
                                                                                                       Matches
                                                                                                                                                                                                                   RESULT 31
                                                                                                                                                                                                                                 AAE38352
SXSS
                                                                                                                                                                                                                                                셤
                                                                                                                                        8
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; V27A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprise activating a KATP channel by administering to an individual a kappa-
                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mccabe RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "The C-terminus is either a carboxyl group
                                                                                                            ö
                                               Length 27;
                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Layer RT,
                                            97.5%; Score 117; DB 6; 59.3%; Pred. No. 0.0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Temple DL,
                                                                                                         11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Snail Kappa-conotoxin PVIIA analogue V27A.
                                                                                                                                                                      1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                  1 CRIPNOKCFQHLDDCCARKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                        Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1, Page 28; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                               AAU10217 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-SEP-1999; 99US-0155135P.
20-JUL-2000; 2000US-0219438P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-SEP-2000; 2000WO-US025827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conotoxin PVIIA peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (COGN-) COGNETIX INC.
Query Match
Best Local Similarity
16; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-648090/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conus purpurascens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cornell-Bell AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200121648-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU10217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jones RR
                                                                                                                                                                                                                                                                                                                                                  AAU10217

IID AAU1

AAU10217

XXX AAU1

XXX AAU1

YXX Carre

XXX Carre

XXX Carre

XXX Carre

XXX Carre

XXX Carre

XXX Carre

YY MOd

                                                                                                                                                                      ઠ
                                                                                                                                                                                                                            용
```

```
The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arriththmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, neuropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral ecrebral ischaemia, coronary artery bypass graft (CASG) surgery, ischaemic heart disease, asthma, and congestive heart failure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             heart of a mammal comprises
                                                                                                                                                                                                                           Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetee; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96.7%; Score 116; DB 6; Length 27; larity 61.5%; Pred. No. 0.0019; Conservative 10; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mcintosh JM;
                                                                                                                                                                                                Conus purpurascens kappa-PVIIA analogue peptide, V27A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protection and preservation of an organ e.g. heart of a use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CXIXNOXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |:|:||:||:||:||CRIPNOKCFOHLDDCCSRKCNRFNKC 26
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 8; 32pp; English.
                                                                                                  Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jones RM,
                                                                                                 AAE38357 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JAN-2003; 2003WO-US002384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JAN-2002; 2002US-0352219P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (COGN-) COGNETIX INC. (UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                /label= Hyp
                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pemberton-Goodman KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-679464/64.
                                                                                                                                                                                                                                                                                                                                Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
es 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                             WO2003063782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Olivera BM;
                                                                                                                               AAE38357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
                                                                                 AAE3835.
                 용
                                                                                                  용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
```

34

ö

ö

Gaps

ö

Length 27;

Score 116; DB 4; Length 27 Pred. No. 0.0019; 9; Mismatches 0; Indels

96.7%;

15 Similarity 65.4

Query Match Best Local & Matches CXIXNQXCXQXLDDCCSXXCNXXNXC 26

δ

e= "H " = gr,

3-pa⁻

ed-E

```
.
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The roots and it I with the distribution of the activities of APP characteristics of the activities of
                                                                                                                   anus is either a carboxyl gramp of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nil; kappa-PV11A-related conotoxin; urinary incont... nee;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; (1,43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cornection of Adv. Pembetten F., Temple Discharger Fig. Accessed to Johns Fig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Section 1 and 1 an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Mitch
Best Local Timilitity 63.0%; Pit 1. No. 0.0023;
Matches 17; Conservative 9; Aismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Comiss purpurascens kappa-PVII. ....logue peptide, 13A.
                                                                                                       une 13A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ·.
::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ... 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 standard; peptice; 27 ....
                                                                                                                   Liastin (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5-0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 com Kaxaxian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   issuice of excit

issue actimisterii

'Vian' peptide or its a...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 - ...P-Sabs; SaudNO-US...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sa. . . The comproxins are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 40111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . : I: I I
. nCFOHLDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ....X INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 7.71
                                                                                                                                                                                                                                                                                                                                             .83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence : / /w;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 . ... - 25 unl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (COC., ) C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF54338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Putt. C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 11 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3922398888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . <u>:</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ther a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :::: 5
```

: -

FEBR 57

2

SOC.

de

::

rin Xin

. - _ = U

.....

อั

```
Conus purpurascens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU10216
   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   원
                                                                                                                                                                                                                                                                                                                                                                      The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, neptropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral ecebral schaemia, coronary artery bypass graft (CABG) surgery, ischeemic heart disease, asthma and congestive heart failure. Sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart diseaes; cerebral ischaemia, anxiety disorder; diabetes; organ protectant, arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.8%; Score 115; DB 6; Length 27; 59.3%; Pred. No. 0.0023;
                                                                                                                                                                                                                                                         Mcintosh JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conus purpurascens kappa-PVIIA analogue peptide, L12A.
                                                                                                                                                                                                                                                         Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                   Disclosure, Page 6; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE38354 standard; peptide; 27 AA
                                                                                                                                                                                                                                                         Jones RM,
                                                                                                                                                                           28-JAN-2003; 2003WO-US002384.
                                                                                                                                                                                                 29-JAN-2002; 2002US-0352219P.
                                                                                                                                                                                                                       (COGN-) COGNETIX INC.
(UTAH ) UNIV UTAH RES FOUND.
                                                                                                      /label= Hyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16; Conservative
                                                                                                                                                                                                                                                         Pemberton-Goodman KE,
                                                                                                                                                                                                                                                                                            WPI; 2003-679464/64.
                                                            Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                              WO2003063782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 27 AA;
                                                                                 Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-NOV-2003
                                                                                                                                                     07-AUG-2003
                                                                                                                                                                                                                                                                     Olivera BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE38354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
   ઠે
```

```
organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, acute heart failure, peripheral circulation disturbance, hypertension, angina, carebral ecrebral schammia, coronary artery bypass graft (CABG) surgery, ischammic heart disease, asthma and congestive heart dialure. The present sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; Q10A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to kappa-PVIIA-related conotoxins and their use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                       Jones RM, Temple DL, Mcintosh JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.8%; Score 115; DB 6; 59.3%; Pred. No. 0.0023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Snail Kappa-conotoxin PVIIA analogue Q10A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CRIPNOKCFQHADDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CXIXNQXCXQXLDDCCSXXCNXXNXCV
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ŕ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Page 8; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU10216 standard; peptide; 27
                                                                                                                                                                                                                       28-JAN-2003; 2003WO-US002384.
                                                                                                                                                                                                                                                                              29-JAN-2002; 2002US-0352219P
                                                       /label= Hyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 59.37
These 16; Conservative
                                                                                                                                                                                                                                                                                                                                      COGNETIX INC.
UNIV UTAH RES
                                                                                                                                                                                                                                                                                                                                                                                                                       Pemberton-Goodman KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-679464/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conus purpurascens.
                                                                                                           WO2003063782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 27 AA;
                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JAN-2002
                                                                                                                                                                07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Olivera BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU10216;
                                                                                                                                                                                                                                                                                                                                      COGN-)
                                                                                                                                                                                                                                                                                                                                                                   (UTAH)
```

ö

Mccabe RT;

```
The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conctoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                                                                                                                                                                                                                         Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappaconotoxin PVIIA peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Purple cone snail, kappa-PVIIA-related conotoxin, urinary incontinence; ischemic heart disease, cerebral ischaemia, anxiety disorder; diabetes; organ protectant, arrhythmia, reperfusion injury; hypertension, angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure;
                                                                                                                                                                                  Layer RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conus purpurascens kappa-PVIIA analogue peptide, Q10A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 114; DB 4;
Pred. No. 0.0028;
                                                                                                                                                                                  Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CXIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRIXNAKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE38356 standard; peptide; 27 AA
                                                                                                                                                                                Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 28; 46pp; English.
                                            21-SEP-2000; 2000WO-US025827.
                                                                                   22-SEP-1999; 99US-0155135P
20-JUL-2000; 2000US-0219438P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JAN-2003; 2003WO-US002384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JAN-2002; 2002US-0352219P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 63.0°
Matches 17, Conservative
                                                                                                                                         (COGN-) COGNETIX INC
                                                                                                                                                                                                                                       WPI; 2001-648090/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (COGN-) COGNETIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conus purpurascens
                                                                                                                                                                              Cornell-Bell AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003063782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Modified-site
        29-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-AUG-2003.
                                                                                                                                                                                                  Jones RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE38356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE38356
        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, coular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
                                                                                                                                                                                                                                                                                                                                                              Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a Karp channel by administering to an individual a kappaconotoxin PVIIA peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
cerebral ischaemia; ocular ischaemia; asthma; Q6A.
        ล
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "The C-terminus is either a carboxyl group or an
amide group"
/note= "The C-terminus is either a carboxyl group or amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                         Mccabe RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                     Temple DL, Layer RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 114; DB 4;
Pred. No. 0.0028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Snail Kappa-conotoxin PVIIA analogue Q6A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |:||||:|:|:|
CRIXNQKCFAHLDDCCSRKCNRFNKCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                   Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 28; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU10210 standard; peptide; 27
                                                                                                                               21-SEP-2000; 2000WO-US025827.
                                                                                                                                                                      22-SEP-1999; 99US-0155135P.
20-JUL-2000; 2000US-0219438P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          analogue of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 63.0
                                                                                                                                                                                                                             (COGN-) COGNETIX INC.
                                                                                                                                                                                                                                                                                                                          WPI; 2001-648090/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conus purpurascens.
Synthetic.
                                                                                                                                                                                                                                                               Cornell-Bell AH,
                                                    WO200121648-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200121648-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                    22-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-JAN-2002
                                                                                           29-MAR-2001
                                                                                                                                                                                                                                                                                     Jones RR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU10210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
```

RESULT 39 AAU1021 ID AA

ò 셤 ö

Gaps

ö

Length 27; 1; Indels

```
22-SEP-1999; 99US-0155135P.
20-JUL-2000; 2000US-0219438P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-SEP-2000; 2000WO-US025827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                16-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (COGN-) COGNETIX INC.
 WPI; 2003-679464/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-648090/74.
                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cornell-Bell AH,
                                                                                                                                                                                                                                                Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200121648-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                           AAU10213;
                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jones RR;
                                                                                                                                                                                                                                                                                             Matches
 g
                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                      ö
                                                                             Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving sometic ells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neptropathy, acute heart failure, peripheral circulation disturbance, hypertension, angina, cerebral ecrebral schemmia, coronary artery bypass graft (ARG) surgery, ischammia, coronary artery bypass graft (ARG) surgery, ischammia, coronary artery bypass graft (ARG) surgery, ischammia, coronary artery bypass graft (ARG) surgery, eschammia, coronary artery bypass graft (ARG) surgery, ischammia, coronary artery bypass graft (ARG) surgery,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure;
                                                                                                                                         The invention relates to kappa-PVIIA-related conotoxins and their use
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                 DB 6; Length 27;
                        Mcintosh JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mcintosh JM;
                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conus purpurascens kappa-PVIIA analogue peptide, Q6A.
                                                                                                                                                                                                                                                                                                                              95.0%; Score 114; DB 6; 59.3%; Pred. No. 0.0028; ive 10; Mismatches
                        Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                          |:|:||:||:|| CRIPNOKCFAHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                              1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                 Disclosure; Page 8; 32pp; English.
                        Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE38350 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JAN-2003; 2003WO-US002384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JAN-2002; 2002US-0352219P
(UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (COGN-) COGNETIX INC.
(UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Hyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pemberton-Goodman KE,
                        Pemberton-Goodman KE,
                                                         NPI; 2003-679464/64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conus purpurascens.
                                                                                                                                                                                                                                                                                                                                          Local Similarity
Les 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003063782-A2
                                                                                                                                                                                                                                                                                                        Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-AUG-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-NOV-2003
                                   Olivera BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Olivera BM;
                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE38350
                                                                                                                                                                                                                                                                                                                                              Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 41
                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                              8
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; N24A.
Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                         related concoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, cerebral ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The presen sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                  The invention relates to kappa-PVIIA-related conotoxins and their use a organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "The C-terminus is either a carboxyl group or an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treating disorders associated with radical depolarization of excitable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mccabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Layer RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.0%; Score 114; DB 6; 59.3%; Pred. No. 0.0028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Snail Kappa-conotoxin PVIIA analogue N24A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                   Disclosure; Page 7; 32pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU10213 standard; peptide; 27 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pemberton KE,
```

```
The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conctoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-
                                                                                              Claim 1; Page 28; 46pp; English.
                                                conotoxin PVIIA peptide
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 27 AA;
```

93.3%; Query Match Best Local Similarity 63.0° Matches 17; Conservative

1 CXIXNOXCXQXLDDCCSXXCNXXNXCV 27 ઠે 셤

43

AAU10209 standard; peptide; 27

Ą.

(first entry) 16-JAN-2002 AAU10209;

Snail Kappa-conotoxin PVIIA analogue D14A.

Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP charnel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; D14A.

Conus purpurascens. Synthetic.

/note= "The C-terminus is either a carboxyl group or an amide group" note= "Hyroxyproline" Location/Qualifiers Modified-site Modified-site

WO200121648-A1

29-MAR-2001

21-SEP-2000; 2000WO-US025827.

22-SEP-1999; 99US-0155135P. 20-JUL-2000; 2000US-0219438P.

(COGN-) COGNETIX INC

Mccabe RT; Layer RT, Temple DL, Pemberton KE, Cornell-Bell AH, Jones RR;

WPI; 2001-648090/74.

Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappaconotoxin PVIIA, peptide

Claim 1; Page 28; 46pp; English

```
ö
              The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                              93.3%; Score 112; DB 4;
63.0%; Pred. No. 0.0041;
ive 9; Mismatches 1
                                                                                                                                                                                                                                                                                                                                         1 CXIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                 27
                                                                                                                                                                                                                                                                                                                                                                |:||||:|:|:||
| CRIXNQKCFQHLDACCSRKCNRFNKCV
                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 63.0'
                                                                                                                                                                                                                      Sequence 27 AA;
****************
                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                             ద
```

RESULT 44 AAU10219

ö

Gaps

ö

Length 27; 1; Indels

Score 112; DB 4; Pred. No. 0.0041; 9; Mismatches AAU10219 standard; peptide; 27 AA

AAU10219;

16-JAN-2002 (first entry)

Snail Kappa-conotoxin PVIIA analogue N5A

Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; NSA.

Conus purpurascens

Synthetic.

/note= "The C-terminus is either a carboxyl group 'note= "Hyroxyproline" Location/Qualifiers amide group" Modified-site Modified-site

an

or

WO200121648-A1

29-MAR-2001

21-SEP-2000; 2000WO-US025827.

22-SEP-1999; 99US-0155135P. 20-JUL-2000; 2000US-0219438P.

(COGN-) COGNETIX INC.

Mccabe Layer RT, Temple DL, Pemberton KE, Cornell-Bell AH, Jones RR;

RT;

WPI; 2001-648090/74.

Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappaconotoxin PVIIA peptide

Claim 1; Page 28; 46pp; English.

The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active

```
27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 27
                                                                                                                                                                                                                                                                                                                                                                                                                           29-MAR-2001
                                                                                                                                                                             AAU10211;
              Sequence
                                                                             -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jones RR
                                                                                                                                   RESULT 46
   X S
                                                                                                                                                       ð
                                                                                                셤
                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                                                                                                                                                                                                                                                  Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; D13A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-
                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "The C-terminus is either a carboxyl group or an amide group"
salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to treating disorders associated with radical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mccabe RT;
                                                                                                             ö
                                                                                     Score 112; DB 4; Length 27; Pred. No. 0.0041; 9; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Layer RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Temple DL,
                                                                                                                                                                                                                                                                              Snail Kappa-conotoxin PVIIA analogue D13A.
                                                                                                                                 1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                              |:|| |:|:||:|||||||||::||::||:||
CRIXAQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                     'note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                            AAU10215 standard; peptide; 27 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 28; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-SEP-1999; 99US-0155135P.
20-JUL-2000; 2000US-0219438P.
                                                                                       93.3%;
63.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-SEP-2000; 2000WO-US025827
                                                                                                                                                                                                                                                        (first entry)
                                             analogue of the invention
                                                                                                            17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         conotoxin PVIIA peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (COGN-) COGNETIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-648090/74.
                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                               Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cornell-Bell AH,
                                                                 Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200121648-A1
                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                        16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-MAR-2001
                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jones RR;
                                                                                                                                                                                                                                  AAU10215;
                                                                                                             Matches
                                                                                                                                                                                     88888888
                                                                                                                                                     용
                                                                                                                                   ઠે
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with cradical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Purple cone snall, kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; N21A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /notes "The C-terminus is either a carboxyl group or an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treating disorders associated with radical depolarization of excitable
                                                                                                  Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mccabe RT;
                                                                                                  ö
                                                 Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 27;
                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Layer RT,
                                                                                                  ;
                                              Score 112; DB 4;
Pred. No. 0.0041;
9; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 112; DB 4;
Pred. No. 0.0041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Snail Kappa-conotoxin PVIIA analogue N21A.
                                                                                                                                                      CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                  |:||||:|:||:||:|| |||||::||::||:||
CRIXNQKCFQHLADCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                           Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 28; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pemberton KE,
                                                                                                                                                                                                                                                                                                                                         AAU10211 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.3%;
                                              Query Match
Best Local Similarity 63.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-SEP-2000; 2000WO-US025827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0155135P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JUL-2000; 2000US-0219438P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activating a KATP channe
conotoxin PVIIA peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (COGN-) COGNETIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-648090/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conus purpurascens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cornell-Bell AH,
Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200121648-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                              16-JAN-2002
```

Conus purpurascens kappa-PVIIA analogue peptide, N21A.

(first entry)

20-NOV-2003

AAE38351;

AAE38351 standard; peptide; 27 AA.

RESULT 48

AAE38351

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, utinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbanes, hypertension, angina, cerebral cerebral ischaemia, coronary artery bypass graft (GABG) surgery, ischaemic heart disease, aschma and congestive heart failure. The present sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                          Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
        Gaps
        ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.3%; Score 112; DB 6; Length 27; 59.3%; Pred. No. 0.0041; ive 10; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mcintosh JM;
      Indels
                                                                                                                                                                                                                                            Conus purpurascens kappa-PVIIA analogue peptide, N24A.
        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Temple DL,
     Mismatches
                                 1 CXIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                    1 CRIXNQKCFQHLDDCCSRKCARFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                  Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 7; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jones RM,
     9.
                                                                                                                                             AAE38353 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JAN-2003; 2003WO-US002384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JAN-2002; 2002US-0352219P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COGNETIX INC.
UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Hyp
                                                                                                                                                                                                             (first entry)
   17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 59.3
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pemberton-Goodman KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-679464/64.
                                                                                                                                                                                                                                                                                                                                                                            Conus purpurascens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003063782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                          Key
Modified-site
                                                                                                                                                                                                               20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Olivera BM;
                                                                                                                                                                               AAE38353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (COGN-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GTAH )
Matches
                                                                                                                                 AAE38353
                                                                                                                                                            ð
                                                              g
```

```
ò
                                                                                                          Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, utinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, incontinence, reperfusion injury, peripheral circulation disturbances, hypertension, angina, cerebral echaemia, coronary artery bypass graft (CABG) surgery, ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The present sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mcintosh JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.3%; Score 112; DB 6; Length 27; 59.3%; Pred. No. 0.0041; ive 10; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jones RM, Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CXIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 7; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 49
AAE38355
ID AAE38355 standard; peptide; 27 AA.
                                                                                                                                                                                                                                                                                                                                                                            28-JAN-2003; 2003WO-US002384.
                                                                                                                                                                                                                                                                                                                                                                                                           29-JAN-2002; 2002US-0352219P.
                                                                                                                                                                                                                                                                                                                                                                                                                                        (COGN-) COGNETIX INC. (UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                              /label= Hyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity 59.3
16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pemberton-Goodman KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-679464/64.
                                                                                                                                                                                                               Conus purpurascens,
                                                                                                                                                                                                                                                                                                             WO2003063782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 27 AA;
                                                                                                                                                                                                                                               Key
Modified-site
                                                                                                                                                                                                                                                                                                                                             07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Olivera BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
```

ö

Gaps

; 0

1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27 |:|:|:||:||:||CRIPNOKCFQHLDDCCSRKCNRFAKCV 27

8

```
Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                           Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
 Conus purpurascens kappa-PVIIA analogue peptide, D14A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 7; 32pp; English
                                                                                                                                                                                                                                                                   28-JAN-2003; 2003WO-US002384
                                                                                                                                                                                                                                                                                                29-JAN-2002; 2002US-0352219P
                                                                                                                                                                                                                                                                                                                                                                         Pemberton-Goodman KE,
                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-679464/64.
                                                                                                                    purpurascens
                                                                                                                                                                                                          WO2003063782-A2
                                                                                                                                                  Key
Modified-site
                                                                                                                                                                                                                                        07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                        Olivera BM
                                                                                                                                                                                                                                                                                                                              COGN-
                                                                                                                                                                                                                                                                                                                                             UTAH )
                                                                                                                      Conus
 The invention relates to kappa-PVIIA-related conotoxins and their use as protectings. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation discurbances, hyperension, angina, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, cerebral ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The present sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                  Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mcintosh JM;
                                                                        Conus purpurascens kappa-PVIIA analogue peptide, D13A.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Temple DL,
                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 8; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Jones RM,
                                                                                                                                                                                                                                                                                                                                                                       29-JAN-2002; 2002US-0352219P.
                                                                                                                                                                                                                                                                                                                                           28-JAN-2003; 2003WO-US002384
                                                                                                                                                                                                                                                                                                                                                                                                    (COGN-) COGNETIX INC. (UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                     /label= Hyp
                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Pemberton-Goodman KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-679464/64.
                                                                                                                                                                                              Conus purpurascens.
                                                                                                                                                                                                                                                                                 WO2003063782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 27 AA;
                                                                                                                                                                                                                                      Modified-site
                                         20-NOV-2003
                                                                                                                                                                                                                                                                                                              07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Olivera BM;
               AAE38355;
```

Mcintosh JM;

Temple DL,

Jones RM,

FOUND.

COGNETIX INC. UNIV UTAH RES

Location/Qualifiers

/label= Hyp

```
ô
                                                                                                                                                                                                                                   present
                organ protectants. The invertion also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, escebati ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, aethma and congestive heart failure. The presensequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     snail; kappa-PVIIA-related conotoxin; urinary incontinence;
The invention relates to kappa-PVIIA-related conotoxins and their use
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                       Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conus purpurascens kappa-PVIIA analogue peptide, N5A.
                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                          93.3%; Score 112; DB 6; 59.3%; Pred. No. 0.0041;
                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CXIXNQXCXQXLDDCCSXXCNXXNXCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ź
                                                                                                                                                                                                                                                                                                                                                                                                                       10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE38359 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity >>..
Best Local Similarity >>..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                            Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE38359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Purple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE38359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
```

ö

Gaps

ö

1; Indels

10; Mismatches

16; Conservative

ઠે g

Local Similarity

Query Match Best Loc Matches

|:|:|:||:|:|:|CRIPNOKCFOHLADCCSRKCNRFNKCV 27 1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27

Ş

AAE38349 standard; peptide; 27

(first entry)

20-NOV-2003

AAE38349;

RESULT 50
AAE38349
ID AAE3
XX
AC AAE3
XX
OT 20-N

93.3%; Score 112; DB 6; Length 27; 59.3%; Pred. No. 0.0041;

Miljanich GP,

Valentino KL,

Gohil K,

Singh T,

92WO-US011349. 91US-00814759

/note= "Amidated C-terminal"

Location/Qualifiers

```
Use of omega-cono-peptide(s) which selectively inhibit voltage-gated calcium channels - to induce analgesia, enhance opiate analgesics, treat
                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 2; 90pp; English.
                                                                                                                                                                                                                                                                                                                       WPI; 1993-227270/28.
                                                                                                                                                                                                                                                         (NEUR-) NEUREX CORP
                        Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                          Modified-site
                                                                                                                                                                                          30-DEC-1992;
                                                                                                                                                                                                                         30-DEC-1991;
                                                                                                                          WO9313128-A1
                                                                                                                                                         08-JUL-1993
                                                                                                                                                                                                                                                                                       Justice A,
                                                                                                                                                                                                                                                                                                                                                                                         pain etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR37774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNX-202.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 53
AAR37774
        유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral cerebral isohaemia, coronary artery bypass graft (CABG) surgery, ischaemia cononary artery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The present sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                               Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVXIA-binding site.
retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                  Mcintosh JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 112; DB 6; Length 27;
Pred. No. 0.0041;
9; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                  Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CXIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 8; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR39628 standard; peptide; 26 AA
                                                                                                                                                                                                                                                                                                                                Jones RM,
                                                                                                                                                                                                                  28-JAN-2003; 2003WO-US002384
                                                                                                                                                                                                                                                 29-JAN-2002; 2002US-0352219P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.3%;
                                                                                                                                                                                                                                                                              (COGN-) COGNETIX INC.
(UTAH ) UNIV UTAH RES FOUND.
                                                                                                                /label= Hyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17; Conservative
                                                                                                                                                                                                                                                                                                                                Pemberton-Goodman KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-679464/64.
                                                 Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                               WO2003063782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 27 AA;
                                                                                              Modified-site
                                                                                                                                                                                 07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                 Olivera BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-2003
20-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR39628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR39628
ID AAR3
XX
AC AAR3
XX
DT 25-b
DT 20-I
XX
XX
CW COME
KW COME
KW CAI
KW Din
KW Din
KW Din
KW CAI
```

```
ö
The sequences given in AAR39608-30 are omega conopeptides (OCTS) and derivatives of these, which may be used to produce analgesia in a mammal. These OCTS inhibit voltage-gated calcium channels selectively in neuronal tissue. This is shown by the peptides ability to stimulate contraction in guinea pig ileum and to bind to OCT WVIIA binding sites present in neuronal tissue. OCTs are components of peptide toxins derived from marine snails of the genus Conus, and act as calcium channel blockers. These OCTs may be used to replace opiods in the treatment of chronic pain or to reduce the opiod dosage required. This helps to reduce dependence on and tolerance to opiod narcotics. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ischaemia; neuronal; omega-conotoxin; OCT; MVIIA; MVIIC; MVIID; GVIA; GVIIA; GVIIA; VVIA; SVIIA; TVIA; SVIB; SNX-207; stroke; delayed treatment; antihistamine; blood pressure; N-type voltage-gated Ca currents; N-channel mediated neurotransmitter release.
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                   67.5%; Score 81; DB 2; Length 26; 34.6%; Pred. No. 2; 4; Indels ive 13; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                      56
                                                                                                                                                                                                                                                                                                                                                                                                          1 CXIXNQXCXQXLDDCCSXXCNXXNXC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR37774 standard; peptide; 26
                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 34.00.
Best Local Similarity
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
                                                                                                                                                                                                                                                            Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                  field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-2003
08-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
```

Omega conopeptide; OCT; analgesia; inhibition; voltage-gated; calcium channel; neurone; contraction; guinea pig; ileum; MVIIA; binding site; toxin; marine; snail; Conus; opiod; chronic pain;

SNX-202.

셤 ઠ

Synthetic

Kristipati R;

```
peptides from Conus sp. (cone snais). The peptides and their analogues are used as analgesics acting by blocking N-type voltage-sensitive are used as analgesics acting by blocking N-type voltage-sensitive calcium channels. The Ocs can be used to treat neuropathic pain as a result of e.g. insult to the spinal cord or peripheral nerves, cancer, bone degenerative diseases, AIDS, reflex sympatheric dystrophy, herpes coster neuropathy, diabetic neuropathy administered in a medicament via an hyperalgesia. The OCs are preferably administered in a medicament via an chyperalgesia. The OCs are preferably administered epidurally in the absence of a permeation enhancer, at doses that are comparable to effective analgesic doses using intrathecal administration. OC formulations comparising an OC and a carboxylic administration. OC They also confer stability to solutions containing them for prolonged
                                                                                                                                                                                                                                                                        Stable omega conopeptide compositions - for producing analgesia and for inhibiting progression of neuropathic pain disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Omega conopeptide, analgesic, treatment, neuropathic pain; inhibition, neuronal damage; schizophrenia; tardive dyskinesia; analgesia; acute dystonic reactions; inflammation; epilepsy.
                                                                                                                                                                    Adriaenssens PI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 67.5%; Score 81; DB Local Similarity 34.6%; Pred. No. 2; es 9; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treatment methods and long-term storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | ::: |:|::: ||||::| :: :|
| CKLKGQSCSRLMYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                 3, Gohil K,
Luther RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW12985
ID AAW12985 standard; peptide; 26 AA
                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 4; 47pp; English.
                        96WO-US011041
                                                             95US-00496847
96US-00613400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93US-00049794.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91US-00814759.
92WO-US011349.
                                                                                                                                                                    Bowersox SS,
Pettus MR, Lu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Omega conopeptide SNX-202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
                                                                                                                            (NEUR-) NEUREX CORP.
                                                                                                                                                                                                                               WPI; 1997-100012/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NEUR-) NEUREX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 26 AA;
                                                               27-JUN-1995;
                                                                                     08-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-DEC-1991;
30-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
22-APR-1997
                                                                                                                                                                    Amstutz GA,
Gadbois T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JS5587454-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW12985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 55
    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                      The C-terminal is amidated. Ischaemia-related neuronal damage in mammals is reduced by admin., 4-24 hr after onset of ischaemia, of a cpd. (I) which binds selectively to an omega-conotoxin (OCT) WIIA site in neuronal tissue. (I) has selectivity at least 100 expressed as ratio of binding affinity for the WIIA site to that for the WIIC site. (I) is one of the OCTS WIIA, GVIA, GVIA or RVIA or it is the cpd. SNX-207. (I) is esp. used to reduce neuronal damage caused by stroke. By delaying admin. for some time (compare USSOS403 where cpds. are given within 1 hr of the onset of ischaemia) a greater redn. in neuronal damage is achieved. (I) is admin. e.g. by intracerebroventricular (ICV) infection at 0.1-20 microg/kg, but can also be given i.v. (opt. after treatment with antihisteramines to minimise redn. in blood pressure caused by (I)). (I) is also at least as effective as the specified conotoxins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for (1) selective inhibition of N-type voltage-gated Ca currents in neuronal tissue and (2) selective inhibition of N-channel mediated neurotransmitter release in neuronal tissue. Primary sequences of omegaconopeptides are given in harm 152. Several analog omega-conopeptides are given in ARR17762-6. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                     Redn. of neuronal damage caused by ischaemia – by admin. of cpds. that
bind specifically to omega-conotoxin MVIIA binding sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conopeptide; cone snail; pain; analgesic; neuropathy; epidural; N-type voltage-sensitive calcium channel; block; Conus.
                                                                                                                                                                                                                               Bitner RS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNX-202, omega conopeptide derivative used for pain relief.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67.5%; Score 81; DB 2; Length 26; 34.6%; Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                               Valentino KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fox JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Fig 2; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW19570 standard; peptide; 26 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "amidated"
                                                                                92WO-US009766
                                                                                                                        91US-00789913
92US-00916478
                                                                                                                                                                                                                               Bowersox SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 9; Conserva
                                                                                                                                                                                     (NEUR-) NEUREX CORP.
                                                                                                                                                                                                                                                                                              WPI; 1993-182487/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
Modified-site
                                                                                                                                                                                                                               Miljanich GP,
Yamashiro DH;
                                                                                   12-NOV-1992;
WO9310145-A1
                                                                                                                        12-NOV-1991;
                                                                                                                                              17-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9701351-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-OCT-1997
                                           27-MAY-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW19570;
```

Query Match Best Loc Matches

RESULT 54

원 ઠ

ö

Gaps

ö

DB 2; Length 26; 4; Indels

78

Page

```
88888888888888
                                                                                                                                                                                           셤
                                                                                                                                                                        à
                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                           Conus genus, marine snail; cone snail; omega-conopeptide; analgesia; noscieeptive pain; neuropathic pain; neuropal tissue; conotoxin; inflammation; schizophrenia; tardive dyskinesia; acute dystonic reaction; rheumatoid arthritis; epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treatment of inflammation, comprises administration of omega-conopeptide - effective to block voltage-gated calcium channels, bind with high affinity to omega-conopeptide binding site, and inhibit neuro=transmitter
                                                                                                         especially for treating neuropathic pain. The peptide, which can be prepared by solid phase synthesis, can also be used to inhibit neuronal damage and treat schizophrenia, tardive dyskinesia, acute dystonic reactions, inflammation and epilepsy. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                             Gaps
                                                                                                 peptide is an omega conopeptide, useful as an analgesic,
                                             - useful as analgesics, esp. for treating
                                                                                                                                                                                                                              ö
    Ë
    Singh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Singh
                                                                                                                                                                                                       2; Length 26;
                                                                                                                                                                                                                             Indels
   Justice A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Justice A,
                                                                                                                                                                                                                                                                                                                                                                                                       genus analogue omega-conopeptide SNX-202.
                                                                                                                                                                                                     67.5%; Score 81; DB 34.6%; Pred. No. 2;
                                                                                                                                                                                                                           Mismatches
  Valentino KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gohil KC,
                                                                                                                                                                                                                                                 26
                                                                                                                                                                                                                                                                      26
                                                                           Disclosure; Col 51-52; 58pp; English
                                                                                                                                                                                                                                                              1 CKLKGQSCSRLMYDCCSGSCGRSGKC
                                                                                                                                                                                                                                                1 CXIXNOXCXOXLDDCCSXXCNXXNXC
                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                           13;
                                                                                                                                                                                                                                                                                                                          AAW72625 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91US-00814759.
93US-00049794.
96US-00675354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96US-00742774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Valentino KL,
                                                                                                                                                                                                                                                                                                                                                                       (revised)
(first entry)
                                                                                                                                                                                                   Query Match
Best Local Similarity 34.6
Matches 9; Conservative
Miljanich GP,
                                             Omega cono:peptide(s)
                      WPI; 1997-064830/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NEUR-) NEUREX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-582596/49.
                                                        neuropathic pain.
                                                                                                                                                                              Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Miljanich GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996;
                                                                                                  The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                     27-AUG-2003
06-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-APR-1993;
03-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US5824645-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-0CT-1998
 Gohil KC,
                                                                                                                                                                                                                                                                                                                                                AAW72625;
                                                                                                                                                                                                                                                                                                                                                                                                       Conus
                                                                                                                                                                                                                                                                                                     RESULT 56
à
                                                                                                                                                                                                                                                                    셤
```

A method has been developed for the treatment of inflammation in a subject. The method comprises administration of an omega-conopeptide effective to: (i) block voltage-gated calcium channels; (ii) bind with high affinity to an omega-conopeptide binding site; and (iii) inhibit neurotransmitter release from nervous tissue. The method is used to treat

Disclosure, Fig 2; 58pp; English.

release

```
inflammation and associated pain. The treatment can also be used to produce analgesia (especially in subjects experiencing neuropathic pain); and to treat schizophrenia, tardive dyskinesia and acute dystonic reactions, rheumatoid arthritis, and epilepsy. The present sequence represents an analogue omega-conopeptide. Omega-conopeptides are components of peptide toxins produced by marine snails of the genus Conus, and which act as calcium channel blockers. (Updated on 27-AUG-2003
                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequences AAW95574-589 represent sequences of analog omega-conopeptides. Omega-conopeptides are components of peptide toxins produced by marine snails of the genus Conus, and which act as calcium channel blockers. The invention relates to a method of producing analgesia in a mammal that comprises administering an omega conopeptide having activities in (a) inhibiting electrically stimulated contraction of guinea pig ileum and (b) selectively binding to omega conopeptide MVIIA binding sites in neuronal tissue, where these activities are within the ranges of those of omega-conotoxins MVIIA and TVIA. The method is used for treating chronic pain, especially neuropathic pain
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Omega-conopeptide; peptide toxin; snail; calcium channel blocker; analgesia; guinea pig ileum; omega-conotoxin; pain; neuropathic.
                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Production of analgesia in mammal - by administration of omega
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Singh T;
                                                                                                                                                                                   Length 26;
                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Justice A,
                                                                                                                                                                                                                   4.
                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "C-terminal amide"
                                                                                                                                                                                 67.5%; Score 81; 34.6%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Valentino KL,
                                                                                                                                                                                                                                              1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                  Disclosure; Fig 2A-B; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                               Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Analog omega-conopeptide SNX-202.
                                                                                                                                                                                                                                                                                                                                                            AAW95584 standard; protein; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96US-00675354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91US-00814759.
                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gohil KC,
                                                                                                                 to correct OS field.)
                                                                                                                                                              (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NEUR-) NEUREX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-120002/10.
                                                                                                                                                   Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Miljanich GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                        29-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US5859186-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide(s)
                                                                                                                                                                                                                                                                                                                                                                                          AAW95584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conus sp.
                                                                                                                                                                                                                                                                                                                            RESULT 57
                                                                                                                                                                                                                                                                                                                                              AAW95584
```

```
AAB14370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Singh T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                      Best Local
Matches
                                                                                                                 AAB14370
                                                                                                        RESULT
                                                                                                                                      ઠે
                                                                     셤
                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A method has been developed of selecting a test compound for treating inflammation. The method comprises measuring the activity of the test compound in blocking voltage-gated calcium channels, binding to the omega conopeptide binding site and inhibiting norepinephrine (noradrenaline) release from nervous tissue. The method is useful for selecting compounds for treating inflammation. The selected compounds are capable of producing analgesia caused by selected compounds are capable of pain. Analgesia caused by selected compounds may reduce the reliance on opioid analgesia caused by selected compounds may reduce the reliance on opioid analgesic agents of the prior art which cause dependency and tolerance, requiring potentially dangerous increases in opioid doses to achieve the analgesic effect. The present sequence represents an omega conopeptide given in the present invention
                                                                                                                                                                                                                    Omega conopeptide, analgesic, nociceptive, neuropathic, pain; conotoxin, marine snail, peptide toxin; inflammation; binding; voltage-gated calcium channel; inhibition; norepinephrine; noradrenaline;
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Measuring the activity of test compounds in blocking voltage-gated calcium channels, binding to the omega conopeptide binding site and inhibiting norepinephrine (noradrenaline) release for treating
                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gohil KC;
                      Length 26;
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Miljanich GP,
                       5.
                     67.5%; Score 81; DB 34.6%; Pred. No. 2; ive 13; Mismatches
                                                              1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                          Valentino KL,
                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                  Analogue omega conopeptide SNX-202.
                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                               /note= "amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 2; 47pp; English
                                                                                                                                      AAY56496 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                                                             91US-00814759.
93US-00049794.
96US-00675354.
96US-00742774.
                                                                                                                                                                                                                                                                                                                                                                                                           98US-00138439
                                                                                                                                                                               entry)
                                            Conservative
                                                                                                                                                                                                                                                                                                        1. .16
8. .20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ELAN-) ELAN PHARM INC
Query Match

Query Match

Gast Local Similarity

9; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Justice A, Singh T,
                                                                                                                                                                              (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-038270/03
                                                                                                                                                                                                                                                     anti-inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 26 AA;
                                                                                                                                                                                                                                                                                                     Disulfide-bond
                                                                                                                                                                                                                                                                                                               Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                           21-AUG-1998;
                                                                                                                                                                              16-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                30-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                         15-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                  USS994305-A.
                                                                                                                                                                                                                                                                                                                                                                                       30-NOV-1999
                                                                                                                                                         AAY56496;
                                                                                                                                                                                                                                                                         Conus sp
                                                                                                                 RESULT 58
                                                                                                                          à
                                                                                 셤
```

67.5%; Score 81; DB 3; Length 26;

Query Match

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                       Marine snail; omega-conopeptide; calcium channel blocker; SNX-202; toxin; analgesic; antiinflammatory; anticonvulsant; neuroleptic; norepinephrine release inhibitor; schizophrenia; tardive dyskinesia; acute dystonic reaction; inflammation; epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is an omega-conopeptide analogue. Omega-conopeptides are components of peptide toxins produced marine snails of the genus forous. Omega-conopeptides and their derivatives act as calcium channel blockers and may be useful for producing analoguia in nociceptive and neuropathic pain. The peptides bind to omega-conopeptide binding sites, which are present mainly in neuronal tissue, and inhibit norephine release from nervous tissue. Conopeptides such as MVIIA and TVIA are effective as therapeutic agents for treating neurogenic conditions such as schizophrenia, tardiave dyskinesia and acute dystonic reactions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Selecting a compound for producing analgesia involves measuring activity of test compound in blocking voltage-gated calcium channels, binding to omega conopeptide binding site and inhibiting norepinephrine release.
                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Justice A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 26;
                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Miljanich GP,
                          4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3;
34.6%; Pred. No. 2; ive 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.5%; Score 81; DB 34.6%; Pred. No. 2; ive 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "C-terminal amide"
                                                                    26
                                                                                                 CKLKGQSCSRLMYDCCSGSCGRSGKC
                                                                      CXIXNOXCXOXIDDCCSXXCNXXNXC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Valentino KL,
                                                                                                                                                                                                                                          Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 2; 58pp; English
                                                                                                                                                                                                                                       AAB14370 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91US-00814759.
93US-00049794.
96US-00675354.
96US-00742774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-00298017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-00138439
                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                             Omega-conopeptide SNX-202
                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             as schizophrenia, tardive inflammation and epilepsy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 34.6 Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .16
8. .20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ELAN-) ELAN PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gohil KC,
Similarity
9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-490177/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-APR-1993;
03-JUL-1996;
01-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-APR-1999;
                                                                                                                                                                                                                                                                                                                                  06-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US6087091-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conus sp.
Synthetic.
```

Ą

(first entry)

```
The present sequence represents an omega-conopeptide analogue. Omega-conopeptides are components of peptide toxins which act as voltage-gated calcium channel inhibitors. The peptides are used to enhance the analgesic effect produced by an opiate in a mammalian subject. The method comprises administering to the subject an omega-conopeptide which is able to inhibit electrically stimulated contraction of the guinea pig ileum and bind to omega-conopeptides are useful for enhancing the analgesic effect produced by an opiate. Omega-conopeptides may also be used in the treatment of pain, in reducing neuronal damage related to an ischemic condition in mammals, and in treating schizophrenia, tardive dyskinesia and acute dystonic reactions, inflammation and epilepsy
                                                                                                                                                                                                                                                                                         /note= "amidated residue"
  26
             Disclosure; Col 51-52; 58pp; English.
  1 CXIXNOXCXQXLDDCCSXXCNXXNXC
                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Valentino KL,
                                                                             AAB19462 standard; peptide; 26 AA
                                                                                                                                                                                                                                                                                                                                                                                             93US-00049794.
93US-00081863.
96US-00675354.
                                                                                                                                                                                                                                                                                                                                                                                                                              96US-00742774.
98US-00138439.
99US-00298017.
                                                                                                                                                                                                                                                                                                                                                             99US-00392979
                                                                                                                                                                                                                                                                                                                                                                                  91US-00814759
                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gohil KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-030946/04.
                                                                                                                                                                                                                                                                Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ELAN-) ELAN
                                                                                                                                                                                                                                                                                                                                                           09-SEP-1999;
                                                                                                                           06-MAR-2001
                                                                                                                                                                                                                                                                                                              US6136786-A.
                                                                                                                                                                                                                                                                                                                                    24-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                         21-AUG-1998;
23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                              15-APR-1993
23-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                  30-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                               01-NON-10
                                                                                                                                                                                                                                Synthetic.
                                                                                                    AAB19462;
                                                                                                                                                                                                           epilepsy.
                                                                                                                                                                                                                                             Conus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Singh T,
                                                                   AAB19462
                                                                                        ò
                    g
```

```
neuroprotective; cerebroprotective; cardiovascular; antiinflammatory; antimpraine; antidabetic; tranquiliser; vulnerary; antipsychotic; anxiolytic; neuroleptic; voltage gated ion channel; saziure; epilepsy; neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia; stroke; cerebrovascular accident; brain trauma; spinal chord trauma; drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain; migralne; inflammation; cardiovascular disorder; psychiatric disorder; psychosis; anxiety; schizophrenia.
                                                                                                                                                                                                                 Omega-conopeptide; analgesic; anticonvulsant; vasotropic;
                                                                                                                                                                                      Omega-conopeptide S6.2 toxin sequence.
                | ::: |:|:::: ||||::| ::| | CKLKGQSCSRLMYDCCSGSCGRSGKC
1 CXIXNQXCXQXLDDCCSXXCNXXNXC
                                                                                               ABB96887 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JUL-2001; 2001WO-US023041.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-2000; 2000US-0219616P.
05-FEB-2001; 2001US-0265888P.
                                                                                                                                                                                                                                                                                                                                                              Conus striatus.
                                                                                                                                                                                                                                                                                                                                                                                         WO200207675-A2
                                                                                                                                                         12-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                     31-JAN-2002
                                                                                                                            ABB96887;
                                                                     RESULT 61
                                                                                   ABB96887
                                                                                                 셤
                                                                                                                                                                                                      Omega-conopeptide, voltage-gated calcium channel inhibitor, analgesic; peptide toxin; opiate; pain; neuronal damage; ischemic condition; schizophrenia; tardive dyskinesia; acute dystonic reaction; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enhancing analgesia produced by opiates by administering an omega-
conopeptide that inhibits electrically stimulated contraction of guinea
pig ilium and binds to omega-conopeptide MVIIA binding sites in neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Justice A;
                                                                                                                                                                              Sequence of an omega-conopeptide analogue designated SNX-202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Miljanich GP,
```

```
The invention relates to isolated omega-conopeptides, nucleic acid
sequences encoding them, and propeptide sequences. The activity of the
peptides of the invention may be described as, analgesic, anticonvulsant,
vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular,
antinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary,
antipsychotic, anxiolytic and neuroleptic. Peptides of the invention act
by modulating the activity of voltage gated ion channels. They may be
used for treating or preventing disorders associated with voltage gated
ion channels such as neurological disorders, e.g. seizure (associated
with epilepsy), neurotoxic injury associated with conditions of hypoxia,
anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal
chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic
conditions of migraine; inflammation or cardiovascular disorders
They may also be used for treating psychiatric disorders e.g. psychosis,
anxiety or schizophrenia. The analgesic agents of the invention show
diminished side effects and toxicity, and are non-addictive. The
sequences given in records ABB96807-ABB96905 represent omega-conopeptide
                                                                                                                                                                                                                                                                                                                                                                                                 New omega-conopeptides useful for treating disorders associated with voltage gated ion channels e.g. pain, inflammation, neurologic or cardiovascular disorders.
                                                                                                                                                            Shon K;
                                                                                                                                                      Mcintosh JM, Watkins M, Garrett JE, Jones RM, Cartier GE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1(a); Page 72; 195pp; English.
(UTAH ) UNIV UTAH RES FOUND. (COGN-) COGNETIX INC.
                                                                                                                                                                                                                                                                                                   WPI; 2002-257318/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                toxin sequences
                                                                                                                                                      Olivera BM,
                                                                                                                                                                                                     Jacobsen R,
```

Query Match

ö

Gaps ;

67.5%; Score 81; DB 4; Length 26; 34.6%; Pred. No. 2; 4; Indels ive 13; Mismatches 4; Indels

Best Local Similarity 34.6 Matches 9; Conservative

Query Match

Sequence 26 AA;

Length 67.5%; Score 81; DB 5;

Sequence 30 AA;

```
The invention relates to isolated omega-conopeptides, nucleic acid sequences encoding them, and propeptide sequences. The activity of the sequences encoding them, and propeptide sequences. The activity of the peptides of the invention may be described as analgesic, anticonvulsant, vasotropic, cardiant, neuroprotective, cerebropotective, cardiovascular, antinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary, antinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary, antinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary, by modulating the activity of voltage gated ion channels. They may be used for treating or preventing disorders associated with voltage gated ion channels such as neurological disorders, e.g. seizure (associated with epilepsy), neurotoxic injury associated with conditions of hypoxia, anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal coverts; pain e.g. migraine; inflammation or cardiovascular disorders. They may also be used for treating psychiatric disorders e.g. psychosis, anxiety or schizophrenia. The analgesic agents of the invention show sequences given in records ABB95695-ABB96697 represent omega-conopeptide propertide sequences
                        ö
                                                                                                                                                                                                                                                                                                                                                Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant; neuroprotective; carebroprotective; cardiovascular; antiinflammatory; antimigraine; antidabetic; tranquilisaer; vulnerary; antipsychotic; anxiolytic; neuroleptic; voltage gated ion channel; seizure; epileps; neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia; stroke; cerebrovascular accident; brain trauma; spinal chord trauma; drowning; sulfocation; perinatal asphyxia; hypoglycaemic event; pain; migraine; inflammation; cardiovascular disorder; psychiatric disorder; psychosis; anxiety; schizophrenia.
                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           omega-conopeptides useful for treating disorders associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           voltage gated ion channels e.g. pain, inflammation, neurologic or cardiovascular disorders.
                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Garrett JE, Shon K;
                        Indela
                        4,
  Pred. No. 2;
                                                          1 CXIXNOXCXQXLDDCCSXXCNXXNXC 26
                                                                                | ::: |:|:::: |||||::| :::| CKLKGQSCRRTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Watkins M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1(c); Page 62; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cartier GE;
                                                                                                                                                                                                                                                                                                             Omega-conopeptide S6.2 propeptide.
                                                                                                                                                                                             ABB96679 standard; peptide; 30 AA
llarity 34.6%; Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-2000; 2000US-0219616P.
05-FEB-2001; 2001US-0265888P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-JUL-2001; 2001WO-US023041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UTAH ) UNIV UTAH RES FOUND. (COGN-) COGNETIX INC.
                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Olivera BM, Mcintosh JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-257318/30.
Similarity
9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ABL98938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conus striatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200207675-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-JAN-2002.
                                                                                                                                                                                                                                                                       12-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jacobsen R,
                                                                                                                                                                                                                                   ABB96679;
  Best Local
Matches
                                                                                                                                                        RESULT 62
                                                                                                                                                                             ABB96679
                                                                                            g
                                                                                                                                                                                             ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequences given in AAR39608-30 are omega conopeptides (OCT8) and derivatives of these, which may be used to produce analgesia in a mammal. These OCT8 inhibit voltage-gated calcium channels selectively in neuronal tissue. This is shown by the peptides ability to stimulate contraction in guinea pig ileum and to bind to OCT MVIIA binding sites present in neuronal tissue. OCT8-are components of peptide toxins derived from marine snalls of the genus Conus, and act as calcium channel blockers. These OCT8 may be used to replace opiods in the treatment of chronic pain or to reduce the opiod dosage required. This helps to reduce dependence on and tolerance to opiod narcotics. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of omega-cono-peptide(s) which selectively inhibit voltage-gated calcium channels - to induce analgesia, enhance opiate analgesics, treat
                               Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                    Omega conopeptide; OCT; analgesia; inhibition; voltage-gated; calcium channel; neurone; contraction; guinea pig; ileum; MVIIA; binding site; toxin; marine; snail; Conus; opiod; chronic pain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                               ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Miljanich GP
 Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 26;
                            Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
,
67.5%; Score 81; DB 5; 34.6%; Pred. No. 2.2; ive 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Valentino KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64.2%; Score 77; DB; 34.6%; Pred. No. 4.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12; Mismatches
                                                        1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                          CKLKGQSCRRTMYDCCSGSCGRRGKC
                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                        AAR39615 standard; peptide; 26 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gohil K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 1; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92WO-US011349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91US-00814759
                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Conservative
 Query Match 67.5
Best Local Similarity 34.6
Matches 9; Conservative
                                                                                                                                                                                                                  (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Singh T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NEUR-) NEUREX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1993-227270/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09313128-A1.
                                                                                                                                                                                                               25-MAR-2003
20-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-JUL-1993
                                                                                                                                                                                                                                                           SVIB/SNX183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Justice A,
                                                                                                                                                                                                                                                                                                                                   narcotics.
                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pain etc.
                                                                                                                                                                                     AAR39615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                              RESULT 63
                                                                                                                                          AAR39615
                                                         8
                                                                                 a
```

1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26

ð

Ş

(revised)
(first entry)

```
1 CKLKGQSCRKTSYDCCSGSCGRSGKC 25
                                                                                                                                                                                                Disclosure; Fig 1; 103pp; English.
                         AAR37760 standard; peptide; 26
                                                                                                                                                      (NEUR-) NEUREX CORP.
                                                                                                                                                                           WPI; 1993-182487/22.
                                                                                               Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                       Sequence 26 AA;
                                                                                                                                                              Miljanich GP,
Yamashiro DH;
                                                       SVIB/SNX-183
                                                                                                                WO9310145-A1.
                                                                                                                                 12-NOV-1992;
                                                                                                                                         12-NOV-1991;
17-JUL-1992;
                                          25-MAR-2003
08-SEP-1993
                                                                                                                         27-MAY-1993.
                                                                                    Synthetic
                                  AAR37760;
                 RESULT 64
                      AAR37760
                         g
```

Bowersox SS,

92WO-US009766. 91US-00789913.

Location/Qualifiers

1. .16 8. .20 15. .26

```
AAW19544-W19553 are naturally occurring omega conopeptides (OCS) isolated from Conus sp. (cone snails). The peptides and their analogues are used as analogasics acting by blocking N-type voltage-sensitive calcium channels. The OCS can be used to treat neuropathic pain as a result of e.g. insult to the spinal cord or peripheral nerves, cancer, bone of degenerative diseases. AIDS. reflex sympathetic dystrophy, herpes zoster neuropathy, diabetic neuropathy, hyperesthesia, allodynia or hyperalgesia. The OCS are preferably administered in a medicament via an cypianis route in a continuous influsion or sustained release formulation. The OCS can provide pain relief when administered epidurally in the absence of a permeation enhancer, at doses that are comparable to conference of a permeation of and a carboxylic acid buffer anti-oxidant. They also confer stability to solutions containing them for prolonged concern methods and long-term storage. (Updated on 27-NUG-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stable omega conopeptide compositions - for producing analgesia and inhibiting progression of neuropathic pain disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SS, Gohil K, Adriaenssens PI, Kristipati
Luther RR;
                                                                                                                                                                                                                                                                                                                                                            Conopeptide, cone snail; pain; analgesic; neuropathy; epidural; N-type voltage-sensitive calcium channel; block; Conus.
                                                                                                                                                                                                                                                                                                                    Natural omega-conopeptide SVIB/SNX-183 used for pain relief.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64.2%; Score 77; DB 2; Length 26; 34.6%; Pred. No. 4.4; ive 12; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "optionally amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Fig 2, Fig 3; 47pp; English:
    56
                          | ::: |:|::: | | | | | | :: | :: | CKLKGQSCRKTSYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CXIXNOXCXQXLDDCCSXXCNXXNXC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
26
                                                                                                                                                          AAW19551 standard; peptide; 26 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96WO-US011041.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95US-00496847.
96US-00613400.
                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amstutz GA, Bowersox S
Gadbois T, Pettus MR,
                                                                                                                                                                                                                                                  27-AUG-2003 (revised)
13-OCT-1997 (first en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NEUR-) NEUREX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-100012/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9701351-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27~JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-JAN-1997.
                                                                                                                                                                                                       AAW19551;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Conus.
                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ischaemia-related neuronal damage in mammals is reduced by admin., 4-24

In after onset of ischaemia, of a cpd. (1) which binds selectively to an omega-conotoxin (OCT) WIISA site in neuronal fissue. (1) has selectivity at least 100 expressed as ratio of binding affinity for the MVIIA site to the MVIIA site in the CCT MVIIA site in the OCTS MVIIA, MVIIB, GVIIA, GVIIA, OR TANA or it is the cpd. SNX-207. (I) is esp. used to reduce neuronal damage caused by stroke. By delaying admin. for some time (compare US5051403 where opds. are given within 1 hr of the onset of ischaemia) a contracerebroventricular (ICV) injection at 0.1-20 microg/Ks, but can also be given i.v. (opt. after treatment with antihistamines to minimise redn. In blood pressure caused by (I)). (I) is also at least as effective as the specified conotoxins for (1) selective inhibition of N-Farnary caused and conopeptides are given in haRR37752-62. Several analog omega-conopeptides are given in AAR37752-62. Several analog correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                           Ischaemia, neuronal, omega-conotoxin, OCT; MVIIA, MVIIC; MVIID, MVIIB, GVIA, GVIIA; RVIA, SVIA, TVIA, SVIB, SNX-207; stroke, delayed treatment, antihistamine; blood pressure; N-type voltage-gated Ca currents; N-channel mediated neurotransmitter release.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Redn. of neuronal damage caused by ischaemia - by admin. of cpds. that bind specifically to omega-conotoxin MVIIA binding sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fox JA, Valentino KL, Bitner RS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

64.2%; Score 77; DB 2; Length 26;
Best Local Similarity 34.6%; Pred. No. 4.4;
Matches 9; Conservative 12; Mismatches 5; Indels
```

ö

Gaps

.. 0

```
Sequence 26 AA;
                                                                                                                     Miljanich GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
Modified-site
                                                             30-DEC-1991;
15-APR-1993;
03-JUL-1996;
                                            01-NOV-1996;
       US5824645-A.
                          20-0CT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5859186-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW95571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conus ap.
                                                                                                                                                                                                                                                                                                                                          field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW9557
%XCCCCCCCCCCCX%X44444X4X4X4X4X4X4X4XAXAXAXAX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conus genus; marine snail; cone snail; omega-conopeptide; analgesia;
nociceptive pain; neuropathic pain; neuronal tissue; conotoxin;
inflammation; schizophrenia; tardive dyskinesia; acute dystonic reaction;
                                                                                                                                                                                                                                                                                                                                                          The present peptide is an omega conopeptide, useful as an analgesic, especially for treating neuropathic pain. The peptide, which can be prepared by solid phase synthesis, can also be used to inhibit neuronal damage and treat schizophrenia, tardive dyskinesia, acute dystonic reactions, inflammation and epilepsy. (Updated on 25-MAR-2003 to correct
                                                                                                           Omega conopeptide; analgesic; treatment; neuropathic pain; inhibition; neuronal damage; schizophrenia; tardive dyskinesia; analgesia; acute dystonic reactions; inflammation; epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                              Omega cono:peptide(s) - useful as analgesics, esp. for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                          Singh
                                                                                                                                                                                                                                                                                                                                                                                                                                              64.2%; Score 77; DB 2; Length 26; 34.6%; Pred. No. 4.4; ive 12; Mismatches 5; Indels
                                                                                                                                                                                                                                                                           Justice A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conus genus natural omega-conopeptide SVIB/SNX-183.
                                                                                                                                                                                                                                                                          Valentino KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |::: |:|::: | | | | | |:: | :: : | CKLKGOSCRKTSYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                          Disclosure; Col 45-46; 58pp; English.
                         AAW12974 standard; peptide; 26 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW72612 standard; peptide; 26 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rheumatoid arthritis; epilepsy.
                                                                                                                                                                                                          93US-00049794.
                                                                                                                                                                                                                          91US-00814759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
(first entry)
                                                                        (first entry)
                                                                                        Omega conopeptide SNX-183.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 34...
Best Local Similarity 34...
                                                                                                                                                                                                                                                                          Miljanich GP,
                                                               (revised)
                                                                                                                                                                                                                                                       (NEUR-) NEUREX CORP.
                                                                                                                                                                                                                                                                                             WPI; 1997-064830/06
                                                                                                                                                                                                                                                                                                                         neuropathic pain.
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 26 AA;
                                                                                                                                                                                                          LS-APR-1993;
                                                                                                                                                                                                                           30-DEC-1991;
                                                                                                                                                                                                                                   30-DEC-1992;
                                                              25-MAR-2003
22-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-AUG-2003
06-JAN-1999
                                                                                                                                                                    US5587454-A
                                                                                                                                                                                       24-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                           field.)
                                                                                                                                                                                                                                                                         Gohil KC,
                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW72612;
                                           AAW12974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conus
       RESULT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW72612
                AAW129'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A method has been developed for the treatment of inflammation in a subject. The method comprises administration of an omega-conopeptide effective to: (i) block voltage-gated calcium channels; (ii) bind with high affinity to an omega-conopeptide binding site, and (iii) inhibit neurotransmitter release from nervous tissue. The method is used to treat inflammation and associated pain. The treatment can also be used to produce analgesia (especially in subjects experiencing neuropathic pain); and to treat schizophrenia, tardive dyskinesia and acute dystonic reactions, rheumatoid arthritis, and epilepsy. The present sequence represents a natural omega-conopeptide. Omega-conopeptides are components of peptide toxins produced by marine snalls of the genus Conue, and which act as calcium channel blockers. (Updated on 27-AUG-2001 to correct OS
                                                                                                                                                                                                                                                                                                                                                                      Treatment of inflammation, comprises administration of omega-conopeptide - effective to block voltage-gated calcium channels, bind with high affinity to omega-conopeptide binding site, and inhibit neuro-transmitter release.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Omega-conopeptide; peptide toxin; snail; calcium channel blocker; analgesia; guinea pig ileum; omega-conotoxin; pain; neuropathic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
0
                                                                                                                                                                                                                                                                  Justice A, Singh T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 34.6%; Pred. No. 4.4;
Matches 9; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26
/note= "C-terminal amide"
                                                                                                                                                                                                                                                                      Gohil KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Fig 1; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Omega-conopeptide SVIB/SNX-183.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW95571 standard; protein; 26
                                                              91US-00814759.
93US-00049794.
96US-00675354.
                                                                                                                                                                                                                                                                  Valentino KL,
96US-00742774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                       WPI; 1998-582596/49.
                                                                                                                                                                                                    (NEUR-) NEUREX CORP
```

Page 34

peptide(s)

```
A method has been developed of selecting a test compound for treating inflammation. The method comprises measuring the activity of the test compound in blocking voltage-gated calcium channels, binding to the omega conopeptide binding site and inhibiting norepinephrine (noradrenaline) release from nervous tissue. The method is useful for selecting compounds for treating inflammation. The selected compounds are capable of producing analgesia caused by selected compounds may reduce the reliance on opioid analgesic agents of the prior art which cause dependency and tolerance, requiring potentially dangerous increases in opioid doses to achieve the analgesic effect. The present sequence represents an omega conopeptide given in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marine snail; omega-conopeptide; calcium channel blocker; SVIB; SNX-183; toxin; analgesic; antilnilammatory; anticonvulsant; neuroleptic; norepinephrine release inhibitor; schizophrenia; tardive dyskinesia; acute dystonic reaction; inflammation; epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Selecting a compound for producing analgesia involves measuring activity
         calcium channels, binding to the omega conopeptide binding site and inhibiting norepinephrine (noradrenaline) release for treating inflammation.
                                                                                                                                                                                                                                                                                                                                                                                               3; Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Miljanich GP,
                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                                                                                                                                                               12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                           ilarity 34.6%; Score 77; 34.6%; Pred. No. Conservative 12; Mismatci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |::: |:|:: ||||::: | CKLKGQSCRKTSYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CXIXNOXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Valentino KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB14359 standard; peptide; 26 AA.
                                                                                Disclosure, Fig 1; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Omega-conopeptide SVIB/SNX-183.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93US-00049794.
96US-00675354.
96US-00742774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-00298017.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91US-00814759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-00138439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .16
8. .20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ELAN-) ELAN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gohil KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-490177/43.
                                                                                                                                                                                                                                                                                                                                                       Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US6087091-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-APR-1993;
03-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB14359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Singh T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB14359
         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                     Sequences AAW95564-573 represent primary sequences of natural omegaconopeptides. Omega-conopeptides are components of peptide toxins produced by marine snails of the genus Conus, and which act as calcium channel blockers. The invention relates to a method of producing analgesia in a mammal that comprises administering an omega conopeptide having activities in (a) inhibiting electrically stimulated contraction of guinea pig ileum and (b) selectrically inding to omega conopeptide WIIA binding sites in neuronal tissue, where these activities are within used for treating chronic pain, especially neuropathic pain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neuropathic; pain; conotoxin;
binding;
norepinephrine; noradrenaline;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                             Production of analgesia in mammal - by administration of omega cono-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Measuring the activity of test compounds in blocking voltage-gated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
0
                                                                                                                                Singh T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.2%; Score 77; DB 2; Length 26; 34.6%; Pred. No. 4.4; ive 12; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gohil
                                                                                                                              Justice A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Miljanich GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Omega conopeptide; analgesic; nociceptive; marine snall; peptide toxin; inflammation; voltage-gated calcium channel; inhibition; anti-inflammatory.
                                                                                                                              Valentino KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Natural omega conopeptide SVIB/SNX-183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Valentino KL,
                                                                                                                                                                                                                                                         Disclosure, Fig 1B; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY56480 standard; peptide; 26 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91US-00814759.
93US-00049794.
96US-00675354.
96US-00742774.
 96US-00675354
                                    91US-00814759
93US-00049794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-00138439,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Conservative
                                                                                                                            Gohil KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ELAN-) ELAN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Singh T,
                                                                                        (NEUR-) NEUREX CORP
                                                                                                                                                             WPI; 1999-120002/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-038270/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 26 AA;
                                                                                                                          Miljanich GP,
03-JUL-1996;
                                                     15-APR-1993;
                                  30-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-APR-1993;
03-JUL-1996;
01-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US5994305-A
```

AAY56480;

RESULT 69 **AAY564**80

Matches

ò 셤 Justice A;

30-NOV-1999

Conus sp.

Justice A,

ö

0; Gaps

```
ö
                                                                                      The present sequence is an omega-conopeptide from marine snails of the genus Conus. Omega-conopeptides are components of peptide toxins produced by the cone snails, and which act as calcium channel blockers. Natural omega-conopeptides and their derivatives may be useful for producing analgesia in nociceptive and neuropathic pain. The peptides bind to omega-conopeptide binding sites, which are present mainly in neuronal tissue, and inhibit norepinephrine release from nervous tissue. Conopeptides such as MVIIA and TVIA are effective as therapeutic agents for treating neurogenic conditions such as schizophrenia, tardive dyskinesia and acute dystonic reactions, inflammation and epilepsy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (III) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptide s.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity.
     S
of test compound in blocking voltage-gated calcium channels, binding omega conopeptide binding site and inhibiting norepinephrine release.
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thibaudeau K;
                                                                                                                                                                                                                                                                                                                                    Length 26;
                                                                                                                                                                                                                                                                                                                                                                        5; Indels
                                                                                                                                                                                                                                                                                                                                      77; DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Holmes DL,
                                                                                                                                                                                                                                                                                                                                  64.2%; Score 77; DB 34.6%; Pred. No. 4.4; ive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 653-654; 733pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                  | ::: |:|::: | | | | | | :: | :: : | CKLKGOSCRKTSYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                               CXIXNOXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Milner PG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB92221 standard; peptide; 26 AA
                                                       Example 4; Fig 1; 58pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0134406P.
99US-0153406P.
99US-0159783P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Toxin peptide SEQ ID NO:1397.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-MAY-2000; 2000WO-US013576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                     Local Similarity 34.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bridon DP, Ezrin AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CONJ-) CONJUCHEM INC
                                                                                                                                                                                                                                                                                               Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200069900-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-MAY-1999;
10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-NOV-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB92221;
                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ношо
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                음
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Omega-conopeptide; voltage-gated calcium channel inhibitor; analgesic; peptide toxin; opiate; pain; neuronal damage; ischemic condition; schizophrenia; tardive dyskinesia; acute dystonic reaction; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enhancing analgesia produced by opiates by administering an omega-
conopeptide that inhibits electrically stimulated contraction of guinea
pig ilium and binds to omega-conopeptide MVIIA binding sites in neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents an omega-conopeptide. Omega-conopeptides
vivo for the treatment of various disorders. Endogenous therapeutic peptides are not sultable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention
                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Justice A;
                                                                                                                                                                                                                                                                                                                                                                                                                        Primary sequence of a natural omega-conopeptide SVIB/SNX-183.
                                                                                                                                                                            Length 26;
                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Miljanich GP,
                                                                                                                                                                                                         ..
2
                                                                                                                                                                            DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "amidated C-terminal"
                                                                                                                                                                                                       12; Mismatches
                                                                                                                                                                            64.2%; Score 77;
                                                                                                                                                                                                                                   1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gohil KC, Valentino KL,
                                                                                                                                                                                                                                                                                                                                       Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 1; 58pp; English.
                                                                                                                                                                                                                                                                                                                                      AAB19449 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93US-00049794.
93US-00081863.
96US-00675354.
96US-00742774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-00392979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91US-00814759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-00298017
                                                                                                                                                                                           34.68;
                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ELAN-) ELAN PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-030946/04.
                                                                                                                                                                                          Best Local Similarity
Matches 9; Conserv
                                                                                                                                                Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                             06-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US6136786-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -AUG-1998
                                                                                                                                                                                                                                                                                                                                                                  AAB19449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Singh T,
                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               epilepsy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissues
                                                                                                                                                                                                                                                                                                                        AAB19449
     888888888888888
                                                                                                                                                                                                                                                              용
                                                                                                                                                                                                                                                                                                                                       CXSXC11111XBXBXBXBXBXBXBXBXBX1111111111X8XXXXXXBXBXBXCCX
                                                                                                                                                                                                                                     8
```

Omega-conopeptide S6.2 generic toxin sequence.

(first entry)

12-JUL-2002

ABB96786;

ABB96786 standard; peptide; 26 AA.

```
are components of peptide toxins which act as voltage-gated calcium channel inhibitors. The peptides are used to enhance the analgesic effect produced by an optate in a mammalian subject. The method comprises administering to the subject an omega-conopeptide which is able to inhibit electrically stimulated contraction of the guinea pig ileum and bind to omega-conopeptide MVIIA binding sites present in neuronal tissue. Omega-conopeptides are useful for enhancing the analgesic effect produced by an opiate. Omega-conopeptides may also be used in the treatment of pain, in reducing neuronal damage related to an ischemic condition in memmals, and in treating schizophrenia, tardive dyskinesia and acute
                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention comprises peptides having calcium channel blocking activities which are derived from the venomous saliva of assassin bugs. The calcium channel blocking peptides of the invention are useful for treating stenocardia, hypertension, myocarditis, arrhythmia and cerebral ischaemia. The present amino acid sequence represents a cone snail wconotoxin peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cone snail; venomous saliva; calcium channel blocking activity; stenocardia; hypertension; myocarditis; arrhythmia; cerebral ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A new peptide derived from venomous saliva of assassin bug, has calcium
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                            64.2%; Score 77; DB 4; Length 26; 34.6%; Pred. No. 4.4;
                                                                                                                                                                                                                                                                                  5; Indels
                                                                                                                                                                            dystonic reactions, inflammation and epilepsy
                                                                                                                                                                                                                                                         34.6%; Preq. ....
                                                                                                                                                                                                                                                                                                                1 CXIXNOXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                  |::: |:|:: |||||:: | CKLKGQSCRKTSYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cone snail w-conotoxin peptide SVIB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, Page 4; 26pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAO15126 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-SEP-2000; 2000JP-00266187.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-SEP-2000; 2000JP-00266187.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      blocking activity.
                                                                                                                                                                                                                                                                              9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-421068/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SUNR ) SUNTORY LTD
                                                                                                                                                                                                                                                            Best_Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                            Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JP2002080499-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            w-conotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-MAR-2002,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA015126;
                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      channel
                                                                                                                                                                                                                                                                                                                                                                                                                   AA015126
                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                               В
```

```
peptices of the invention may be described as a malegest, anticonviolant, vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular, antiinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary, antiinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary, on inspectoric, anxiolytic and neuroleptic. Peptides of the invention act by modulating the activity of voltage gated ion channels. They may be used for treating or preventing disorders associated with voltage gated ion channels such as neurological disorders, e.g. saizure (associated with epilepsy), neurotoxic injury associated with conditions of hypoxia, anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic events; pain e.g. migraine; inflammation or cardiovascular disorders. They may also be used for treating psychiatric disorders e.g. psychosis, anxiety or schizophrenia. The analgesic agents of the invention show analysis and effects and toxicity, and are non-addictive. The sequences given in records ABB96698-ABB96806 represent omega-conopeptide generic toxin sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= OTHER / 1251-Tyr, mono-iodo-Tyr or di-iodo-Tyr or O-iodo-Tyr or O-sulpho-Tyr or O-Phospho-Tyr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to isolated omega-conopeptides, nucleic acid sequences encoding them, and propeptide sequences. The activity of the peptides of the invention may be described as, analgesic, anticonvulsant,
                                                                                                                                                                      neuroprotective, cerebroprotective, cardiovascular; antinflammatory, antinformed antinflammatory, antinframe, antinflammatory, antinfraine; antinflammatory, antinfraine; antidabetic; tranquiliser; vulnerary; antipsychotic; anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy; neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia; stroke; cerebrovascular accident; brain trauma; spinal chord trauma; drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain; migraine; inflammation; cardiovascular disorder; psychiatric disorder; psychosis; anxiety; schizophrenia.
                                                                                                                                                        Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New omega-conopeptides useful for treating disorders associated voltage gated ion channels e.g. pain, inflammation, neurologic o cardiovascular disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          꽃
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Garrett JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M, Watkins M,
Cartier GE;
                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Page 62; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JUL-2001; 2001WO-US023041.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-2000; 2000US-0219616P.
05-FEB-2001; 2001US-0265888P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ę,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mcintosh J
Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UTAH ) UNIV UTAH RES
(COGN-) COGNETIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-257318/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                         Conus striatus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200207675-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Olivera BM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jacobsen R,
```

ö

Gaps

ö

64.2%; Score 77; DB 5; Length 26; 34.6%; Pred. No. 4.4; ive 12; Mismatches 5; Indels

Query Match
Best Local Similarity 34.6'
Matches 9; Conservative

8

```
RESULT 76
                                                                                   원
                                                              ò
                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method for detecting or measuring the form of Motch that mediates Norch signal transduction in a sample of cells. The method involves detecting or measuring the expression of a Notch heterodimer containing reducing agent-sensitive linkage in the cells and comparing detected or measured expression to the detected or measured expression of full-length Notch in the cells. The present sequence is Xenopus Notch/Xotch (XenN) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or
                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detecting or measuring forms of Notch mediating Notch signal transduction, by comparing detected or measured expression of Notch heterodimer containing reducing agent-sensitive linkage to detected measured expression of full-length Notch.
                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                               2172. .2175
/note= "Nuclear localisation signal (NLS)"
2216. .2218 .--- '---'isation signal, BNTS"
   Length 26;
                         4; Indels
                                                                                                                                                                                                                                                                                                                                                         /noce="EGF repeat"
1447. 1561
Anote= "Lin-12/Notch repeat (LN)"
1728. 1749
Anote = Transmembrane (TN) domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2451. .2509
/note= "PEST-containing region"
61.7%; Score 74; DB 5;
34.6%; Pred. No. 8;
ive 13; Mismatches
                                                                                                                                                                                                                                                                                                                          20. .2523 _____Mature N2 protein"
/note= "Mature N2 protein"
20. .1425
                                                                                                                                                                                                             Xenopus sp. Notch/Xotch (XenN) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                          1870. .2082
/note= "Ankyrin repeat"
                                                  56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 3; 63pp; English.
                                                              | ::: |:|:::: | | | | | | :: | ::: | CKLKGQSCRRTMXDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                . .19
|abel= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rand MD;
                                                                                                                                                                                                                                      Notch; signal transduction; detection
                                                  1 CXIXNOXCXOXLDDCCSXXCNXXNXC
                                                                                                                                     ADL26915 standard; protein; 2523 AA
                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qi H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-00121457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-00899232
                                                                                                                                                                                      (first entry)
                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Artavanis-Tsakonas S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-178437/17.
           Local Similarity
nes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYYA ) UNIV YALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US6692919-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-FEB-2004
                                                                                                                                                                                                                                                               Xenopus sp.
                                                                                                                                                             ADL26915;
 Query Match
                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                         Matches
                                                                                                             RESULT 75
                                                                                                                        셤
```

Sequence 2523 AA;

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= OTHER
/note= "OTHER is Tyr, 1251-Tyr, mono-iodo-Tyr or di-iodo-
Tyr or O-sulpho-Tyr or O-Phospho-Tyr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated omega-conopeptides, nucleic acid sequences encoding them, and propeptide sequences. The activity of the peptides of the invention may be described as, analgesic, anticonvulsant, vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular, antinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary, antinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary, by modulating the activity of voltage gated ion channels. They may be used for treating or preventing disorders associated with voltage gated with epilepsy), neurological disorders, e.g. seizure (associated with epilepsy), neurotoxic injury associated with conditions of hypoxia, anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic
                                                                                                                                                                                                                                                                                                                                                                       neuroprotective; cerebroprotective; cardiovascular; antiinflammatory; antimurane; antidabetic; tranquiliser; vulnerary; antipsychotic; anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy; neurological disorder; neurotoxic injury; hypoxia; anoxia; schaemia; stroke; cerebrovascular accident; brain trauma; spinal chord trauma; drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain; migraine; inflammation; cardiovascular disorder; psychosis; anxiety; schizophrenia.
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New omega-conopeptides useful for treating disorders associated with voltage gated ion channels e.g. pain, inflammation, neurologic or cardiovascular disorders.
                                                                                                                                                                                                                                                                                                                                                           cardiant;
                                    ö
 Length 2523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shon K;
                                                                                                                                                                                                                                                                                                                                                           Omega-conopeptide; analgesic; anticonvulsant; vasotropic;
                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Garrett JE,
                                                                                                                                                                                                                                                                                                                      Omega-conopeptide w-SVIB generic toxin sequence.
Query Match 60.0%; Score 72; DB 8; Best Local Similarity 34.6%; Pred. No. 7e+02; Matches 9; Conservative 12; Mismatches
                                                                                             247 GFSGQNCEENIDDCPSNNCRNGGTCV 272
                                                                       2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M, Watkins M,
Cartier GE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Page 63; 195pp; English.
                                                                                                                                                                                                      ABB96790 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JUL-2001; 2001WO-US023041.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-2000; 2000US-0219616P
05-FEB-2001; 2001US-0265888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UNIV UTAH RES FOUND.
COGNETIX INC.
                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mcintosh JM,
Jones RM, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-257318/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conus striatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200207675-A2
                                                                                                                                                                                                                                                                                 12-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Olivera BM,
Jacobsen R,
                                                                                                                                                                                                                                            ABB96790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UTAH ) 1
(COGN-) (
```

დ ო

ö

Gaps

; 0

Length 26; Indels

5

57.5%; Score by; 23.30.8%; Pred. No. 22; tive 12; Mismatches

Similarity 30.8 8; Conservative

56 26

| : : : | :::: | | | | | :: | :: : : | CKGKGAPCRKTMYDCCSGSCGRRGKC 1 CXIXNQXCXQXLDDCCSXXCNXXNXC

Ź 56

(revised)
(first entry)

```
Omega conopeptide; OCT; analgesia; inhibition; voltage-gated; calcium channel; neurone; contraction; guinea pig; ileum; MVIIA; binding site; toxin; marine; snall; Conus; opiod; chronic pain;
                                                                                                                    AAR39617 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                  (NEUR-) NEUREX CORP.
   Sequence 26 AA;
                                                                                                                                                                                                                                                                         Disulfide-bond
                                                                                                                                                                                                                                                                                                   Disulfide-bond
                                                                                                                                                                                                                                                                                                             Disulfide-bond
                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                10-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                30-DEC-1992;
                                                                                                                                                                                                                                                                                                                             WO9313128-A1
                                                                                                                                                      25-MAR-2003
20-DEC-1993
                   Query Match
Best Local S
                                                                                                                                                                                                                              narcotics.
                                                                                                                                                                                                                                               Synthetic
                                                                                                                                      AAR39617;
                                                                                                                                                                                  SNX231.
                                      Matches
                                                                                                                     g
                                                        ò
                                                                                                    .
0
events; pain e.g. migraine; inflammation or cardiovascular disorders. They may also be used for treating psychiatric disorders e.g. psychosis, anxiety or schizophrenia. The analgesic agents of the invention show diminished side effects and toxicity, and are non-addictive. The sequences given in records ABB96698-A3B96806 represent omega-conopeptide generic toxin sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of omega-cono-peptide(s) which selectively inhibit voltage-gated calcium channels - to induce analgesia, enhance opiate analgesics, treat
                                                                                                    Gaps
                                                                                                                                                                                                                                                           Omega conopeptide, OCT; analgesia; inhibition; voltage-gated, calcium channel, neurone; contraction; guinea pig; ileum; MVIIA; binding site; toxin; marine; snail; Conus; opiod; chronic pain;
                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GP;
                                                                                 5; Length 26
                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Miljanich
                                                                                                  5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Valentino KL,
                                                                              58.3%; Score 70; DB 34.6%; Pred. No. 18; ive 12; Mismatches
                                                                                                                 1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                           |::: |::: |:|::: | | | | |:: | :: : | CKLKGQSCRKTSXDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                             AAR39616 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gohil K,
                                                                                                                                                                                                                                                                                                                                                                                                         92WO-US011349
                                                                                                                                                                                                                                                                                                                                                                                                                          91US-00814759
                                                                                                                                                                                                                 (revised)
(first entry)
                                                                                                 Conservative
                                                                   Query Match
Best Local Similarity
9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Justice A, Singh T,
                                                                                                                                                                                                                                                                                                                                                                                                                                          (NEUR-) NEUREX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1993-227270/28
                                                              A.
                                                                                                                                                                                                                                                                                                                                Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                        30-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                         30-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                    WO9313128-A1
                                                              Sequence 26
                                                                                                                                                                                                                                           MVIIC/SNX230
                                                                                                                                                                                                                25-MAR-2003
20-DEC-1993
                                                                                                                                                                                                                                                                                        narcotics.
                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                AAR39616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pain etc.
                                                                                                                                                            RESULT 77
                                                                                                                                                                      AAR39616
                                                                                                                                                                             8$$$$$$$$$$
                                                                                                                                 g
                                                                                                                  ð
```

Location/Qualifiers

"4Hyp"

/note= " 8. .20 15. .26 1. .16

92WO-US011349. 91US-00814759.

```
The sequences given in AAR39608-30 are omega conopeptides (OCTS) and derivatives of these, which may be used to produce analgesia in a mammal. These OCTs inhibit voltage-gated calcium channels selectively in neuronal tissue. This is shown by the peptides ability to stimulate contraction in guinea pig ileum and to bind to OCT MVIIA binding sites present in neuronal tissue. OCTs are components of peptide toxins derived from marine snails of the genus Conus, and act as calcium channel blockers. These OCTs may be used to replace opiods in the treatment of chronic pain or to reduce the opiod dosage required. This helps to reduce dependence on and tolerance to opiod narcotics. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                      Use of omega-cono-peptide(s) which selectively inhibit voltage-gated calcium channels - to induce analgesia, enhance opiate analgesics, treat
         Miljanich GP;
Valentino KL,
Gohil K,
                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 1; 90pp; English.
Singh T,
                                                                                   WPI; 1993-227270/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 26 AA;
Justice A,
                                                                                                                                                                                                                                                                  pain etc.
```

ö

Gaps

ö

Length 26; 6; Indels

57.5%; Score 69; DB 2; 30.8%; Pred. No. 22; iive 12; Mismatches

Conservative

Query Match Best Local Similarity Matches 8; Conserv

The sequences given in AAR39608-30 are omega conopeptides (OCTS) and derivatives of these, which may be used to produce analgesia in a mammal. These OCTs inhibit voltage-gated calcium channels selectively in neuronal tissue. This is shown by the peptides ability to stimulate contraction in guinea pig ileum and to bind to OCT WVIIA binding sites present in neuronal tissue. OCTs are components of peptide toxins derived from marine snails of the genus Conus, and act as calcium channel blockers. These OCTs may be used to replace opiods in the treatment of chronic pain or to reduce the opiod dosage required. This helps to reduce dependence on and tolerance to opiod narcotics. (Updated on 25-MAR-2003 to correct PN field.)

Claim 1; Fig 1; 90pp; English.

Gaps

ö

Length 26; Indels

..

57.5%; Score 69; DB 30.8%; Pred. No. 22; ive 12; Mismatches

Conservative

Ź

(first entry)

(revised)

ò 셤

```
Ischaemia, neuronal, omega-conotoxin, OCT, MVIIA, MVIIC; MVIID; MVIIB; GVIA; GVIIA, RVIA; SVIA; TVIA; SVIB; SMX-207; stroke; delayed treatment, antihistamine, blood pressure; N-type voltage-gated Ca currents; N-channel mediated neurotransmitter release.
                                                                                                                                                       AAR37761 standard; peptide; 26
Query Match
Best Local Similarity
The 8; Conserve
                                                                                                                                                                                                                                                                                                                                                                               Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                 MVIIC/SNX-230.
                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9310145-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JUL-1992;
                                                                                                                                                                                                         25-MAR-2003
08-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-MAY-1993
                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                 AAR37761;
                                                                                                                              RESULT 80
                                                                                                                                             AAR37761
                                                                                       g
                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hr after onset of ischaemia, of a cpd. (I) which binds selectively to an onega-conotoxin (OCT) MVIIA site in neuronal tissue. (I) has selectivity at least 100 expressed as ratio of binding affinity for the MVIIA site to that for the MVIIA site. (I) is one of the OCTS MVIIA, MVIIB, GVIA, GVIIA or RVIA or it is the cpd. SNX-207. (I) is esp. used to reduce neuronal cansed by stroke. By delaying admin. for some time (compare C USSO51403 where cpds. are given within 1 hr of the onset of ischaemia) a creater redn. in neuronal damage is achieved. (I) is admin. e.g. by compare compare compare compare compared in reacrebroventricular (ICV) injection at 0.1-20 microg/Kg, but can also compared in the compared compared in neuronal damage is achieved. (I) is admin. e.g. by compared to optimize a compared compared in holood pressure caused by (II). (I) is also at least as effective as the specified conotoxins for (I) selective inhibition of N-type voltage. C dard currents in neuronal tissue and (2) selective inhibition of N-type voltage. C channel mediated neurotransmitter release in neuronal tissue. Primary compared by film of N-RN37752-62. Several analog compared by the compared on ARR37752-62. Several analog compared by the compared on ARR37753-76. (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                   Ischaemia; neuronal; omega-conotoxin; OCT; MVIIA; MVIIC; MVIID; MVIIB; QCIA; GVIIA; RVIA; SVIA; TVIA; SVIB; SNX-207; stroke; delayed treatment; antihistamine; blood pressure; N-type voltage-gated Ca currents; N-channel mediated neurotransmitter release.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Redn. of neuronal damage caused by ischaemia - by admin. of cpds. that bind specifically to omega-conotoxin MVIIA binding sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fox JA, Valentino KL, Bitner RS;
                                                                                                                                                                                                                                                                                                                                                                    note= "hydroxyproline"
                                       | : : : | : : : | | | | | : : : | CKGKGAPCRKTMYDCCSGSCGRRGKC 26
                         CXIXNOXCXOXIDDCCSXXCNXXNXC
                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 1; 103pp; English.
                                                                                                                 AAR37762 standard; peptide; 26 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92WO-US009766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91US-00789913
92US-00916478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bowersox SS,
                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                  .20
                                                                                                                                                                                                                                                                                                                                            1. .16
                                                                                                                                                                    (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NEUR-) NEUREX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1993-182487/22.
                                                                                                                                                                                                                                                                                                                                         Disulfide-bond
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                             Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Miljanich GP,
Yamashiro DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-NOV-1991;
17-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                        A09310145-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                27-MAY-1993.
                                                                                                                                                                    25-MAR-2003
                                                                                                                                                                                 08-SEP-1993
                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                          AAR37762;
                                                                                                                                                                                                                                                                                                                               Key
                                                                                                      AAR37762
                                                                                         RESULT
```

Location/Qualifiers

92WO-US009766. 91US-00789913.

```
rechaemia-related neuronal damage in manmals is reduced by admin., 4-24

hr after onset of ischaemia, of a cpd. (I) which binds selectively to an onega-conocton (OCT) WVITA site in neuronal tissue. (I) has selectivity

c mega-conocton (OCT) WVITA site in neuronal tissue. (I) has selectivity

c that for the WVIIC site. (I) is one of the OCTS MVIIA, MVIIB, GVIA, GVIIA

or RVAR or it is the cpd. SNX-207. (I) is esp. used to reduce neuronal

damage caused by stroke. By delaying admin. for some time (compare

US5051403 where cpds. are given within 1 hr of the onset of ischaemia) a

c greater redn. in neuronal damage is achieved. (I) is admin. e.g. by

intracerebroventricular (ICV) injection at 0.1-20 microg/kg, but can also

be given i.v. (opt. after treatment with antihistamines to minimise redn.

in blood pressure caused by (I)). (I) is also at least as effective as

the specified conocoxins for (I) selective inhibition of N-type voltage-

gated Ca currents in neuronal tissue and (2) selective inhibition of N-

channel mediated neurotransmitter release in neuronal tissue. Primary

sequences of omega-conopeptides are given in AAR37752-62. Several analog

correct PN field.)
                                                                                                                                                                                                                                                                                                                                                    Redn. of neuronal damage caused by ischaemia - by admin. of cpds. that
bind specifically to omega-conotoxin MVIIA binding sites.
                                                                                               Bitner RS;
                                                                                               Bowersox SS, Fox JA, Valentino KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Fig 1, 103pp; English.
                                                                                                                                                                                                                                                         WPI; 1993-182487/22.
(NEUR-) NEUREX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 26 AA;
                                                                                               Miljanich GP,
Yamashiro DH;
```

correct PN field.) Sequence 26 AA;

```
Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                     15-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                               30-DEC-1991;
30-DEC-1992;
                                                                                                  25-MAR-2003
22-APR-1997
                                                                                                                                                                                                                                                                                                    US5587454-A
                                                                                                                                                                                                                                                                                                                             24-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-AUG-2003
06-JAN-1999
                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gohil KC,
                                                                        AAW12987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW72614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 83
                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM19544-W19553 are naturally occurring omega conopeptides (OCS) isolated from Conus sp. (cone snails). The peptides and their analogues are used as analgesics acting by blocking N-rype voltage-sensitive calcium channels. The OCs can be used to treat neuropathic pain as a result of e.g. insult to the spinal cord or peripheral nerves, cancer, bone curropathy, diabetic neuropathy, hyperesthesia, allodynia or neuropathy, diabetic neuropathy, hyperesthesia, allodynia or hyperalgesia. The OCs are preferably administered in a medicament via an optimuous infusion or sustained release formulation. The OCs can provide pain relief when administered epidurally in the absence of a permeation enhancer, at doses that are comparable to effective analgesic doses using intrathecal administration. OC effective analgesic doses using intrathecal administration. OC commulations comprising an OC and a carboxylic acid buffer anti-oxidant. They also confer stability to solutions containing them for prolonged created and peace of a permeation that are considered to a containing them for prolonged created and peace of a permeation that are considered to a containing them for prolonged created and peace of a permeation that are considered to a containing them for prolonged created and an analyses of treatment metcheds and long-term storage. (Updated on 27-AUG-2003 to
                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stable omega conopeptide compositions - for producing analgesia and for inhibiting progression of neuropathic pain disorders.
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adriaenssens PI, Kristipati R;
                                 ;
0
                                                                                                                                                                                                                                                                   Conopeptide; cone snail; pain; analgesic; neuropathy; epidural; N-type voltage-sensitive calcium channel; block; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
                                                                                                                                                                                                                                          Natural omega-conopeptide MVIIC/SNX-230 used for pain relief.
     Length 26;
                              6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Indels
      2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
22;
DB '
  57.5%; Score 69; DB 30.8%; Pred. No. 22; tive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.5%; Score 69; DB 30.8%; Pred. No. 22; ive 12; Mismatches
                                                      1 CXIXNOXCXQXLDDCCSXXCNXXNXC 25
                                                                     1 CXIXNQNCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |: : :|::: |||||::| :: :|
CKGKGAPCRKTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Gohil K,
Luther RR;
                                                                                                                                              AAW19552 standard; peptide; 26 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 2; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                       96WO-US011041
                                                                                                                                                                                                                                                                                                                                                                                                               95US-00496847,
96US-00613400.
                                                                                                                                                                                                                  (first entry)
             Best Local Similarity 30.88 Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bowersox SS,
Pettus MR, Lu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Conservative
                                                                                                                                                                                                      (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NEUR-) NEUREX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-100012/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                   WO9701351-A1.
                                                                                                                                                                                                                                                                                                                                                                                                               27-JUN-1995;
08-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                      26-JUN-1996;
                                                                                                                                                                                                   27-AUG-2003
13-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amstutz GA,
Gadbois T,
                                                                                                                                                                                                                                                                                                                                                           16-JAN-1997
                                                                                                                                                                         AAW19552;
    Query Match
                                                                                                                       RESULT 81
                                                                                                                                   AAW19552
                                                                                                                                                            à
                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present peptide is an omega conopeptide, useful as an analgesic, especially for treating neuropathic pain. The peptide, which can be prepared by solid phase synthesis, can also be used to inhibit neuronal damage and treat schizophrenia, tardive dyskinesia, acute dystonic reactions, inflammation and epilepsy. In a rat paw formalin test, the peptide had an EDSO of greater than 1.0 microg in phase 1, and greater than 1.0 microg in phase 1, and greater than 1.0 microg in phase 2 (by intrathecal administration). (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                         Omega conopeptide; analgesic; treatment; neuropathic pain; inhibition; neuronal damage; schizophrenia; tardive dyskinesia; analgesia; acute dystonic reactions; inflammation; epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Omega cono:peptide(s) - useful as analgesics, esp. for treating neuropathic pain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Singh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57.5%; Score 69; DB 2; Length 26; 34.6%; Pred. No. 22; ive 11; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conus genus natural omega-conopeptide MVIIC/SNX-230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Justice A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Valentino KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | i · i | | i · i · | | | | i · i | cKGKGAXCRKTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Col 53-54; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
AAW12987 standard; peptide; 26 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW72614 standard; peptide; 26 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93US-00049794.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91US-00814759.
92WO-US011349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Hyp
                                                                                                                                     (first entry)
                                                                                                                                                                                            Omega conopeptide SNX-231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 57.5
Best Local Similarity 34.6
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Miljanich GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-064830/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NEUR-) NEUREX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW72614
ID AAW7
XX
AC AAW7
XX
DT 27-P
DT 06-J
XX
DE CONU
```

```
ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                              A method has been developed for the treatment of inflammation in a subject. The method comprises administration of an omega-conopeptide effective to: (i) block voltage-gated calcium channels; (ii) bind with high affinity to an omega-conopeptide binding site; and (iii) inhibit neurotransmitter release from nervous tissue. The method is used to treatmention and associated pain. The treatment can also be used to produce analgesia (especially in subjects experiencing neuropathic pain); and to treat schizophrenia, tardive dyskinesia and acute dystonic reactions, rheumatoid arthritis, and epilepsy. The present sequence represents a natural omega-conopeptide. Omega-conopeptides are components of peptide toxins produced by marine snalls of the genus Conus, and which act as calcium channel blockers. (Updated on 27-AUG-2001 to correct OS
         Conus genus; marine snail; cone snail; omega-conopeptide; analgesia; nocideptive pain; neuropathic pain; neuronal tissue; conotoxin; inflammation; schizophrenia; tardive dyskinesia; acute dystonic reaction; rheumatoid arthritis; epilepsy;
                                                                                                                                                                                                                                                                    Treatment of inflammation, comprises administration of omega-conopeptide - effective to block voltage-gated calcium channels, bind with high affinity to omega-conopeptide binding site, and inhibit neuro-transmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conus genus, marine snail; cone snail; omega-conopeptide; analgesia; ordiceptive pain; neuropathic pain; neuronal tissue; conotoxin; inflammation; schizophrenia; tardive dyskinesia; acute dystonic reaction; rheumatoid arthritis; epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                          Singh T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Indels
                                                                                                                                                                                                                           Justice A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genus natural omega-conopeptide SVX-231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.5%; Score 69; DB 30.8%; Pred. No. 22; ive 12; Mismatches
                                                                                                                                                                                                                          Gohil KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |: : : | : : : | | | | | : : | : : : | CKGKGAPCRKTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW72613 standard; peptide; 26 AA
                                                                                                                                                                                                                                                                                                                            Disclosure, Fig 1, 58pp; English.
                                                                                                                                                       91US-00814759.
93US-00049794.
96US-00675354.
                                                                                                                                                                                                                          Valentino KL,
                                                                                                                                  96US-00742774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

Query Match

Best Local Similarity 30.00,

Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
(first entry)
                                                                                                                                                                                                                                                 WPI; 1998-582596/49.
                                                                                                                                                                                                     (NEUR-) NEUREX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 26 AA;
                                                                                                                                                                                                                          Miljanich GP,
                                                                                                                                 01-NOV-1996;
                                                                                                                                                       30-DEC-1991;
15-APR-1993;
                                                                                                                                                                              03-JUL-1996;
                                                                                       US5824645-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-AUG-2003
06-JAN-1999
                                                                                                             20-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW72613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Н
                                                                                                                                                                                                                                                                                                       release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       field.)
                                                                 Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
```

```
A method has been developed for the treatment of inflammation in a subject. The method comprises administration of an omega-conopeptide effective to: (i) block voltage-gated calcium channels; (ii) bind with high affinity to an omega-conopeptide binding site; and (iii) inhibit neurotransmitter release from nervous tissue. The method is used to treat inflammation and associated pain. The treatment can also be used to produce analgesia (specially in subjects experiencing neuropathic pain); and to treat schizophrenia, tradive dyskinesia and acute dystonic reactions, rheumatoid arthritis, and epilepsy. The present sequence represents a natural omega-conopeptide. Omega-conopeptides are components of peptide toxins produced by marine snails of the genus Conus, and which act as calcium channel blockers. (Updated on 27-AUG-2003 to correct OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treatment of inflammation, comprises administration of omega-conopeptide - effective to block voltage-gated calcium channels, bind with high affinity to omega-conopeptide binding site, and inhibit neuro-transmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Omega-conopeptide; peptide toxin; snail; calcium channel blocker; analgesia; guinea pig ileum; omega-conotoxin; pain; neuropathic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                               Ŧ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Singh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Justice A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.5%; Score 69; DB 30.8%; Pred. No. 22; ive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gohil KC,
                                              /label= Hyp
/note= "hydroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | : : : | | | | | : : : : | CKGKGAPCRTMYDCCSGSCGRRGKC
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 1; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW95572 standard; protein; 26
                                                                                                                                                                                                                                                                                 91US-00814759.
93US-00049794.
96US-00675354.
                                                                                                                                                                                                                                   96US-00742774.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Valentino KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= 4Hyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Omega-conopeptide SNX-231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 30.8
hes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              (NEUR-) NEUREX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-582596/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 26 AA;
Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                               Miljanich GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Modified-Bite
                                                                                                                                                                                                                                   01-NOV-1996;
                                                                                                                                                                                                                                                                                       30-DEC-1991;
                                                                                                                                                                                                                                                                                                               15-APR-1993;
03-JUL-1996;
                                                                                                                            US5824645-A
                                                                                                                                                                                20-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW95572:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 85
AAW95572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
```

```
Valentino KL, Miljanich GP,
   93US-00049794.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-00138439
                                                                                                                                                                                                                                                                                                                                       AAY56482 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                          8; Conservative
                                       Gohil KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ELAN-) ELAN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Justice A, Singh T,
                                                        WPI; 1999-120002/10
                     (NEUR-) NEUREX CORP
                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-038270/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Misc-difference
                                                                                                                                                                                                                       Sequence 26 AA;
                                      Miljanich GP,
   15-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                           16-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US5994305-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5-APR-1993
                                                                                   peptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conus sp
                                                                                                                                                                                                                                                                                                                     RESULT 87
   ð
                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                Sequences AAW95564-573 represent primary sequences of natural omegaconopeptides. Omega-conopeptides are components of peptide toxins produced by marine snails of the genus Conus, and which act as calcium channel blockers. The invention relates to a method of producing analgesia in a mammal that comprises administering an omega conopeptide having activities in (a) inhibiting electrically stimulated contraction of guinea pig ileum and (b) alectrically binding to omega conopeptide WVIA binding sites in neuronal tissue, where these activities are within the ranges of those of omega-conotoxins WVIA and TVIA. The method is
                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Omega-conopeptide; peptide toxin; snail; calcium channel blocker; analgesia; guinea pig ileum; omega-conotoxin; pain; neuropathic.
                                                                                                                                                                      Production of analgesia in mammal - by administration of omega
                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                 used for treating chronic pain, especially neuropathic pain
                                                                                                                                                                                                                                                                                                                                    Justice A,
'hote= "4-Hydroxyproline"
                 /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "C-terminal amide'
                                                                                                                                    Valentino KE,
                                                                                                                                                                                                                                                                                                                                                                         <u>5</u>
                                                                                                                                                                                                                                                                                                                                                                                   CKGKGAPCRKTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                       CXIXNOXCXOXTDDCCSXXCNXXNXC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                 Disclosure, Fig 1B; 59pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW95573 standard; protein; 26
                                                                       96US-00675354
                                                                                        91US-00814759
93US-00049794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ·96US-00675354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91US-00814759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Omega-conopeptide SNX-230
                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                  Gohil KC,
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                 (NEUR-) NEUREX CORP.
                                                                                                                                                    WPI; 1999-120002/10.
                                                                                                                                                                                                                                                                                                                   Sequence 26 AA;
                                                                                                                                  Miljanich GP,
         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
Modified-site
                                                                      03-JUL-1996;
                                                                                       30-DEC-1991;
15-APR-1993;
                                   US5859186-A.
                                                     12-JAN-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-MAR-1999
                                                                                                                                                                                peptide(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US5859186-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW95573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conus sp.
```

셤 ò

```
Sequences AAW95564-573 represent primary sequences of natural omegaconopeptides. Omega-conopeptides are components of peptide toxins produced by marine snails of the genus Conus, and which act as calcium channel blockers. The invention relates to a method of producing analgesia in a mammal that comprises administering an omega conopeptide having activities in (a) inhibiting electrically stimulated contraction of guinea pig ileum and (b) selectrivaly binding to omega conopeptide WIIA binding sites in neuronal tissue, where these activities are within used for treating chronic pain, especially neuropathic pain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      binding;
norepinephrine; noradrenaline;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuropathic; pain; conotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                    cono-
                                                                                                                    omega
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.5%; Score 69; DB 2; Length 26; 30.8%; Pred. No. 22;
                                                                                                           Production of analgesia in mammal - by administration of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
Justice A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Omega conopeptide; analgesic; nociceptive; marine snall; peptide toxin; inflammation; voltage-gated calcium channel; inhibition; anti-inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Mismatches
Valentino KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "unspecified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CKGKGAPCRKTMYDCCSGSCGRRGKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
7
                                                                                                                                                                                          Disclosure, Fig 1B; 59pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Natural omega conopeptide SNX-231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91US-00814759.
93US-00049794.
96US-00675354.
96US-00742774.
```

Gohil KC;

ó

```
test compounds in blocking voltage-gated to the omega conopeptide binding site and (noradrenaline) release for treating
Measuring the activity of calcium channels, binding inhibiting norepinephrine
                                                                                         inflammation
```

Disclosure; Fig 1; 47pp; English

A method has been developed of selecting a test compound for treating inflammation. The method comprises measuring the activity of the test compound in blocking voltage-gated calcium channels, binding to the omega conopeptide binding site and inhibiting norepinephrine (noradrenaline) release from nervous tissue. The method is useful for selecting compounds for treating inflammation. The selected compounds are capable of producing analgesia in a mammalian subject with chronic or intractable pain. Analgesic agents of the prior art which cause dependency and tolerance, requiring potentially dangerous increases in opioid doses to achieve the analgesic effect. The present sequence represents an omega conopeptide given in the present invention

Sequence 26 AA;

Gaps ö 57.5%; Score 69; DB 3; Length 26; 34.6%; Pred. No. 22; ive 11; Mismatches 6; Indels CXIXNQXCXQXLDDCCSXXCNXXNXC 26 | : : | | : : : | | | | | : : : | CKGKGAXCRYIMYDCCSGSCGRRGKC 26 Conservative Local Similarity Query Match ઠ 8

AAY5648:

AAYS6481 standard; peptide; 26

AAY56481;

(first entry) 16-FEB-2000

Natural omega conopeptide MVIIC/SNX-230.

neuropathic; pain; conotoxin; binding; norepinephrine; noradrenaline; Omega conopeptide; analgesic; nociceptive; marine snall; peptide toxin; inflammation; voltage-gated calcium channel; inhibition; anti-inflammatory.

Conus

US5994305-A

30-NOV-1999

21-AUG-1998;

91US-00814759 30-DEC-1991; 15-APR-1993

98US-00138439

93US-00049794 96US-00675354 96US-00742774 01-NOV-1996;

(ELAN-) ELAN PHARM INC.

Gohil KC;

Valentino KL, Miljanich GP,

Justice A, Singh T, WPI; 2000-038270/03 Measuring the activity of test compounds in blocking voltage-gated calcium channels, binding to the omega conopeptide binding site and inhibiting norepinephrine (noradrenaline) release for treating inflammation

Disclosure; Fig 1; 47pp; English.

A method has been developed of selecting a test compound for treating

inflammation. The method comprises measuring the activity of the test compound in blocking voltage-gated calcium channels, binding to the omega conopeptide binding site and inhibiting norepinephrine (noradrenaline) release from nervous tissue. The method is useful for selecting compounds for treating inflammation. The selected compounds are capable of producing analgesia in a mammalian subject with chronic or intractable pain. Analgesia caused by selected compounds may reduce the reliance on opioid analgesic agents of the prior art which cause dependency and tolerance, requiring potentially dangerous increases in opioid doses to achieve the analgesic effect. The present sequence represents an omega conopeptide given in the present invention

Sequence 26 AA;

0; Gaps Length 26; Indels . . , DB 12; Mismatches 57.5%; Score 69; 30.8%; Pred. No. 8; Conservative Query Match Best Local Similarity Matches

ö

1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26

g

ð

RESULT 89 AAY43715

ö

Ź AAY43715 standard; peptide; 26

AAY43715;

(first entry) 11-FEB-2000 Amino acid sequence of an omega-conotoxin MVIIC.

Omega-conotoxin; venom; predatory marine snail; N-type calcium channel; neuronal damage reduction; ischemia; analgesia; opiate analgesia; schizophrenia; stimulant induced psychosis; hypertension; inflammation; bronchotension; neuropathic pain; voltage sensitive calcium channel

Conus magus

WO9954350-A1

28-OCT-1999

99WO-AU000288 16-APR-1999; 98AU-00002989.

16-APR-1998; 01-FEB-1999;

QUEENSLAND (UYQU) UNIV

Nielsen KJ; Alewood PF, Lewis RJ, Drinkwater RD,

WPI; 2000-013226/01.

Novel peptides used for the treatment of disorders and diseases where blockage of the N-type calcium channels is required.

Disclosure; Page 12; 81pp; English.

The present sequence represents an omega-conotoxin. Omega-conotoxins are isolated from venoms of predatory marine snails, and have a selectivity for N-type calcium channels over P/O type channels, and so block N-type calcium channels. The omega-conotoxins of the invention can be used in any disease or disorder where blockage of N-type calcium channels is required, e.g. in the reduction of neuronal damage following ischemia, production of analgesia, or enhancement of opiate analgesia, in the treatment of schizophrenia, stimulant induced psychoses, hypertension, inflammation, and diseases which cause bronchotension, and also in the inhibition of progression of neuropathic pain. They can also be used in screen to identify compounds with activity at N-type voltage sensitive calcium channels Pred. No.

30.8%;

Local

Best

ö

Gaps

Tue Apr 19 09:12:32 2005

g

```
The present sequence is an omega-conopeptide from marine snails of the genus Conus. Omega-conopeptides are components of peptide toxins produced by the cone snails, and which act as calcium channel blockers. Natural comega-conopeptides and their derivatives may be useful for producing analgesia in nociceptive and neuropathic pain. The peptides bind to omega-conopeptide binding sites, which are present mainly in neuronal tissue, and inhibit norepinephrine release from nervous tissue. Conopeptides such as MVIIA and TVIA are effective as therapeutic agents for treating neurogenic conditions such as schizophrenia, tardive dyskinesia and acute dystonic reactions, inflammation and epilepsy
                                                                                                                                                                                                                                                                                                    Marine snail; omega-conopeptide; calcium channel blocker; MVIIC; SNX-230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Selecting a compound for producing analgesia involves measuring activity of test compound in blocking voltage-gated calcium channels, binding to omega conopeptide binding site and inhibiting norepinephrine release.
                                                                                                                                                                                                                                                                                                                   toxin; analgesic, antiinflammatory; anticonvulsant; neuroleptic; norepinephrine release inhibitor; schizophrenia; tardive dyskinesia; acute dystonic reaction; inflammation; epilepsy.
                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Justice A;
                             57.5%; Score 69; DB 3; Length 26; 30.8%; Pred. No. 22;
                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Miljanich GP,
                                                             . 9
                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "C-terminal amide"
                                                                                        5
                                                                                                     1 CXIXNOXCXQXLDDCCSXXCNXXNXC
                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Valentino KL,
                                                                                                                                                                                         Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 1; 58pp; English.
                                                                                                                                                                                                                                                                            Omega-conopeptide MVIIC/SNX-230.
                                                          12;
                                                                                                                                                                                     AAB14377 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91US-00814759.
93US-00049794.
96US-00675354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-00298017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96US-00742774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-00138439
                                                                                                                                                                                                                                              (first entry)
                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Selecting a compound for of test compound in block
                                                                                                                                                                                                                                                                                                                                                                                                                         1. .16
8. .20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ELAN-) ELAN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gohil KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-490177/43,
                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 Disulfide-bond
Disulfide-bond
Disulfide-bond
Sequence 26 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                               06-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-APR-1993;
03-JUL-1996;
01-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US6087091-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JUL-2000
                                                          ..
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-AUG-1998
                                                                                                                                                                                                                   AAB14377;
                                                                                                                                                                                                                                                                                                                                                                             gg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Singh T,
                                                                                                                                                                                                                                                                                                                                                                          Conus
                                                          Matches
                                                                                                                                                           RESULT 90
                                                                                                                                                                                                                                                                                                                                                                                                        ۴ę
                                                                                                                                                                         AAB1437
                                                                                                                                                                                                    à
                                                                                                                g
```

Length 26;

DB 3;

57.5%; Score 69;

Sequence 26 AA;

Query Match

```
ö
                                                                                                                                                                                                                                       Marine snail; omega-conopeptide; calcium channel blocker; SNX-231; toxin; analgesic; antiinflammatory; anticonvulsant; neuroleptic; norepinephrine release inhibitor; schizophrenia; tardive dyskinesia; acute dystonic reaction; inflammation; epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is an omega-conopeptide from marine snails of the genus Conus. Omega-conopeptides are components of peptide toxins produced by the cone snails, and which act as calcium channel blockers. Natural omega-conopeptides and their derivatives may be useful for producing analgesia in nociceptive and neuropathic pain. The peptides bind to omega-conopeptide binding sites, which are present mainly in neuronal tissue, and inhibit norrepinephrine release from nervous tissue. Conopeptides such as MVIIA and TVIA are effective as therapeutic agents for treating neurogenic conditions such as schizophrenia, tardive dyskinesia and acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Selecting a compound for producing analgesia involves measuring activity of test compound in blocking voltage-gated calcium channels, binding to omega conopeptide binding site and inhibiting norepinephrine release.
                Gaps
                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Justice A;
                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 26;
                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Miljanich GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          э
Э
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dystonic reactions, inflammation and epilepsy
 d. No. 22;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "C-terminal amide"
                                        26
                                                                 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 69;
Pred. No.
                                                     |: : :|::: ||||::| :: :|| CKGKGAPCRKTMYDCCSGSCGRRGKC
                                       1 CXIXNQXCXQXLDDCCSXXCNXXNXC
                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Valentino KL,
                                                                                                                                   Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Fig 1; 58pp; English.
              12;
                                                                                                                                  AAB14372 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91US-00814759.
93US-00049794.
96US-00675354.
96US-00742774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-00298017.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.5%;
                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                 Omega-conopeptide SNX-231
               Conservative
                                                                                                                                                                                                                                                                                                                                                                            label=
                                                                                                                                                                                                                                                                                                                                                     1. .16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ELAN-) ELAN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-490177/43.
Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gohil KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                  Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                      Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                      Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                      06-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        US6087091-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-APR-1993
03-JUL-1996
                                                                                                                                                           AAB14372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Singh T,
                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                          Conus
            Matches
                                                                                                                                                                                                                                                                                                                                       Key
                                                                                                                   AAB14372
                                                                                                       RESULT
                                                                                                                                             ò
                                                             g
```

Ā

(first entry)

ò 셤

```
Omega-conopeptide, voltage-gated calcium channel inhibitor; analgesic; peptide toxin; opiate; pain; neuronal damage; ischemic condition; schizophrenia; tardive dyskinesia; acute dystonic reaction; inflammation;
                                                                                                                                                                 Primary sequence of a natural omega-conopeptide SNX-231
                                                       AAB19450 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                   Disulfide-bond
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                          Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                              06-MAR-2001
                                                                                          AAB19450;
                                                                                                                                                                                                                                                                                                 Conus sp.
                                                                                                                                                                                                                                                               epilepsy
                   RESULT 93
AAB19450
                                                                        %XCCCCCCCCCCX8X4444X8X5BX888B88X6X8X4444444444X8X8X6X6X6X6X6X6X6X6X8X6X6X8X6X6X8X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a modified therapeutic peptide (I)

comprising a therapeutically active amino acid region (III) and a
reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
a less therapeutically active amino acid region (IV), which covalently
conds with amino/hydroxyl/thiol groups on blood components to form a
peptidase stabilised therapeutic peptide composed of 3-50 amino acids.

(I) are useful for modifying therapeutic peptides e.g. hormones, growth
factors and neurotransmitters, to protect them from peptidase activity in
vivo for the treatment of various disorders. Endogenous therapeutic
convolor the treatment of various disorders. Endogenous therapeutic
convolor the treatment of various disorders is athey require frequent
administration due to rapid degradation by peptidases in the body.
Condifying and attaching therapeutic peptides to albumin prevents or
reduces the action of peptidases to increase length of activity (half
IIfe) and specificity as bonding to large molecules decreases
interacellular uptake and interference with physiological processes.
AAB90829 to AAB92441 represent invention
 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity.
   Gaps
                                                                                                                                                                                                                                                                                                                Protection, endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thibaudeau K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.5%; Score 69; DB 4; Length 26; 30.8%; Pred. No. 22; cive 12; Mismatches 6; Indels
 Indels
   . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Holmes DL,
11; Mismatches
                                    1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                       |: : ||::: ||||::| || CKGKGAXCRKTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 653; 733pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Milner PG,
                                                                                                                                                                    Ź
                                                                                                                                                                 AAB92220 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0134406P.
99US-0153406P.
99US-0159783P.
                                                                                                                                                                                                                                                                                Toxin peptide SEQ ID NO:1396.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-MAY-2000; 2000WO-US013576.
                                                                                                                                                                                                                                          (first entry)
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bridon DP, Ezrin AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CONJ-) CONJUCHEM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-112059/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200069900-A2
                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-SEP-1999;
15-OCT-1999;
                                                                                                                                                                                                                                           22-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                       AAB92220;
Matches
```

/note= "amidated C-terminal"

/label= Hyp /note= "hydroxyproline"

8. .20 15. .26

Location/Qualifiers

1. .16

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents an omega-conopeptide. Omega-conopeptides are components of peptide toxins which act as voltage-gated calcium channel inhibitors. The peptides are used to enhance the analgesic effect produced by an opiate in a mammalian subject. The method comprises administering to the subject an omega-conopeptide which is able to linhibit electrically stimulated contraction of the guinea pig ileum and bind to omega-conopeptide MVITA binding sites present in neuronal its sue omega-conopeptides are useful for enhancing the analgesic effect produced by an opiate. Omega-conopeptides may also be used in the treatment of pain, in reducing schusophical damage related to an ischemic condition in mammals, and in treating schizophrenia, tardive dyskinesia and acute dystonic reactions, inflammation and epilepsy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enhancing analgesia produced by opiates by administering an omega-
conopeptide that inhibits electrically stimulated contraction of guinea
pig ilium and binds to omega-conopeptide MVIIA binding sites in neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Justice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Miljanich GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

S7.5%; Score 69; DB
Best Local Similarity 30.8%; Pred. No. 22;
Matches 8; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Valentino KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 1; 58pp; English.
                                                                                                                                                                                                 93US-00049794.
93US-00081863.
96US-00675354.
96US-00742774.
98US-00138439.
                                                                                                                99US-00392979
                                                                                                                                                                                                                                                                                                                                                                                                            (ELAN-) ELAN PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-030946/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gohil KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 26 AA;
                                                                                                                09-SEP-1999;
                                                                                                                                                                                                    15-APR-1993;
23-JUN-1993;
JS6136786-A.
                                                      24-OCT-2000
                                                                                                                                                                         30-DEC-1991
                                                                                                                                                                                                                                                              03-JUL-1996
                                                                                                                                                                                                                                                                                         01-NOV-1996
                                                                                                                                                                                                                                                                                                                       21-AUG-1998
                                                                                                                                                                                                                                                                                                                                                23-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Singh T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissues.
```

ö

Gaps

. 0

CXIXNQXCXQXLDDCCSXXCNXXNXC 26 |: : : | : : : | | | | | : : : | CKGKGAPCRKTMYDCCSGSCGRRGKC 26

-

ò

Conservative

Gaps

ö

Indels

. 9

us-10-627-685a-1.rag

AAB19451;

94

ò 음 AAB1945

Conus sp.

Key

```
The invention comprises peptides having calcium channel blocking activities which are derived from the venomous saliva of assassin bugs. The calcium channel blocking peptides of the invention are useful for treating stenocardia, hypertension, myocarditis, arrhythmia and cerebral ischaemia. The present amino acid sequence represents a cone snail wconotoxin peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conotoxin; MVIIC; peptide library; disulphide bond; biological activity;
                                                                                                                                                                                                                                                                                                                                    Cone snail; venomous saliva; calcium channel blocking activity; stenocardia; hypertension; myocarditis; arrhythmia; cerebral ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A new peptide derived from venomous saliva of assassin bug, channel blocking activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.5%; Score 69; DB 5; Length 26; 30.8%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Omega-conotoxin MVIIC peptide sequence SEQ ID NO:1.
 ed. No. 22;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12; Mismatches
   Pred. No.
                                                                            |: : :|::: ||||::| :: :|
CKGKGAPCRKTMYDCCSGSCGRRGKC 26
                                                     1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cone snail w-conotoxin peptide MVIIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 4; 26pp; Japanese.
                                                                                                                                                                                      AAO15125 standard; peptide; 26 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG68252 standard; peptide; 26
 30.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-SEP-2000; 2000JP-00266187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-SEP-2000; 2000JP-00266187
                                                                                                                                                                                                                                                               (first entry)
                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-421068/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SUNR ) SUNTORY LID
Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  JP2002080499-A.
                                                                                                                                                                                                                                                             22-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                               w-conotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-FEB-2002
                                                                                                                                                                                                                          AA015125;
                                                                                                                                                                                                                                                                                                                                                                                                                 Conus sp.
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG68252;
                   Matches
                                                                                                                                               RESULT 95
                                                                                                                                                                   AA015125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG68252
                                                                                                                                                                                                        ò
                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SXXXXXXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents an omega-conopeptide. Omega-conopeptides are components of peptide toxins which act as voltage-gated calcium channel inhibitors. The peptides are used to enhance the analgesic effect produced by an opiate in a mammalian subject. The method comprises administering to the subject an omega-conopeptide which is able to inhibit electrically stimulated contraction of the guinea pig ileum and bind to omega-conopeptide MVIAb binding sites present in neuronal tissue. Omega-conopeptides are useful for enhancing the analgesic effect produced by an opiate. Omega-conopeptides may also be used in the treatment of pain, in reducing neuronal damage related to an ischemic condition in mammals, and in treating schizophrenia, tardive dyskinesia and acute dystonic reactions, inflammation and epilepsy
                                                                                                                                                                                                                                                                                         Omega-conopeptide; voltage-gated calcium channel inhibitor; analgesic; peptide toxin; opiate; pain; neuronal damage; ischemic condition; schizophrenia; tardive dyskinesia; acute dystonic reaction; inflammation; epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enhancing analgesia produced by opiates by administering an omega-
conopeptide that inhibits electrically stimulated contraction of guinea
pig ilium and binds to omega-conopeptide MVIIA binding sites in neuronal
tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Justice A;
                                                                                                                                                                                                                                                     Primary sequence of a natural omega-conopeptide SNX-230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Valentino KL, Miljanich GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "amidated C-te:rminal"
           CXIXNOXCXQXLDDCCSXXCNXXNXC 26
                               Location/Qualifiers
                                                                                                                                             Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 1; 58pp; English.
                                                                                                                                         AAB19451 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93US-00049794.
93US-00081863.
96US-00675354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96US-00138439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-00392979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91US-00814759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-00298017
                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                              . .16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ELAN-) ELAN PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gohil KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-030946/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Disulfide-bond
Disulfide-bond
Disulfide-bond
Modifide-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 26 AA;
                                                                                                                                                                                                                06-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US6136786-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-APR-1993
23-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-JUL-1996
```

Singh T,

has calcium

ö

Gaps

; 0

Indels

..

calcium channel blocker.

Conus sp

Length 26;

DB 4;

57.5%; Score 69;

Query Match

Olivera BM, Hillyard DR;

93US-00092215.

93US-00092215

```
New omega-conotoxin peptide(s) - which target P-type and N-type calcium ion channels, used for distinguishing calcium channels or for diagnosis.
                                                                                                                                                                                                                                                                                                                                                                   Example 1; Col 29-30; 21pp; English.
                                                                                                                                                                                                                                       Monje VD, Imperial JS,
                                                                                                                                                                                                   (UTAH ) UNIV UTAH.
                                                                                                                             16-JUL-1993;
                                                                                                                                                               16-JUL-1993;
                      Conus magus.
                                                       US5591821-A.
                                                                                           07-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADP04517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a method for manufacturing a peptide

[Ibrary comprising a peptide (I) having 2 or more intramolecular

[Ibrary comprising a peptide (I) having 2 or more intramolecular

[Ibrary comprising and its variants (V). The method comprises

[Ibrary and its variants (V). The method comprises

[Ibrary obtained by the above said method; (2) screening for mutant

[Ibrary obtained by the above said method; (2) screening for mutant

[Ibrary obtained by the above said method; (2) screening for mutant

[Ibrary obtained by the above said method; (3) a mutant peptide obtained

[Ibrary obtained by the above said method; and (4) a calcium channel blocker

[Ibrary obtaining of screening method; and (4) a calcium channel blocker

[Ibrary with a wild type peptide. The method is useful for

[Ibrary obtaining of screening method; and (4) a calcium channel blocker

[Ibrary obtaining of screening method; and for screening peptides with increased

[Ibrary obtaining of screening method; and for screening nethod is suitable

[Ibrary obtaining of screening method; and for screening peptides with increased

[Ibrary obtaining of screening method; and for screening method is suitable

[Ibrary obtaining of screening method; and for screening method is suitable

[Ibrary obtaining of screening method; and for screening method; and the screening method; and for screening method; and for screening method; and the screening method; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents an omega-conotoxin MVIIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Omega-conotoxin; conus; Conus magus; alpha-conotoxin; mu-conotoxin; nicotinic acetylcholine receptor; venom; skeletal muscle; inhibitor; sodium ion channel; presynaptic neuronal calcium ion channel; therapy; P-like subtype; N-type channel; respiratory rhythm; respiratory control; neural developmental syndrome; respiratory crisis; Lambert-Eaton myasthenic syndrome.
                                                                                                                                                                                                                                                                                                                                                                                    peptide mixture for synthesizing peptide of interest and its variants, forming intramolecular disulphide bonds between peptides and separating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              simultaneously, The present sequence represents an omega-conotoxin MYLI
peptide which is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                   Manufacturing peptide library, by introducing mutant amino acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.5%; Score 69; DB 30.8%; Pred. No. 22; ive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Full length omega-conotoxin MVIIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW12803 standard; peptide; 29 AA
                                                                                                            /note= "amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example; Fig 1; 11pp; Japanese.
                                                                                                                                                                                                                   13-MAR-2000; 2000JP-00068023.
                                                                                                                                                                                                                                                       13-MAR-2000; 2000JP-00068023.
                                                                                                                                                                                                                                                                                           (MITU ) MITSUBISHI CHEM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-APR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Conservative
                                    1. .16
8. .20
15. .26
                                                                                                                                                                                                                                                                                                                               WPI; 2002-044564/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                  Disulfide-bond
Disulfide-bond
Disulfide-bond
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 26 AA;
                                                                                                                                            JP2001253899-A
                                                                                                                                                                                18-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW12803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 97
AAW12803
ID AAW120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for p
simul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
&&&&&&&&
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
```

```
AAW12800-W12804 represent omega-conotoxins isolated from Conus magus.

This sequence represents the MVIIC Conus magus omega-conotoxins. Conus verom contains three types of disulphide rich peptides, these are the alpha-conotoxins target and block the nicotinic acetylcholine receptors, the author conotoxins target and block the nicotinic acetylcholine receptors, the mucro conotoxins target and block the skeletal muscle sodium ion channels, and the comparation are receptors, the mucro conotoxins target and block the presynaptic neuronal calcium con channels. The omega-conotoxin peptides of the invention can target P-CC like subtypes of calcium ion channels, as well as the N-type channels can also be used for distinguishing the types of calcium ion channels. The presence or absence of sites for the peptides can be calcions, thereby characterising calcium ion channel expressing calls into various types. As these sequences affect the control of respiratory rhythms in vivo, they can be used to evaluate abnormalities in respiratory control which are particularly severe in the neonatal period. The peptides can also be used for assessing neural everyphental syndromes that result in respiratory crisis, and can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sea squirt protein with tissue specific expression in development Seq112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sea squirt; regeneration medicine; gene therapy; cell proliferation; differentiation; reproduction; environmental measurement; water survey.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      used to diagnose the Lambert-Eaton myasthenic syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.5%; Score 69; DB 30.8%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | : : : | : : : | CKGKGAPCRKTMYDCCSGSCGRRGKC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADP04517 standard; protein; 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-JUL-2002; 2002JP-00222593.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ciona intestinalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 29 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JP2004057129-A.
```

```
31-AUG-2000; 2000US-0229614P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-JAN-2001; 2001US-0265395P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 30.55
Best Local Similarity
Since Si Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                     Nickoloff BJ, Miele L;
                                                                                                                                                                               WPI; 2002-339659/37,
                                                                                                                                                                                                                   N-PSDB; ABL40768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2444 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200268649-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-SEP-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 100
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XX AX XX DE XX XX BY XX 
                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to novel genes and the encoded proteins thereof
that are derived from the sea squirt Ciona intestinalis. Specifically, it
refers to those genes that are expressed in the tissues or organs of the
cas squirt during its developmental phase. The present invention
describes the identification of these genes as useful for elucidation of
the mechanism of development and hence for developing reseneration
medicines and gene therapy techniques. Accordingly, they can be used in
the research of various genetic diseases, as well as the analysis of cell
proliferation, differentiation and reproduction. Furthermore, such
compositions can be useful for environmental measurements and water
surveys, particularly for sea water surveys, and also for the preparation
of transformed sea squirt for improving edibility of sea squirt such as
Halocynthia roretzi. This polypeptide sequence is a sea squirt protein
sequence that has tissue specific expression during development, given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
                                                                                                                                                                                                                                Novel gene cluster which is specifically expressed in tissue or organ during developmental phase of sea squirt, useful for elucidation of mechanism of development of tissue or organ of sea squirt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell differentiation, notch; epidermis; cytostatic; dermatological; epithelial; skin; cancer; gamma secretase; notch-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57.1%; Score 68.5; DB 8;
33.3%; Pred. No. 2.4e+02;
ive 14; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Thr, Ala, Pro or Ser
/note= "encoded by NCC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260 CAICNEFCN-ATNECQASTCAPYCNIC 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CXIXNQXCXQXLDDC----CSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 112; 1846pp; Japanese.
                                                                       (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'label= Gln, Arg, Pro o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "encoded by GSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Constitutively active notch-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB07821 standard; protein; 2444 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'label= Gly or Ala
                31-JUL-2002; 2002JP-00222593.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-AUG-2001; 2001WO-US027246.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 33.3
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference 891
                                                                                                                                                                     N-PSDB; ADP04516.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 342 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200218544-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-MAR 32002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB07821;
```

RESULT 99

ઠે

```
The invention relates to a method of inducing differentiation of at least one spithelial cell. The method involves exogenously providing at least one source of at least one Notch agonist to at least one epithelial cell, whereby the Notch pathway is activated within at least one epithelial cell, whereby the Notch pathway is activated within at least one epithelial cell, whereby the Notch pathway is activated within at least one epithelial cell, cell so that the differentiation of the cell is induced. Methods of producing differentiated epidermis; for assaying for genetic propensity of a patient to develop a disorder associated with epithelial barrier formation; for retarding progression of skin cancer and for diagnosing aggressive melanoma are also provided. The methods are useful for inducing differentiation of at least one epithelial cell e.g. a charching actions of epithelial cell within cutaneous epithelial tissue or dermal equivalent, or within extracutaneous epithelial tissue or dermal equivalent, or within extracutaneous epithelial. The methods are useful retarding the progression of skin cancer such as aggressive melanoma, aggressive cutaneous T-cell lymphoma (CTCL), aggressive squamous cell carcinoma, or aggressive basal cell carcinoma, by preferably administering an antagonist of the Notch pathway concarticities.
                                                                                                                                                                                                                                                                                                                                                Inducing differentiation of epithelial cell useful for inducing barrier formation within epithelium for treating psoriasis, sunburn, involves exogenously providing a source of a Notch agonist to the epithelial cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes; inflammation; autoimmune disorder; allergy; blood disorder; acquired immunodeficiency syndrome; AIDS; obesity; asthma; immunoglobulin (1g)A nephropathy; cirrhosis; arthritis; Alzheimer's disease; infection; str.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56.7%; Score 68; DB 5; Length 2444; 30.8%; Pred. No. 1.5e+03; ive 12; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 GFTGQNCEENIDDCPGNNCKNGGACV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human NOVX protein homologue SegID 469.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                constitutively active notch-1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 10; Page 50-66; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADI16933 standard; protein; 2444 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-JAN-2002; 2002WO-US002785.
(LOYO ) UNIV LOYOLA CHICAGO
```

```
2001US-0278652P.
2001US-0278775P.
2001US-0278778P.
2001US-0279882P.
                                                                                                                                                   2001US-0279884P.
2001US-0280147P.
2001US-0282992P.
2001US-0283083P.
                                                                2001US-0271855P.
2001US-0272788P.
2001US-0273046P.
                2001US-0266406P.
2001US-0266767P.
                                                                                                        2001US-0276448P.
                                                                                                                                                                         2001US-0285133P.
2001US-0285749P.
2001US-0288327P.
                                                            2001US-0271839P
                                                                                                                                                                                          2001US-0288504P
                                                                                                                                                                                                2001US-0294047P
                                                                                                                                                                                                                                                2001US-0315470P
                          2001US-026
2001US-026
2001US-026
               02-FEB-2001; 2
05-FEB-2001; 2
07-FEB-2001; 2
07-FEB-2001; 2
08-FEB-2001; 2
                                                15-FEB-2001;
26-FEB-2001;
27-FEB-2001;
                                                                                                                                                                                                         08-JUN-2001;
18-JUN-2001;
                                                                                                                                                                   11-APR-2001;
20-APR-2001;
                                                                                                                                                                                                                                16-AUG-2001;
16-AUG-2001;
                                                                                                                                        26-MAR-2001;
29-MAR-2001;
                                                                                                                                                   29-MAR-2001;
                                                                                                                                                                                    03-MAY-2001;
                                                                                                                                                                                                                    19-JUN-2001;
                                                                                                                                                                                                                          13-AUG-2001;
                                                                                                                                                                                                                                                28-AUG-2001;
                                                                                                                                                                                                                                                                      12-SEP-2001;
```

(CURA-) CURAGEN CORP.

Burgess CE Shimkets RA; li L, Miller CE; c AR, Pena CEA; Zerhusen BD, Patturajan M, Shimket garu M, Anderson DW, Rasteslil L, N Gusev VY, Colman SD, Wolenc AR, I sobrook JP, Lepley DM, Rieger DK, Padigaru M, Ander RJ, Gusev VY, Cc , Alsobrook JP, I Spytek KA, Taupier RJ, Li L, Games Gerlach VL, Tauplen ... Tchernev VT,

WPI; 2002-706998/76.

New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or pharmacogenomics.

Disclosure; SEQ ID NO 469; 1498pp; English.

This invention relates to a novel nucleic acids, and encoded polypeptides thereof, which have properties related to the stimulation of biochemical or physiological responses in a cell, tissue, organ or organism.

diagnostic and prognostic assays and furthermore in the treatment of diagnostic and prognostic assays and furthermore in the treatment of diagnostic and prognostic assays and furthermore in the treatment of diagnostic and diagnostic as well as methods to modulate their expression using antisense oligos, riboxymes and peptide nucleic acids. The NOWX polypeptides, polynucleotides and antibodies are useful in treating or preventing NoWX-associated disorders, e.g. cardiomyopathy, atherosclerosis, cancer and diabetes. Furthermore, they may be used in treating or preventing diseases such as inflammation, autoimmune to disorders, albrodiances. Purthermore, they may be used in treating or preventing diseases such as inflammation, autoimmune and isorders, albrodiances, and epithepsy, Accordingly, these molecules have many activities including cytostatic, cardiant, antidiahetic, immunosuppressive, antiallergic, haemostatic, anti-HIV, antidiahetic, antiarteriosclerotic, anorectic, antiaxant and anticonvulsant. In addition, they are useful in screening casasays to identify small molecules that modulate or inhibit, for example, neurogenesis, wound healing and angiogenesis. The nucleic acids are also the incorporation. This polypeptide is a homologue of a human NOVX protein ö Specifically, it refers to the use of biologically active fragments for Gaps ; 0 Query Match 56.7%; Score 68; DB 5; Length 2444; Best Local Similarity 30.8%; Pred. No. 1.5e+03; Matches 8; Conservative 12; Mismatches 6; Indels 248 GFTGONCEENIDDCPGNNCKNGGACV 273 2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27 Search completed: April 18, 2005, 20:33:43 Job time : 127.5 secs Sequence 2444 AA; of the invention. 셤 8

This Page Blank (uspto)

Š

```
29, Appl
21, Appl
21, Appl
22, Appl
22, Appl
23, Appl
21, Appl
22, Appl
23, Appl
23, Appl
23, Appl
24, Appl
26, Appl
27, Appl
27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9, Appli
9, Appli
1, Appli
2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    364, App
413, App
119, App
2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                Sequence 21, Apsequence 21, Apsequence 20, Apsequence 20, Apsequence 21, Apsequen
   Sequence
Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
US-08-496-847-29
US-08-742-774-21
US-08-742-774-21
US-08-742-774-29
US-08-742-774-29
US-08-675-354-29
US-08-675-316-29
US-08-965-918-29
US-08-965-918-29
US-09-9138-439-29
US-09-9138-439-29
US-09-298-017-29
US-09-298-017-29
US-09-298-017-29
US-09-298-017-29
US-08-103-299-29
US-08-103-298-215-9
US-08-103-298-215-9
US-08-103-298-215-9
US-08-103-298-215-9
US-08-103-298-215-9
US-08-103-29-6
US-08-103-29-6
US-08-103-29-6
US-08-103-29-6
US-08-103-29-103-29-6
US-08-103-29-6
US-08-103-29-103-19
US-08-91-13-19
US-08-91-13-19
US-08-91-13-19
US-08-91-13-19
US-08-91-13-19
US-08-91-13-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-230-652-2
US-09-894-883-364
US-09-894-882-119
US-09-341-461-2
US-09-894-882-324
US-09-894-882-339
US-09-894-882-443
US-09-894-882-443
US-09-894-882-433
US-09-894-882-433
US-09-894-882-433
US-09-894-882-323
US-09-894-882-073
US-09-894-882-073
US-09-894-882-073
US-09-841-612-2
US-09-641-612-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-894-882-404
US-09-894-882-209
US-09-894-882-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2556
2556
2556
2556
2556
321
321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         585
1055
1055
11065
11148
11212
11213
11238
11238
11248
11248
11248
11257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66
65.5
65.5
65.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64.5
64.5
64.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.5
63.5
63.5
63.5
63.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64
   Appl
Appl
Appl
Appl
Appl
Appl
Appli
                                                                                                                                                                                                 April 18, 2005, 20:24:17; Search time 30.5 Seconds (without alignments) 66.083 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence Sequence Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1
Sequence 1
Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       513545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                           GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-619-936-1

US-08-049-913-19

US-08-496-847-19

US-08-75-354-19

US-08-965-918-19

US-08-965-918-19

US-08-965-918-19

US-09-138-439-19

US-09-138-439-19

US-09-398-017-19

US-08-913-8

US-08-96-913-8

US-08-96-913-8

US-08-138-439-8

US-08-965-918-8

US-08-138-439-8

US-09-138-439-8

US-09-138-439-8

US-08-138-432-18

US-08-18-432-18

US-08-18-432-18

US-08-18-432-18

US-08-18-432-18

US-08-18-432-18

US-08-18-432-18

US-08-18-432-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                             US-10-627-685A-1
120
1 CXIXNQXCXQXLDDCCSXXCNXXNXCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum March 0%
Maximum March 100%
Listing first 100 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                         BLOSUM62DX
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patents AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2523
2523
2523
                                                            Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     •
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB
Maximum DB
                                                                                                                                                protein
                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database
                                                                                                                                                                                                          Run on:
```

Result No.

```
RESULT 2
US-07-789-913-19
                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: /product= "4Hyp"
OTHER INFORMATION: /note= "Amino acid 4 may be 4-trans-hydroxyproline."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 120; DB 1; Length 27; Best Local Similarity 66.7%; Pred. No. 9.9e-05; Matches 18; Conservative 9; Mismatches 0; Indels
                                                                                                                                                                            APPLICANT: Terlau, Heinrich
APPLICANT: Shon, Ki-Joon
APPLICANT: Shon, Ki-Joon
APPLICANT: Grilley, Michelle
APPLICANT: Glivera, Baldomero M.
TITLE OF INVENTION: Conctoxin Peptide PVIIA
NUMBER OF SEQUENCES:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
                                                                                                                                                                                                                                                                                                                                                               CITY: Marington
STATE: DC
COUNTRY: U.S.A.
ZOUNTRY: U.S.A.
ZONETER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRIT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,936
FILLING DATE:
                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CXIXNQXCXQXEDDCCSXXCNXXNXCV 27
                                                                                                                 Sequence 1, Application US/08619936
Patent No. 5672682
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 2426C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4848
TELEFAX: 202-962-4848
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disulfide-bond
8..20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Modified-site LOCATION: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , NAME/KEY:
, LOCATION:
US-08-619-936-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
                                                                                                  US-08-619-936-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

```
;
0
                                                                  APPLICANT: Mijanich, George P.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Valentino, Karen L.
APPLICANT: Vamashiro, Lonald H.
TITLE OF INVENTION: Delayed Treatment Method of Reducing TITLE OF INVENTION: Ischemia-Related Neuronal Damage NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.5%; Score 81; DB 1; Length 26; 34.6%; Pred. No. 0.29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATENTIAN DATA:
APPLICATION NUMBER: US/07/789,913
FILING DATE: 1091112
CLASSIFICATION NUMBER: US 07/561,766
FILING DATE: 22-NOV-1990
PRIOR APPLICATION NUMBER: US 07/440,094
FILING DATE: 22-NOV-1989
ATTONEX/AGENT INFORMATION:
NAME: SELATEORY CAPATION
NAME: SELATEORY CAPATION
TELEPHONE: (415) 324-0960
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHRARATERISTICS:
LENGTH: ALSO AUTO acids
LENGTH: ALSO AUTO acids
LENGTH: ALSO AUTO acids
LENGTH: ALSO AUTO acids
                                                                                                                                                                                                                                                                                                           ADDRESSEE: Law Offices of Peter Dehlinger STREET: 350 Cambridge Avenue, Suite 300 CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 67.5%; Score 81; DB Best Local Similarity 34.6%; Pred. No. 0.29 Matches 9; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CKLKGQSCSRLMYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
US-08-049-794-19
Sequence 19, Application US/08049794
Sequence 19, Application US/08049794
Patent No. 5587454
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
Sequence 19, Application US/07789913
Patent No. 5559085
GENERAL INFORMATION:
APPLICANT: Miljanich, George P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                94306
                                                                                                                                                                                                                                                                                                                                                                                                                   S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-07-789-913-19
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: JUGGITCE, ALAN
APPLICANT: JUGGITCE, ALAN
APPLICANT: JUGGITCE, ALAN
APPLICANT: JUGGITCE, TELINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: WILLANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: PAIO Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 67.5%; Score 81; DB 1; Length 26; Best Local Similarity 34.6%; Pred. No. 0.29; Matches 9; Conservative 13; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
                                                                                                 COMPUTER: IBM COMPACLATION OPERATING SYSTEM: DOS SOFTWARE: DOS SOFTWARE: DOS SOFTWARE: DOS SOFTWARE: DOS SOFTWARE: DOS CURRENT APPLICATION NUMBER: US/08/496,847
FILING DATE: 27-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INPORMATION:
NAME: STATEFORM 34,444
REFERENCE/DOCKET NUMBER: 365-0009.31
TELECOMMUNICATION INPORMATION:
TELEPHONE: 650-324-0860
TELEPHONE: 650-324-0860
TELEPHONE: 650-324-0860
TELEPHONE: 262 ID NO: 19:
SEQUENCE CHARACTER/STICS:
LENGTH: 26 amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNX-202, FIGURE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/675,354
RILING DATE: 03-UUL-196
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-APR-15
APPLICATION NUMBER: US 07/814,759
RILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CKLKGÓSCSRLMYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19, Application US/08742774
Patent No. 5824645
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Stratford, Carol A. REGISTRATION NUMBER: 34,444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL: NO ORIGINAL SOURCE: INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-496-847-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bowered, Stephen S.
APPLICANT: Goolin, Kishorchandra
APPLICANT: Goolin, Kishorchandra
APPLICANT: Goolin, Kishorchandra
APPLICANT: Adriaensens, Peter I.
APPLICANT: Adriaensens, Rameabarma
TITLE OF INVENTION: METHODS AND
TITLE OF INVENTION: FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
STREET: 350 Cambridge & Associates
STREET: 350 Cambridge Avenue, Suite 250
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.5%; Score 81; DB 1; Length 26; 34.6%; Pred. No. 0.29; tive 13; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 19930415
CLASSITEATION: 514.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY AGENT INFORMATION:
NAME: Stratford Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE: SNX-202, FIGURE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CKLKGQSCSRLMYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19, Application US/08496847
Patent No. 5795864
GENERAL INFORMATION:
APPLICANT: Amstutz, Gary A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION: (415) 324-0880
TELERAX: (415) 324-0880
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94306-1546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
US-08-496-847-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-049-794-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
```

쉽

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                      Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Amstutz, Gary A.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Gohil, Kishorchandra
APPLICANT: Gohil, Kishorchandra
APPLICANT: Adriaenssens, Peter I.
APPLICANT: Kristipati, Ramsharma
TITLE OF INVENTION: METHODS AND FORMULATIONS FOR PREVEN
TITLE OF INVENTION: PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADBRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                    67.5%; Score 81; DB 2; ilarity 34.6%; Pred. No. 0.29; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.5%; Score 81; DB 2; 34.6%; Pred. No. 0.29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRSESSO for Windows Version 2.0
SAPPLICATION DATE: APPLICATION NUMBER: US/08/965,918
FILING DATE: 07-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13; Mismatches
         INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
TYTORNEY TARGENTA TON:
NAME: Mohr. Judy M.
REGISTRATION NUMBER: 38,563
REFREENCE/POCKET NUMBER: 5865-0009.34
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
                                                                                                                                                           1 CXIXNOXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                       1 CKLKGQSCSRLMYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                           Sequence 19, Application US/08965918
Patent No. 5891849
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19, Application US/09138439
Patent No. 5994305
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 34.68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                    Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Palo Alto
CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: NORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ns
             ,
US-08-675-354-19
                                                                                                                                                                                                                                                                                       JS-08-965-918-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
US-09-138-439-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-965-918-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                             ઠે
                                                                                                                                                                                                요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                              Query Match 67.5%; Score 81; DB 2; Length 26; Best Local Similarity 34.6%; Pred. No. 0.29; Matches 9; Conservative 13; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: GOHIL, KISHOR C
APPLICANT: WILLANITHO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk

COMPUTER: 1BM PC compatible

APPLICATION NUMBER: 1B/08/049,794

FILING DATE: 30-D21-193

APPLICATION NUMBER: 1B/08/049,794

FILING DATE: 30-D2C-1991

FILING DATE: 30-D2C-1991

FILING DATE: 30-D3C-1991

FILING DATE: 30-080

TELEFAN: (415) 324-0860

TELEFAN: (415) 324-0860

TELEFAN: (415) 324-0860

TELEFAN: (415) 324-0960

TELEGRAN: 26 amino acids

TVPR: Amino acids

TVPR: 1DM CATERISTICS:

LENGTH: 26 amino acids
                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHERICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
    5865-0009.30
                                                                                                                                                                                                                                                                                                                                                                                                                     1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19, Application US/08675354
Patent No. 5859186
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
REFERENCE/DOCKET NUMBER: 5:
TELECOMMUNICATION INFORMATION
TELEPHONE: (415) 324-0880
                                      TELEPHONE: (415) 324-0860
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS:
LENGTH: 26 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                  US-08-742-774-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-675-354-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                       ठ
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 67.5%; Score 81; DB 3; Length 26; Best Local Similarity 34.6%; Pred. No. 0.29; Matches 9; Conservative 13; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19, Application US/09298017
Patent No. 6087091
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: GOHIL, KISHOR C
APPLICANT: WALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/298,017
                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASISEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/613,400A
FILLING DATE: 08-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger STREET: 350 Cambridge Avenue, Suite 300 CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
US-08-613-400A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CKLKGOSCSRLMYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5865-0019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,794
FILING DATE:
                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A
REGISCRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 586;
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEPHONE: 650-124-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                         ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-298-017-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 34.6%; Pred. No. 0.29;
Matches 9; Conservative 13; Mismatches 4; Indels
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHILL, KISHOR C
APPLICANT: GOHILL, KISHOR C
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
MUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19, Application US/08613400A
Patent No. 605429
GENERAL INFORMATION:
APPLICANT: Bowersox, S. Scott
APPLICANT: Gadbois, Theresa
APPLICANT: Luther, Robert, R.
APPLICANT: Luther, Robert, R.
TITLE OF INVENTION: IMPROVED EPIDURAL
TITLE OF INVENTION: METHOD OF PRODUCING ANALGESIA
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Eloppy disk

MEDIUM TYPE: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/138,439

FILING DATE: 100 PATA:

APPLICATION NUMBER: US/08/049,794

FILING DATE: 1993-04-15

APPLICATION NUMBER: US 07/814,759

FILING DATE: 30-DEC-1991

ATTORNEY/AGENT INFORMATION:

NAME: Stratford, Carol A.

REGISTRATION NUMBER: 34,444

REGISTRATION NUMBER: 34,0960

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERIFICS:

LEMETHE SEA EMBING ACIDS

L
                                                                                                                                                                                                                                                                                                          ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CXIXNOXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CKLKGÓSCSRLMYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-613-400A-19
                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-138-439-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
```

ઠે

; 0

```
Sequence 8, Application US/07789913
Patent No. 5559095
GENERAL INFORMATION:
APPLICANT: Miljanich, George P.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Valentino, Karen L.
APPLICANT: Valentino, Karen L.
APPLICANT: Walentino, Donald H.
TITLE OF INVENTION: Ischemia-Related Neuronal Damage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 64.2%; Score 77; DB 1; Length 26; Best Local Similarity 34.6%; Pred. No. 0.65; Matches 9; Conservative 12; Mismatches 5; Indels
                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: P43.0A
COMPUTER: F10.0PY disk
COMPUTER: F10.0PY disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: Patentin Pcl-Bos/Ms-Dos
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/789,913
FILING DATE: 19911112
CLASSIFICATION NUMBER: US 07/561,766
FILING DATE: 02-AUG-1990
PRIOR APPLICATION NUMBER: US 07/440,094
FILING DATE: 22-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0005.30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                Ouery Match 67.5%; Score 81; DB 3; Best Local Similarity 34.6%; Pred. No. 0.29; Matches 9; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Law Offices of Peter Dehlinger STREET: 350 Cambridge Avenue, Suite 300 CITY: Palo Alto STATE: CA
                                  HYPOTHETICAL: NO
HORGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
US-09-392-979A-19
                                                                                                                                                                                                                                                                          1 CXIXNOXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 26 amino acide
            MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE: INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                     JS-07-789-913-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-07-789-913-8
                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19, Application US/09392979A

Patent No. 6136786

GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN'
APPLICANT: GOHIL, KISHOR C
APPLICANT: WALENTINO, KAREN L
APPLICANT: WALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: BETANCHOS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENTANCHO OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Deblinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIE: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRATI APPLICATION DATA:
APPLICATION NUMBER: US/09/392,979A
                                                                                                                                                                                                                                                                                                                                                                                                                          67.5%; Score 81; DB 3; 34.6%; Pred. No. 0.29; tive 13; Mismatches
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
TELEPAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFCATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-04-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                         ; INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
US-09-298-017-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CXIXNOXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CKLKGQSCSRLMYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 67.57
Best Local Similarity 34.67
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                    26 amino acids
                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 350 Camb
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                         HYPOTHETICAL: NORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-392-979A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

ö

Gaps

```
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,847
FILING DATE: 27-JUN-1995
CLASSIFICATION: 514
ATTOMNEY/AGENT INFORMATION:
NAME: Stratford, Carol A
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.31
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.2%; Score 77; DB 1; 34.6%; Pred. No. 0.65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE US-08-496-847-8
             APPLICANT: Kristipati, Ramasharma
TITLE OF INVENTION: METHODS AND
TITLE OF INVENTION: FORMULATIONS FOR PREVE
CORRESPONDENCE 306
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 64.2%; Score 77; DB Best Local Similarity 34.6%; Pred. No. 0.65 Matches 9; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CKLKGOSCRKTSYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/08742774; Patent No. 5824645; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: Patentin Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEBAX: 650-12. U.S. INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: 5 FUNCTH: 26 aming acids
                                                                                                                                                                               STATE: CA
COUNTRY: US
ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-742-774-8
APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                 APPLICANT: SINCH, TELINDER

APPLICANT: GSHILL, KISINDER

APPLICANT: GOHLL, KISHOR C

APPLICANT: VALENTINO, KAREN L

APPLICANT: MILJANICH, GEORGE P

TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND

TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND

TITLE OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Off:

STREPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.2%; Score 77; DB 1; Length 26; 34.6%; Pred. No. 0.65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/049,794
FILING DATE: 19930415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORIGINAL SOURCE:
individual ISOLATE: SVIB/SNX-183, FIGURE 1
US-08-04-794-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APLIANCE DATE: 19930415
CLASSIFICATION: 514
PRIOR APPLICATION DATA: 07/814,759
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTONNEY/AGENT INFORMATION: NAME: Stratford, Carol A. REGISTRATION NUMBER: 34,444
REPERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Mismatches
                   1 CXIXNOXCXQXLDDCCSXXCNXXNXC 26
                                           1 CKLKGQSCRKTSYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/08049794
Patent No. 5587454
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-08-496-847-8
; Sequence 8, Application US/08496847
; Patent No. 5795864
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amstutz, Gary A.
Bowersox, Stephen S.
Gohil, Kishorchandra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Palc
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
```

```
herhods and Perventing Progression of Neuropathic Pain FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR
APPLICANT: WILDANICH, GEORGE P
TITLE OF INVENTION: METHADS OF PRODUCING ANALGESII
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patentin Release #1.0, Version #1.25
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: America. Gary A.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Gondal, Kishorchiandra
APPLICANT: Gondal, Kishorchiandra
APPLICANT: Goldansens, Peter I.
APPLICANT: Kristipati, Ramasharma
TITLE OF INVENTION: METHODS AND FORMULATIONS FOR PREVENTING
TITLE OF INVENTION: PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSE: Dellinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IEBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASESEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,918
FILING DATE: 07-NOV-1997
CLASSIFICATION: 514
ATTOMES/AGENT INFORMATION:
NAME: Mohr, Judy M.
REGISTRATION NUMBER: 38,563
REFERENCE/DOCKET NUMBER: 5865-0009.34
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 34.6%; Pred. No. 0.65;
Matches 9; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE
                                              REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CXIXNOXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/08965918
Patent No. S891849
GENERAL INFORMATION:
                                                                                                                                           (415) 324-0880
                                                                                                                                       TELEPHONE: (415) 324-08
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                        : 26 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US
ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-675-354-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-965-918-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SINGH, TEJINDER
APPLICANT: SINGH, TEJINDER
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: 34
CORRESPONDENCES: 34
CORRESPONDENCES: 34
CORRESPONDENCES: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

64.2%; Score 77; DB 2;
Best Local Similarity 34.6%; Pred. No. 0.65;
Matches 9; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
US-08-742-774-8
                                                           FILING DATE:
CLASSIFICATION
CLASSIFICATION
PRIOR PAPLICATION DATA:
PRIOR PAPLICATION NUMBER: 08/675,354
FILING DATE: 03-JUL-1996
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1933-APR-15
APPLICATION NUMBER: US/08/049,794
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERNENCE/OCKET NUMBER: 34,686
REQUENCE CHARACTERISTICS:
REQUENCE CHARACTERISTICS:
REQUENCE CHARACTERISTICS:
REQUENCE CHARACTERISTICS:
REQUENCE CHARACTERISTICS:
REDERIFORMATION FOR SEQ ID NO:
REDERIFORMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CKLKGÓSCRKTSYDCCSGSCGRSGKC 26
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRÍOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATÉ: 1993.APR-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/08675354
Patent No. 5859186
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINCH, TEJINDER
APPLICANT: GOHILL, KISHOR C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
MOLEGULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
```

à g

```
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-613-400A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                             ö
                                             Gaps
                                             .
0
                                                                                                                                                                                                                APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: WALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSE: LAW OFF:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 34.6%; Pred. No. 0.65;
Matches 9; Conservative 12; Mismatches 5; Indels
Query Match '64.2%; Score 77; DB 2; Length 26; Best Local Similarity 34.6%; Pred. No. 0.65; Matches 9; Conservative 12; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/138,439
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 1993-04-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
APTING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRANION NUMBER: 34444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELEPHONE: (415) 324-0880
TELEPHONE: (415) 324-0880
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                           1 CKLKGOSCRKTSYDCCSGSCGRSGKC 26
                                                                                   1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | ::: |:|::: | | | | | | :: | :: | CKLKGQSCRKTSYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94306
COMPUTER READMELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                           US-09-138-439-8
; Sequence 8, Application US/09138439
Patent No. 5994305
; GENERAL INFORMATION:
APPLICANT: USINGE
APPLICANT: GOHIL, KISHOR C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 26 cmc
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 19
US-08-613-400A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                          유
```

; Sequence 8, Application US/08613400A

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jesus 17-8

Sequence 8, Application US/09298017

Patent No. 6087091

GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: GOHIL, KISHOR C
APPLICANT: GOHIL, KISHOR C
APPLICANT: WALENTION, KAREN L
APPLICANT: WALENTION RETHONS OF PRODUCING ANALGESIA
TITLE OF INVENTION: BENHANCING OPIATE ANALGESIA
TITLE OF INVENTION: BENHANCING OPIATE ANALGESIA
CORRESPONDENCES: 34
CORRESPONDENCE: Jaw Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 34.6%; Pred. No. 0.65;
Matches 9; Conservative 12; Mismatches 5; Indels
APPLICANT: Bowersox, S. Scott
APPLICANT: Gadbois, Theresa
APPLICANT: Gadbois, Theresa
APPLICANT: Luther, Mark, R.
TITLE OF INVENTION: IMPROVED EPIDURAL
TITLE OF INVENTION: METHOD OF PRODUCING ANALGESIA
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/613,400A
FILING DATE: 08-MAR-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
                                                                                                                                                                                   ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 34,444
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0019
TELECOMMUNICATION:
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                ZIP: 94306-1546
ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Dieter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 650-324-0960 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
```

```
Sequence 18, Application US/08185432

Sequence 18, Application US/08185432

Patent No. 5750652

GENERAL INFORMATION:

APPLICANT: Arcavania-Tsakonas, Spyridon

APPLICANT: Diederich, Robert J.

APPLICANT: Matsuno, Kenji

TITLE OF INVENTION: DELFEX PROTEINS, NUCLEIC ACIDS, AND

TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: PENNIE & EDMONDS

STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: FERNIE & EDWONDS
STREET: New York
CITY: New York
CITY: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE: 21-JAN-1994
CLASSIFICATION: S30
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 7326-006
TELECOMMUNICATION NUMBER: 7326-006
TELECOMMUNICATION NUMBER: 7326-006
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
64.2%; Score 77; DB 3;
Best Local Similarity 34.6%; Pred. No. 0.65;
Matches 9; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANGINAL SOURCE:
INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
           FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEPANE: (415) 324-0880
TELEPAN: (415) 324-0860
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 minno acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
US 07/814,759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2523 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                US-09-392-979A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-185-432-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/09392979A
; Sequence 8, Application US/09392979A
; Patent No. 6156786
; GENERAL INFORMATION:
APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: WALENTINO, KAREN L
APPLICANT: WALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: BETHODS OF PRODUCING ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSES: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Sulte 300
CITY: Palo Alto
STATE: CA
ZIP. ALLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64.2%; Score 77; DB 3; Length 26; 34.6%; Pred. No. 0.65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Indels
         ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOCOMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/298,017
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/392,979A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,44
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELEPHONE: (415) 324-0860
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CXIXNQXCXQXLDDCCSXXCNXXNXC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CKLKGQSCRKTSYDCCSGSCGRSGKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
RIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-04-15
                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 34.64
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 26 am. TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-298-017-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

```
ZIP: 94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-049-794-29
                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  유
                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Attavanis-Teakonas, Spyridon
APPLICANT: Oi, Hullin
TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
FILE REFERENCE: 7326-046
FILE REFERENCE: 1997-07-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 2523
                              Gaps
                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                               ö
60.0%; Score 72; DB 1; Length 2523; 34.6%; Pred. No. 1.1e+02; ive 12; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.0%; Score 72; DB 4; Length 2523; 34.6%; Pred. No. 1.1e+02; tive 12; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   Length 2523;
                                                                                                                                                                                                                                                                                                                                                                                                                               5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  60.0%; Score 72; DB 4; 1 34.6%; Pred. No. 1.1e+02; ive 12; Mismatches 5,
                                                                       247 GFSGQNCEENIDDCPSNNCRNGGTCV 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247 GFSGQNCEENIDDCPSNNCRNGGTCV 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 GFSGONCEENIDDCPSNNCRNGGTCV 272
                                                       2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 XIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21, Application US/08049794; Patent No. 5587454
                                                                                                                           RESULT 23
US-08-899-212-3
'Sequence 3, Application US/08899232
'Parent No. 6436650
Query Match
Best Local Similarity 34.61
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 34.6
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Xenopus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Xenopus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 25
US-08-049-794-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 2523
                                                                                                                                                                                                                                                                                                                                                                      US-08-899-232-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-121-457-3
                                                       ò
                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: 7
; TOCATION: 7
j. OTHER INFORMATION: /note= "where X is hydroxyproline"
182-08-049-794-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 29, Application US/08049794

Patent No. 5587454

GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: GOHIL, KISHOR C
APPLICANT: WALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KLSHOR C
APPLICANT: VALENTINO, KESHOR L
APPLICANT: VALENTINO, REORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: BNHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS: ADDRESSE: LAW Offices of Peter Deblinger
                                                                                                                                                                                                                                                                                                                                                                       CURPLIANT TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 19930415
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REFERENCE/POCKET NUMBER: 5865-0009.30
TELEPHONE: (415) 324-0880
TELEPHONE: APACTRIKITICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; DB 1;
                                                                                                                                                                                                   E: Law Offices of Peter Dehlinger
350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

Sect 69; DB

Best Local Similarity 34.6%; Pred. No. 3.4;

Matches 9; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNX-231, FIGURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                STREET: 350 Camb
CITY: Palo Alto
STATE: CA
```

```
Sequence 29, Application US/08496847

Sequence 29, Application US/08496847

Sequence 29, Application US/08496847

GENERAL INFORMATION:
APPLICANT: Ametutz, Gary A.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Advisensens, Peter I.
APPLICANT: Kristipati, Ramasharma
TITLE OF INVENTION: PORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Defilinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 ST.5%; Score 69; DB 1; Length 26; 11 strity 34.6%; Pred. No. 3.4; Conservative 11; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 7
CTHER INFORMATION: /note= "where X is hydroxyproline"
US-08-496-847-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COPERATING SYSTEM: DOS
COPERATING SYSTEM: DOS
SOFTWARE: FastESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,847
FILING DATE: 27-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A
REGISTRATION NUMBER: 34,444
REGISTRATION NUMBER: 5865-0009.31
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE: INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
                                                                                                                        5865-0009.31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CKGKGAXCRKTMYDCCSGSCGRRGKC 26
                                                 NAME: Stratford, Carol A
REGISTRATION NUMBER: 34,444
REFERNENCE/DOCKET NUMBER: 5865
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0860
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                     34,444
                          ATTORNEY/AGENT INFORMATION: NAME: Stratford, Carol A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        650-324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JS-08-496-847-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21, Application US/08496847

| Sequence 21, Application US/08496847
| Patent No. 5795864
| GENERAL INFORMATION:
| APPLICANT: Bowersox, Stephen S. APPLICANT: APPLICANT: Adriaensens, Peter I. APPLICANT: Kristipati, Ramasharma | APPLICANT: Kristipati, Ramasharma | APPLICANT: Kristipati, Ramasharma | APPLICANT: Kristipati, Ramasharma | APPLICANT: Kristipati | APPLICANT: MITTLE OF INVENTION: FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN | NUMBER OF SEQUENCES: 36 CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: Deblinger & Associates | SITE T | APPLICANT: C. ATTLE CANTENT: C. ATTLE CANTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57.5%; Score 69; DB 1; Length 26; 30.8%; Pred. No. 3.4; tive 12; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Indels
                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 19930415
CLASSIFICATION: DATA:
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: SELATION CAPOL.A.
REGISTRATION NUMBER: $865-0009.30
TELEPHONE: (415) 324-0860
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING.SYSTEM: DOS
SOFTWARE: FastSEQ.for Windows Version 2.0
JURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,847
FILING DATE: 27-JUN-1995
3: Law Offices of Peter Dealinger 350 Cambridge Avenue, Suits 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
US-08-049-794-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: C.S. COUNTRY: US
ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 30.8*
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM COM
OPERATING..SYSTEM:
                          STREET: 350 cum
                                                                                                                                                         ZIP: 94306
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-496-847-21
                                                                                                                               COUNTRY:
```

ò g

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA AND
TITLE OF INVENTION: BUHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 26;
                                  Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM ITEE: FIODS/WIS-DOS

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

CONTARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/742,774

FILING DATE: 08/675,354

FILING DATE: 193-ARR-15

APPLICATION NUMBER: US/08/049,794

FILING DATE: 193-ARR-15

APPLICATION NUMBER: US/08/049,794

FILING DATE: 30-DEC-1991

APPLICATION NUMBER: 34,444

REGISTRATION NUMBER: 34,0960

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:

LEMETRIC CHARACTERISTICS:

LEMETRIC CAPARACTERISTICS:

LEMETRIC CAPARACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.5%; Score 69; DB 2; ilarity 30.8%; Pred. No. 3.4; Conservative 12; Mismatches
                                  DB 2;
                                  57.5%; Score 69; DB 34.6%; Pred. No. 3.4; Live 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
                                                                                                                                                                                                                                                  1 CKGKGAXCRKTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |: : :|:::: ||||::| :: :|
CKGKGAPCRKTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                   1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 29, Application US/08742774; Patent No. 5824645; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
Query Match
Best Local Similarity 34.6*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 8, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-742-774-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 31
                                                                                                                                                                                                       ઠ
                                                                                                                                                                                                                                                                            유
                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                57.5%; Score 69; DB 1; Length 26; 30.9%; Pred. No. 3.4; tive 12; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21, Application US/08742774

Patent No. 5824645

GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: GOHIL, KISHOR C
APPLICANT: WALENTINO, KAREN L
APPLICANT: MILJANICH, GEDRGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: /note= "where X is hydroxyproline"
US-08-742-774-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/742,774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Law Offices of Peter Dehlinger
350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION
PRIOR APPLICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/675,354
FILING DATE: 03-JUL-1996
APPLICATION NUMBER: US/08/049,794
FILING DATE: 193-APR-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/ABRIT INFORMATION:
ARGISTRATION NUMBER: 34,444
REGISTRATION NUMBER: 34,444
RECISTRATION NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEC
                         ; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
US-08-496-847-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CKGKGAPCRKTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 30.89
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-742-774-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          유
```

```
APPLICANT: Amstutz, Gary A.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Gohil, Kishorchandra
APPLICANT: Gohil, Kishorchandra
APPLICANT: Adriaenssens, Peter I.
APPLICANT: Adriaenssens, Peter I.
APPLICANT: Mistipal, Ramasharma
TITLE OF INVENTION: METHODS AND FORMULATIONS FOR PREVENTING
TITLE OF INVENTION: PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES:
ADDRESSE: Dehlinger & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.5%; Score 69; DB 2; Length 26; 30.8%; Pred. No. 3.4; tive 12; Mismatches 6; Indels
                                 METHODS OF PRODUCING ANALGESIA AND ENHANCING OPIATE ANALGESIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,354
FILING DATE: 03-JUL-1996
CLASSIFICATION NUMBER: US/08/049,794
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-ARR-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 5865-0009.30
TELEPHONE: (415) 324-0860
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 29:
SEQUIENCE CHARACTERISTICS:
CHARACTERISTICS:
CHARACTERISTICS:
CHARACTERISTICS:
                                                                                                                                                        E: Law Offices of Peter Dehlinger
350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
US-08-675-354-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CKGKGAPCRKTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 21, Application US/08965918
Patent No. 5891849
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF
TITLE OF INVENTION: ENHANCING C
MUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Pet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 30.8%
Since 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                 ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                         STREET: 350 Camb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: US
ZIP: 94306-1546
                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-965-918-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                      APPLICANT: JUNGHALLON:
APPLICANT: JUNGH, TEJINDER
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR
APPLICANT: GHIL, KISHOR
APPLICANT: WILJANICH, GEORGE P
TITLE OF INVENTION: MITHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: BHANCING OPIATE ANALGESIA AND
TITLE OF INVENTION: BHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.5%; Score 69; DB 2; Length 26; 34.6%; Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: 7; COTHER INFORMATION: /note= "where X is hydroxyproline" US-08-675-354-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,354
FILING DATE: 03-ULL-1996
CLASSIFICATION NUMBER: US/08/049,794
FILING DATE: 1393-APR-15
APPLICATION NUMBER: US/08/049,794
FILING DATE: 30-DEC-1991
ATPORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 30-DEC-1991
ATPORNEY/AGENT INFORMATION:
NAME: STEATEFORD CAROL A
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELEPHONE: (415) 324-0860
TELEPRANT (415) 324-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CXIXNOXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21, Application US/08675354
Patent No. 5859186
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 29, Application US/08675354
Patent No. 5859186
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JUSTICE, ALAN
SINGH, TEJINDER
GOHIL, KISHOR C
VALENTINO, KAREN L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-675-354-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
```

```
TYPE: amino acid
TOPOLOGY: 1:-
    TELEPAONE: 650-324-0880
TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 30.8%
Matches 8; Conservative
                                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94306
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
XX: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 35
US-09-138-439-21
                                                                                                                                                                                                                                           US-08-965-918-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-965-918-29
; Sequence 29, Application US/08965918
; Sequence 29, Application US/08965918
; Parent No. 5891849;
GENERAL INFORMATION:
; APPLICANT: Bowersox, Stephen S.
; APPLICANT: Gonil, Kishorchandra
APPLICANT: Adriaenseens, Peter I.
; APPLICANT: Kristipati, Ramasharma
; TITLE OF INVENTION: METHODS AND FORMULATIONS FOR PREVENTING
; TITLE OF INVENTION: PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 57.5%; Score 69; DB 2; Length 26; Best Local Similarity 34.6%; Pred. No. 3.4; Matches 9; Conservative 11; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: /note= "where X is hydroxyproline"
               COMPUTER: IBM COMPACLATOR CONFIGURATING SYSTEM: DOS
SOFTWARE: FastSEQ for windows Version 2.0
SOFTWARE: FastSEQ for windows Version 2.0
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,918
FILING DATE: 07-NOV-1997
CLASSIPICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MOhr, Judy M.
REGISTRATION NUMBER: 38,563
REFERENCE/DOCKET NUMBER: 5865-0009.34
FELECOMMUNICATION INFORMATION:
TELEFAX: 650-324-0860
TELEFAX: 650-324-0860
TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: DISKELLE
COMPUTER: IBM Compatible
OPERATING SYSTEM. DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,918
FILING DATE: 07-NOV-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MOMAL: Judy M.
REGISTRATION NUMBER: 38,563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CKGKGAXCRKTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 58
TELECOMMUNICATION INFORMATION:
1: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Modified-site LOCATION: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-965-918-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

```
Gaps
                                                                                                                                                           ö
                                                                                                  57.5%; Score 69; DB 2; Length 26; 30.9%; Pred. No. 3.4; tive 12; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TELINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
ATITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
ITTLE OF INVENTION: ENHANCING OPIATE ANALGESIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/138,439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-04-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELEPHONE: (415) 324-0880
TELEPHONE: (415) 324-0980
TELEPHONE: CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUDKESSEE: Law Offices of Peter Dehlinger STREET: 350 Cambridge Avenue, Suite 300 CITY: Palo Alto
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
                                                                                                                                                                                                            1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                          1 CKGKGAPCRKTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21, Application US/09138439
```

```
Ouery Match 57.5%; Score 69; DB 3; Length 26; Best Local Similarity 34.6%; Pred. No. 3.4; Matches 9; Conservative 11; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; IOCATION: 7
; OTHER INFORMATION: /note= "where X is hydroxyproline"
VIS-08-613-400A-21
                                                                                   Sequence 21, Application US/08613400A

Patent No. 605429

GENERAL INFORMATION:
APPLICANT: Bowersox, S. Scott
APPLICANT: Gadbois, Theresa
APPLICANT: Luther, Robert, R.
TITLE OF INVENTION: IMPROVED EPIDURAL
TITLE OF INVENTION: METHOD OF PRODUCING ANALGESIA
NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Comparible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSENC FOR Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/613,400A
FILING DATE: 08-MAR-1996
CLASSIFICATION 514
PRICR APPLICATION 514
PRICR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INDIVIDUAL ISOLATE: SNX-231, FIGURE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CKGKGAXCRKTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 29, Application US/08613400A Patent No. 6054429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Stratford, Carol A
REGISTRATION NUMBER: 34,444
REFRENCE/DOCKET NUMBER: 5865
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0860
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bowersox, S. Scott
Gadbois, Theresa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pettus, Mark, R.
Luther, Robert, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Bowersoy
APPLICANT: Gadbois,
APPLICANT: Pettus,
APPLICANT: Luther,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                ns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-613-400A-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.5%; Score 69; DB 2; Length 26; 30.8%; Pred. No. 3.4; tive 12; Mismatches 6; Indels
                                                                                                                Query Match 57.5%; Score 69; DB 2; Length 26; Best Local Similarity 34.6%; Pred. No. 3.4; Matches 9; Conservative 11; Mismatches 6; Indels
; NAME/KEY: Modified-site
; LOCATION: 7
; CIMER INFORMATION: /note= "where X is hydroxyproline"
US-09-138-439-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRODUCING ANALGESIA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/138,439
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: WALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGI
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 1993-04-15
APPLICATION NUMBER: US/08/049,794
FILING DATE: 3-0-EC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
                                                                                                                                                                                                             1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                       1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                 Sequence 29, Application US/09138439
Patent No. 5994305
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 30.8%
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                   US-09-138-439-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-138-439-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                           RESULT 36
                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

. 0

```
.
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 57.5%; Score 69; DB 3; Length 26; Best Local Similarity 34.6%; Pred. No. 3.4; Matches 9; Conservative 11; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: /note= "where X is hydroxyproline" US-09-298-017-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METHODS OF PRODUCING ANALGESIA AND ENHANCING OPIATE ANALGESIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZUCHINIA CONTINUE READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/298,017
     Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 29, Application US/09298017
Sequence 29, Application US/09298017
Patent No. 6087091
APPLICANT: JUSTICE, ALAN
APPLICANT: GOHIL, KISHOR
APPLICANT: GOHIL, KISHOR C
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALA
TITLE OF INVENTION: SHETHODS OF PRODUCING ANALA
TITLE OF INVENTION: SHETHOD ANALA
TITLE OF INVENTION: SHETHODS OF PRODUCING ANALA
TITLE SHETHODS OF SHETHODS OF PRODUCING
                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/298,017
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,794
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REGISTRATION NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Modified-site LOCATION: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C.
APPLICANT: WILDANICH, GEORGE P.
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
STRPETE STRPETE I LAW OFF:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 57.5%; Score 69; DB 3; Length 26; Best Local Similarity 30.8%; Pred. No. 3.4; Matches 8; Conservative 12; Mismatches 6; Indels
     IMPROVED EPIDURAL
METHOD OF PRODUCING ANALGESIA
                                                                                                                                                                                                                                                                                 CITY:
STATE: CA
COUNTRY: US
ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskettee
COMPUTER: IBM COMPALIBLE
COMPUTER: BASTEM for Windows Version 2.0
SOFTWARE: FastENG for Windows Version 2.0
CURRENTING SYSTEM: DOS
SOFTWARE: FASTENG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/613,400A
FILING DATE: 08-MAR-1996
CLASSIFICATION: 5-14
PRIOR APPLICATION INFORMATION:
FILING DATE: 4144
FRICESTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 34,444
REFERENCE/OCKET NUMBER: 3665-0019
TELEFAX: 650-324-0860
TELEFAX: 650-324-0860
FILIERAY: 650-324-0860
FILIERAY
TITLE OF INVENTION: IMPROVED EPIDURAL
TITLE OF INVENTION: METHOD OF PRODUCING AI
WUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
US-08-613-400A-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |: : : |:::: |||||::| :: :|
CKGKGAPCRKTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94306
COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 21, Application US/09298017
Patent No. 6087091
GENERAL INFORMATION:
APPLICANT: SINGH, TEJINDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 35v
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-298-017-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
```

ઠે 요

```
ORIGINAL SOURCE: INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 29, Application US/09392979A Patent No. 6136786 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
                                                                         NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94306
                                                                                                                                                                                                                                                                                                                                                                           RESULT 42
US-09-392-979A-29
                                                   FEATURE:
                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                  57.5%; Score 69; DB 3; Length 26; 30.8%; Pred. No. 3.4; tive 12; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GENGEP E
ITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
ITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
ADDRESSEE: Law Offices of Peter Dehlinger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/392,979A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEE: Law Offices of Peter Dehlinger: 350 Cambridge Avenue, Suite 300 Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION
PRIOR APPLICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-04-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
MOLECTULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
                      REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
TELEPAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-392-979A-21
; Sequence 21, Application US/09392979A
; Patent No. 6136786
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
REGISTRATION NUMBER: 34,444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 30.89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 25 amino acids
amino acid .
3Y: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                          US-09-298-017-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                      ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.5%; Score 69; DB 3; Length 26; 30.8%; Pred. No. 3.4; cive 12; Mismatches 6; Indels
; LOCATION: 7
; OCATION: /note= "where X is hydroxyproline"
(S-09-392-979A-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/392,979A
FILING DATE:
CLASSIFICATION:
                                                                                              Query Match 57.5%; Score 69; DB 3; Best Local Similarity 34.6%; Pred. No. 3.4; Matches 9; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
US-09-392-979A-29
                                                                                                                                                                                                  1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-04-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
RECISTRATION NUMBER: 34,444
RECISTRATION NUMBER: 5865-0009...
TELECOMMUNICATION INFORMATION:
```

```
GENERAL INFORMATION:
APPLICANT: Artavanis-Teakonas, S. et al.
APPLICANT: Artavanis-Teakonas, S. et al.
TITLE OF INVENTION: Therapeutic And Diagnostic Methods
TITLE OF INVENTION: Therapeutic And Diagnostic Methods
TITLE OF INVENTION: Nucleic Acids
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STRIE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.7%; Score 68; DB 1; Length 2556; 30.8%; Pred. No. 2.4e+02;
                                                                                                                 COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,432
FILING DATE: 21-JAN-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Miscrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-006
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 GFTGQNCEENIDDCPGNNCKNGGACV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-083-590A-20; Sequence 20, Application US/08083590A; Patent No. 5786158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (212) 790-9090
TELEFAX: (312) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2556 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 56.7%;
Best Local Similarity 30.8%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 2556 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-185-432-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17, Application US/08185432

Sequence 17, Application US/08185432

Patent No. 5750652

GENERAL INFORMATION:
APPLICANT: Artavanis-Teakonas, Spyridon
APPLICANT: Busseau, Isabelle
APPLICANT: Busseau, Isabelle
APPLICANT: Mateuno, Kenji
TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND
TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND
TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS: 23
CORRESPONDENCE ADDRESS:
STREET: 1155 Avenue of the Americas
CITY: New York
CERTAN OF AUTORITY AND ADDRESSES AND COMPOSITIONS
CORRESPONDENCE ADDRESSES AND COMPOSITIONS
CORRESPONDENCE ADDRESSES AND COMPOSITIONS
CORRESPONDENCE ADDRESSES AND COMPOSITIONS
CORRESPONDENCE ADDRESSES AVENUE & EDWONDS
CORRESPONDENCE ADRESSES AVENUE & EDWONDS
CORRESPONDENCE ADDRESSES AVENUE & EDWONDS
CORRESPONDENCE ADDRESSES AVENUE & EDWONDS
CORRESPONDENCE ADDRES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 57.5%; Score 69; DB 1; Length 29; Best Local Similarity 30.8%; Pred. No. 3.7; Matches 8; Conservative 12; Mismatches 6; Indels
                                                                                                                                                                                                                                            APPLICANT: Olivera, Baldomero M.
APPLICANT: Hillyard, David R.
APPLICANT: Imperial, Julita S.
APPLICANT: Imperial, Julita S.
APPLICANT: Monje, Virginia D.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W., Suite 1000
CITY: Washington
STREE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 2005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/092,215
FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107674
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
   1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                             1 CKGKGAPCRKTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 CKGKGAPCRKTMYDCCSGSCGRRGKC 28
                                                                                                                                                                                                               Sequence 9, Application US/08092215; Patent No. 5591821; GENERAL INFORMATION: APPLICANT: Hillyard, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 202-902 DINORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-08-092-215-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-185-432-17
      ò
                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
```

Gaps

ö

6; Indels

```
SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
US-08-899-232-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 2556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JS-09-121-457-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-121-457-2
                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT Artenants-Tsakonas, S. et al.
ATILE OF INVENTION: Therapeutic And Diagnostic Methods
TITLE OF INVENTION: And Compositions Based On No. 6083904ch Proteins And
TITLE OF INVENTION: Nucleic Acids
                                                                                                                                                                  Gaps
                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ·
0
                                                                                                                    Query Match 56.7%; Score 68; DB 1; Length 2556; Best Local Similarity 30.8%; Pred. No. 2.4e+02; Matches 8; Conservative 12; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3; Length 2556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/532,384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56.7%; Score 68; DB 30.8%; Pred. No. 2.4e tive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:

CLASCIFICATION 1424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/083,590

FILING DATE: 25-JUN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Misrock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 7326-015

TELECOMMUNICATION INFORMATION:

TELESCOMMUNICATION INFORMATION:

TELESA: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 2556 amino acids
                                                                                                                                                                                                                           248 GFTGQNCEENIDDCPGNNCKNGGACV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :: |:|::::|| | ::| | | GFTGQNCEENIDDCPGNNCKNGGACV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                    2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                              Sequence 20, Application US/08532384 Patent No. 6083904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 47
US-08-899-232-2
; Sequence 2, Application US/08899232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 30.89
Matches 8; Conservative
          STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New York
Y: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                        ; TOPOLOGY:
; MOLECULE TYPE
US-08-083-590A-20
                                                                                                                                                                                                                                                                                                      RESULT 46
US-08-532-384-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-532-384-20
                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               요
```

```
| APPLICANT OF LANDARD CORNS OF NOTCH AND METHODS BASED THEREON TITLE OF INVESTIGAT ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON TITLE OF INVESTIGAT ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON TITLE OF INVESTIGATION NOMBER, US/08/899,232 | WINDERS OF SEQ ID NOS; 437-17-23 | SCOTE 68; DB 4; Length 2556; SEQ ID NOS; 437-17-23 | SCOTE 68; DB 4; Length 2556; SEQ ID NOS; 437-17-23 | SCOTE 68; DB 4; Length 2556; SEQ ID NOS; 437-17-23 | SCOTE 68; DB 4; Length 2556; SEQ ID NOS; 437-17-23 | SCOTE 68; DB 4; Length 2556; SEG ID NOS; 437-17-23 | SCOTE 68; DB 4; Length 2556; SEG ID NOS; 437-17-23 | SCOTE 68; DB 4; Length 2556; SEG ID NOS; 437-17-23 | SCOTE 68; DB 4; Length 2556; SEG ID NOS; 437-17-23 | SCOTE 68; DB 4; Length 2556; SEG ID NOS; 437-17-23 | SCOTE 68; DB 4; Length 2556; SEG ID NOS; 437-17-23 | SCOTE 68; DB 4; Length 2556; SEG ID NOS; 437-17-23 | SCOTE 68; DB 4; Length 2556; SEG ID NOS; 437-17-23 | SCOTE 68; DB 4; Length 2556; SEG ID NOS; 447-17-23 | SCOTE 68; DB 4; Length 2556; SEG ID NOS; 447-17-23 | SCOTE 68; DB 4; Length 2556; SEG ID NOS; 447-17-23 | SCOTE 68; DB 4; Length 2556; SEG ID NOS; 447-17-23 | SCOTE 68; DB 4; Length 2556; SEG ID NOS; 447-17-23 | SCOTE 68; DB 4; Length 2556; SEG ID NOS; 447-17-23 | SCOTE 68; DB 4; Length 2556; SEG ID NOS; 447-17-23 | SCOTE 68; DB 4; Length 2556; SEG ID NOS; 447-17-23 | SCOTE 68; DB 4; Length 2556; SEG ID NOS; 447-17-23 | SCOTE 68; DB 4; Length 2556; SEG ID NOS; 447-17-23 | SCOTE 68; DB 4; Length 2556; SEG ID NOS; 447-17-23 | SCOTE 68; DB 4; Length 2556; SEG ID NOS; 447-17-23 | SCOTE 68; DB 4; Length 2556; SEG ID NOS; 447-17-23 | SCOTE 68; DB 4; Length 2556; SEG ID NOS; 447-17-23 | SCOTE 68; DB 4; Length 2556; SEG ID NOS; 457-17-3 | SCOTE 68; DB 4; Length 2556; SEG ID NOS; 653-17-457-2 | SCOTE 68; DB 4; Length 2556; SEG ID NOS; 653-17-457-3 | SCOTE 68; DB 4; Length 2556; SEG ID NOS; 653-17-457-3 | SCOTE 68; DB 4; Length 2556; SEG ID NOS; 653-17-457-3 | SCOTE 68; DB 4; Length 2556; SEG ID NOS; 653-17-457-3 | SCOTE 68; DB 4; SCOTE 68; DB 4; SCOTE 68; DB 4;
```

Length 721;

```
/ Match 55.0%; Score 66; DB 3; I
Local Similarity 32.0%; Pred. No. 1.2e+02;
nes 8; Conservative 11; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOCTUMARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,392
FILING DATE: 22-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                    36 GFSGRNCDDNLDDCTSFPCQNGGTC 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36 GFSGRNCDDNLDDCTSFPCQNGGTC 460
                                                                                                                                                                                                                        2 XIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 XIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/08981392; Patent No. 6262025; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-908-322-5 ; Sequence 5, Application US/09908322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Antler, Adriane M.
REGISTRATION NUMBER: 32,605
REFERENCE, POCKET NUMBER: 73
TELECOMMUNICATION INFORMATION:
TELECHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 721 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                         TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: peptide US-08-981-392-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                      RESULT 52
US-08-981-392-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                   ; MOLECULE T
US-08-872-855-7
                                                                                                                                    Query Match
                                                                                                                                                       Best Loc
Matches
                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ે
                                                                 ö
                                                                                                                                                                                                                                                                                                                                   APPLICANT: Homburger et al.
TILLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
UNRENT APPLICATION NUMBER: US/09/270,767
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PERCENTIN VET: 2.0
                                                                 Gaps
                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/08872855;
Patent No. 6121045;
GENERAL INFORMATION:
APPLICANT: McCarthy, Sean
APPLICANT: Gearing, David
TITLE OF INVENTION: THERAPEUTIC USES THEREFOR
TITLE OF INVENTION: THERAPEUTIC USES THEREFOR
CORRESPONDENCES: 23
CORRESPONDENCES: 23
CORRESPONDENCES: 40654, HOAG & ELLOT LLP
STREET: One Post Office Square
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 321;
                    DB 4; Length 321;
                                                              5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: FILOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN RElease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,855
FILING DATE: 11-UN-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                  Query Match 55.0%; Score 66; DB Best Local Similarity 33.3%; Pred. No. 58; Matches 8; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.0%; Score 66; DB ilarity 33.3%; Pred. No. 58; Conservative 11; Mismatches
                                                                                                                                    :::|:::|| |::|::||
165 TGKNCQHTIDDCASNPCQHGATCV 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :::|:::|| |::||
165 TGKNCQHTIDDCASNPCQHGATCV 188
                                                                                                                                                                                                                      RESULT 50
US-09-270-767-48979
Sequence 48979, Application US/09270767
Pacent No. 6703491
GENERAL INFORMATION:
                                                                                                           4 XNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 XNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT (CREANISM: Drosophila melanogaster US-09-270-767-48979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MALE
TELECOMMUNICATION INFORMATION
TELECHONE: 617-832-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 48979
LENGTH: 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 51
US-08-872-855-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                     엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ish-Horowicz, David
APPLICANT: Henrique, Domingos Manuel Pinto
APPLICANT: Henrique, Domingos Manuel Pinto
APPLICANT: Lewis, Julian
APPLICANT: Artavanie-Teakonas, Spyridon
APPLICANT: Artavanie-Teakonas, Spyridon
APPLICANT: Gray, Grace
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match. 55.0%; Score 66; DB 3; Lei
Best Local Similarity 32.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 11; Mismatches 6;
```

```
1 CXIXN----OXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Therapeutic And Diagrams of Invention: And Compositions Bas TITLE OF INVENTION: Mucleic Acids NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS: ADDRESSE: Pennie & Edmonds STREET: 1155 Avenue of the Americas CITY: New York STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-083-590A-19; Sequence 19, Application US/08083590A; Patent No. 5786158; GENBRAL INFORMATION: APPLICANT: Artavanis-Tsakonas, S. et al.
                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 2471 amino acids amino acids
                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 25.8<sup>†</sup>
Matches 8<sup>‡</sup> Conservative
ZIP: 10036-2711
COMPUTER REDABLE FORM:
MEDIUM TYPE: Flore:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-185-432-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                    TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF VERTEBRATE DELTA GENE AND METHODS BASED THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xu, Tian
Matsuno, Kenji
NVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND
NVENTION: ATTIBODIES, AND RELATED METHODS AND COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 55.0%; Score 66; DB 4; Length 721; Best Local Similarity 32.0%; Pred. No. 1.2e+02; Matches 8; Conservative 11; Mismatches 6; Indels
      GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ISh-Horowicz, David
Henrique, Domingos Manuel Pinto
Lewis, Ullian Hart
Artavanis-Tsakonas, Spyridon
                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/09/908,322
FLING DATE: 17-Jul-2001
CLASSIFICATION: ¢UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Artavanis-Tsakonas, Spyridon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
;
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-908-322-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3: PENNIE & EDMONDS
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     436 GFSGRNCDDNLDDCTSFPCONGGTC 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 XIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 73:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 16, Application US/08185432
Patent No. 5750652
GENERAL INFORMATION:
APPLICANT: Artavanis-Tsakonas, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 721 amino acids
TYPE: amino acid
STRANDEDNESS: «Unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Busseau, Isabelle
Diederich, Robert J.
                                                                                                                                                                                                                                                                                                                                        ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2:
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & I
STREET: 1155 Avenue of
                                                                                                                                                                                                                                                                               CITY: New York
                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 54
US-08-185-432-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
```

```
Therapeutic And Diagnostic Methods
And Compositions Based On No. 5786158ch Proteins And
Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.0%; Score 66; DB 1; Length 2471; 25.8%; Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/083,590A
FILING DATE: 25-JUN 1993
CLASSIFICATION: 435
ATTONNEY/AGENT INPORMATION:
NAME: MASTOCK, S. Lealie
REGISTRATION NUMBER: 18,872
REPERENCE/DOCKET NUMBER: 18,872
REPERENCE/DOCKET NUMBER: 13,66-015
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE: 21-JAN-1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Misrock, S. Leslie

REGISTRATION NUMBER: 18,872

REGISTRATION NUMBER: 18,872

REGISTRATION NUMBER: 18,872

TELEPROM/NICATION INFORMATION:

TELEPAS: (212) 790-9090

TELEPAS: (212) 790-9090

TELEPAS: (212) 790-9090

TELEPAS: 6614 PENNIE

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     324 CVCVNGWSGDDCSENIDDCAFASCTPGSTCI 354
```

```
Sequence 1, Application US/08899232
                                                                                                                                                                                                                      SEQ ID NO 1
LENGTH: 2471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-185-432-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 58
US-09-121-457-1
                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ä
                                                                                                                                                                                                                                                                                                                                                    US-08-532-384-19

Sequence 19, Application US/08532384

Sequence 19, Application US/08532384

GENERAL INFORMATION:

APPLICANT: Artavanis-Tsakonas, S. et al.

TITLE OF INVENTION: Therapeutic And Diagnostic Methods

TITLE OF INVENTION: And Compositions Based On No. 6083904ch Proteins And

TITLE OF INVENTION: Nucleic Acids

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.
                                                                                                                                              Length 2471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.0%; Score 66; DB 3; Length 2471; 25.8%; Pred. No. 3.5e+02; tive 14; Mismatches 5; Indels
                                                                                                                                                                                     5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: 1BM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/532,384
                                                                                                                                          55.0%; Score 66; DB 1; 725.8%; Pred. No. 3.5e+02; tive 14; Mismatches 5
                                                                                                                                                                                                                                                    324 CVCVNGWSGDDCSENIDDCAFASCTPGSTCI 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    324 CVCVNGWSGDDCSENIDDCAFASCTPGSTCI 354
                                                                                                                                                                                                                            1 CXIXN----OXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 55.0%; Score bb; UD Best Local Similarity 25.8%; Pred. No. 3.5e Matches 8; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CXIXN----QXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION NAMES: US/US/322,354
FRIOR APPLICATION 1424
FRIOR APPLICATION DATE:
APPLICATION NUMBER: 08/083,590
FILING DATE: 25-UN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-015
TELECHONE: 212 790-9090
TELECHONE: 212 790-9090
TELEFAX: 212 869864/9741
TELEFAX: 212 869864/9741
FILERAX: 66141 PENIE
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 2471 amino acids
2471 amino acids
                                                                                                                           Query Match
Best Local Similarity 25.89
                                         single
                                                            ; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-083-590A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sir
                     TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-532-384-19
                                                                                                                                                                                                                                                                                                                                    RESULT 56
                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                 ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
```

RESULT 57 US-08-899-232-1

```
APPLICANT: Busseau, Isabelle
APPLICANT: Diederich, Robert J.
APPLICANT: Xu, Tian
APPLICANT: Matsuno, Kenji
TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND
TITLE OF INVENTION: ATTIBODIES, AND RELATED METHODS AND COMPOSITIONS
Patent No. 6436650

APPLICANT: ATLANATION:
APPLICANT: Qi, Huilin
TITLE OF INVENTATION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
FITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
FILE REFERENCE: 7326-046
CURRENT APPLICATION NUMBER: US/08/899,232
NUMBER OF SEQ ID DATE: 1997-07-23
SOFTWARE: PATENT VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Artavanis-Teakonas, S.
APPLICANT: Artavanis-Teakonas, S.
APPLICANT: Qi, H.
APPLICANT: Raid, M.
TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH. AND METHODS BASED THEREON FILE REFERENCE: 7326-073
CURRENT APPLICATION NUMBER: US/09/121,457
CURRENT FILING DATE: 1998-07-23
EARLIER APPLICATION NUMBER: 08/899,232
EARLIER FILING DATE: 1997-07-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 2471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 2471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 55.0%; Score 66; DB 4; Le
Best Local Similarity 25.8%; Pred. No. 3.5e+02;
Matches 8; Conservative 14; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        324 CVCVNGWSGDDCSENIDDCAFASCTPGSTCI 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  324 CVCVNGWSGDDCSENIDDCAFASCTPGSTCI 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CXIXN----QXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CXIXN----QXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 55.0%; Score 66; DB Best Local Similarity 25.8%; Pred. No. 3.5e Matches 8; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19, Application US/08185432
Patent No. 5750652
GENERAL INFORMATION:
APPLICANT: Artavanis-Tsakonas, Spyridon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDNONDS
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09121457
Patent No. 6692919
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
US-08-899-232-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
CRGANISM: Homo sapiens
US-09-121-457-1
```

ó

.; 0

Length 2703;

```
APPLICANT: Rand, M.
TILLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON FILE REFERENCE: 7326-073
CURRENT APPLICATION NUMBER: US/09/121,457
CURRENT FILING DATE: 1998-07-23
EARLIER APPLICATION NUMBER: 08/899,232
RARIER FILING DATE: 1997-07-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 55.0%; Score 66; DB 4; Length 270 Best Local Similarity 29.2%; Pred. No. 3.8e+02; Matches 7; Conservative 12; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INPORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Shetty, Reshma
APPLICANT: Mained
APPLICANT: Mained
APPLICANT: Mained
APPLICANT: Mained
APPLICANT: Matkins, Maren.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    822 TGQKCETNIDDCVTNPCGNGGTCI 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 XNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 168, Application US/09894882
Patent No. 6767895
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Drosophila sp.
US-09-121-457-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 62
US-09-894-882-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INPORMATION:
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Q1, Hullin
TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
CURRENT APPLICATION NUMBER: US/08/899,232
CURRENT FILING DATE: 1997-07-23
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J.8e+02;
L.e 5; Indels
                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,432
FILING DATE: 21-JAN-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INPORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REBERENCE/DOCKET UNMBER: 18,872
RESPERENCE/DOCKET UNMBER: 7326-006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.0%; Score 66; DB 1; 1
29.2%; Pred. No. 3.8e+02;
tive 12; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.0%; Score 66; DB 4;
29.2%; Pred. No. 3.8e+02
tive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         822 TGQKCETNIDDCVTNPCGNGGTCI 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : |:|: |:|| :::| :: | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : | : : | : : | : : | : : | : : | : | : : | : | : | : : | : : | : | : | : | : | : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 XNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 XNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-899-232-4; Sequence 4, Application US/08899232; Patent No. 6436650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (212) 790-9000
TELEFAX: (212) 869-8864/9741
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2703 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 29.27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 29.2'
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-08-185-432-19
                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Drosophila sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                           STATE: New York COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 4
LENGTH: 2703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-899-232-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 61
US-09-121-457-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
```

```
DOCATION: (1)...(36)
CTHER INFORMATION: Xaa at residue 10 is Glu or gamma-carboxy-Glu; Xaa at residues 18
OTHER INFORMATION: , 23 and 36 is Tyr, 1251-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulph
US-09-894-882-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
APPLICANT: Jones, Robert M.
APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US 60/
PRIOR PILING DATE: 2001-06-29
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-14
PRIOR PILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PALENTIN VOIGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 54.6%; Score 65.5; Di
Best Local Similarity 44.4%; Pred. No. 9.2;
Matches 12; Conservative 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CXIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Conus betulinus
PEATURE:
NAME/KEY: PEPTIDE
```

Sequence 4, Application US/09121457; Patent No. 6692919; GENERAL INFORMATION: APPLICANT: Artavanis-Tsakonas, S. APPLICANT: Qi, H.

유

```
GapB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                               ä
                                                                                                                                                                                                                                                                                                              DB 4; Length 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Goodman, Corey
APPLICANT: Kid, Thomas
APPLICANT: Kid, Thomas
APPLICANT: Kid, Thomas
APPLICANT: Tessies. Karja
APPLICANT: Tessies. Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REPRESENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/540, 245A
CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 60/065, 544
PRIOR APPLICATION NUMBER: 60/061, 057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Goodman, Corey
APPLICANT: Kid, Thomas
APPLICANT: Kid, Thomas
APPLICANT: Brose, Katja
APPLICANT: Tessler.Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT FILING DATE: 1998-11-13
EARLIER APPLICATION NUMBER: 60/065,544
EARLIER APPLICATION NUMBER: 60/065,544
EARLIER APPLICATION NUMBER: 60/081,057
EARLIER FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 14
SCOTUMENT: PROBLICATION NUMBER: 60/081,057
EARLIER FILING DATE: 1998-04-07
SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 735;
                                                                                                                                                                                                                                                                                                                                                            Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 54.2%; Score 65; DB 3; Best Local Similarity 26.9%; Pred. No. 1.5e+02; Matches 7; Conservative 13; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                       12; Mismatches
                                                                                                                                                                                                                                                                                                              54.6%; Score 65.5; 33.3%; Pred. No. 17
                                                                                                                                                                                                                                                                                                                                                                                                         1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                    248 GFEGDYCEKNIDDCVNSKCENGGKCV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                         PRIOR FILING DATE: 2000-11-14
PRIOR PELLON DATE: 2000-11-14
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: Patentin version 3.0
SEQ ID NO 167
FILING DATE: 2000-11-08
APPLICATION NUMBER: US 60/247,714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/09540245A Patent No. 6270984 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application US/09191647
Patent No. 6046015
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-191-647-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1998-04-07
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 33.34
Matches 9; Conservative
                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Conus betulinus
US-09-894-882-167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JS-09-540-245A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 65
US-09-191-647-9
                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                         APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: McIncosh, J. Michael
APPLICANT: Matkins, Maren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc. APPLICANT: Walker, Craig S. APPLICANT: Shetty, Reshma
                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: 1-Superfamily Conotoxins FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR PELLING DATE: 2000-06-30
PRIOR FILING DATE: 2000-10-37
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/245,410
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-19
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 54.6%; Score 65.5; E
Best Local Similarity 33.3%; Pred. No. 9.2;
Matches 9; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: I-Superfamily Conotoxins FILE REFERENCE: 2314-238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION WUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
2 CLSLGQRCXRH-SDCCGXLCCFXDKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |: : |:|::: ||| ::| ::::|| CLSLGORCERH-SDCCGYLCCFYDKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
                                                                                                              Sequence 369, Application US/09894882
Patent No. 6767895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 167, Application US/09894882
Patent No. 6767895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jimenez, Elsie C.
McIntosh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
                                                                                                                                                                                                                                                                                                                                                                                  Jones, Robert M.
Shen, Greg S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jones, Robert M.
Shen, Greg S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Conus betulinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-894-882-369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-894-882-167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 369
LENGTH: 36
                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
```

ઠે

```
APPLICANT: Mackins, Marken
APPLICANT: Shen, Greg S.
TITLE OF INVENTIONS: 1-Superfamily Conotoxins
FILE REFERENCE: 2314-238
CURRENT APPLICATION INVERE: US/09/894,882
CURRENT APPLICATION NUMBER: US 60/9894,882
CURRENT APPLICATION NUMBER: US 60/9894,882
PRIOR PILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR PILING DATE: 2000-11-08
PRIOR PAPLICATION NUMBER: US 60/246,581
PRIOR PLILING DATE: 2000-11-08
                                                            348 GCEENLDDCAAATCAPGSTCI 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 364, Application US/09894882
Patent No. 6767895
                                                                                                                                                                     US-09-230-652-2
; Sequence 2, Application US/09230652A
; Patent No. 6537775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JS-09-894-882-364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-230-652-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                            qq
                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q
                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-467-997-1

| Sequence 1, Application US/09467997 |
| Sequence 2, Application US/09467997 |
| Parent No. 6379928 |
| Parent No. 6379928 |
| GENERAL INFORMATION: |
| APPLICANT: Kitajewski, Jan |
| APPLICANT: Kitajewski, Jan |
| APPLICANT: Witajewski, Jan |
| TITLE OF INVENTION: ANGIGGENIC MODULATION BY NOTCH SIGNAL TRANSDUCTION |
| FILE REFERENCE: 53863-A-PCT-08 |
| CURRENT FILING DATE: 1999-12-20 |
| NUMBER OF SEQ ID NOS: 10 |
| SEQ ID NO 1 |
| SEQ ID NO 1 |
| LENGTH: 1964 |
| TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFURCALION:
APPLICANT: Goodman, Corey
APPLICANT: Kid, Thomas
APPLICANT: Kid, Thomas
APPLICANT: Brose, Katja
APPLICANT: Bresier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT APPLICATION NUMBER: U5/09/540,153
CURRENT APPLICATION NUMBER: 09/191,647
PRIOR PILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: 60/081,057
PRIOR FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.2%; Score 65; DB 3; Length 1964; 33.3%; Pred. No. 3.5e+02; Live 12; Mismatches 2; Indels
                                                                                                                                                                                      54.2%; Score 65; DB 3; Length 735; 26.9%; Pred. No. 1.5e+02; tive 13; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.2%; (Score 65; DB 3; Length 735; ilarity 26.9%; Pred. No. 1.5e+02; Conservative 13; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                248 GFEGDYCEKNIDDCVNSKCENGGKCV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   248 GFEGDYCEKNIDDCVNSKCENGGKCV 273
                                                                                                                                                                                                                                                                                 2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/09540153
Patent No. 6270995
                                                                                       ; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-540-245A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-540-153-9
                                                                                                                                                                                    Query Match
Best Local Similarity 26.93
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 33.3
Matches 7; Conservative
NUMBER OF SEQ ID NOS: 20 SOFTWARE: Patentin Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: mouse US-09-467-997-1
       SOFTWARE: Pate
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-540-153-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
```

```
APPLICANT: Tournier-lasserve, Elisabeth
APPLICANT: Journier-lasserve, Elisabeth
APPLICANT: Joutel, Anne
APPLICANT: Joutel, Anne
APPLICANT: Bousesr, Marie-Germaine
APPLICANT: Bousesr, Marie-Germaine
APPLICANT: Bousesr, Marie-Germaine
TITLE OF INVENTION: THERAPEUTIC APPLICATION
TITLE OF INVENTION: THERAPEUTIC APPLICATION
FILE REFERENCE: 03715.0048-00000;
CURRENT APPLICATION NUMBER: US/09/230,652A
CURRENT APPLICATION NUMBER: P99-05-17
EARLIER PILING DATE: 1999-05-17
EARLIER PILING DATE: 1999-04-16
EARLIER APPLICATION NUMBER: PCT/FF97/01433
EARLIER RILING DATE: 1997-07-31
NUMBER OF SEQ ID NOS: 163
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: APPLICATION VARIER: PLING DATE: 1997-07-31
NUMBER OF SEQ ID NOS: 163
SOFTWARE: PATENTING DATE: 1997-07-31
NUMBER OF SEQ ID NOS: 163
SOFTWARE: PATENTING DATE: 1997-07-31
NUMBER OF SEQ ID NOS: 163
SOFTWARE: PATENTING DATE: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Shetty, Reshma
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
APPLICANT: Watkins, Maren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.2%; Score 65; DB 4; 30.0%; Pred. No. 4.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: human ADNc No. 6537775ch 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300 CVCVNGWTGESCSQNIDDCATAVCFHGATC 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 30.0%; Pred. No. 4.1e
Matches 9; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CXIXN----OXCXQXLDDCCSXXCNXXNXC 26
```

```
McIntosh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
         Jimenez, Elsie C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Conus magus
US-09-894-882-119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 74
US-09-894-882-324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-341-461-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                      ä
                                                                                                                                                                                                         DB 4; Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 53.8%; Score 64.5; DB 4; Length 35; Best Local Similarity 33.3%; Pred. No. 11; Matches 6; Indels Matches 6; Indels
                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: McIntosh, J. Michael
APPLICANT: Moithesh, Michael
APPLICANT: Matkins, Maren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 119, Application US/09894882
Patent No. 6767895
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: General Mones, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins FILE FERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT APPLICATION NUMBER: US 60/29
PRIOR PILING DATE: 2001-06-29
PRIOR PELLING DATE: 2000-06-30
PRIOR FILING DATE: 2000-10-27
PRIOR PELLING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR PELLING DATE: 2000-11-08
PRIOR PELLING DATE: 2000-11-08
PRIOR PELLING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-09
PRIOR FILING DATE: 2001-11-09
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOSTWARE: PALENTIN VUMBER: US 60/264,256
PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                                     Query Match 53.8%; Score 64.5; I
Best Local Similarity 33.3%; Pred. No. 10;
Matches 9; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                          1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 413, Application US/09894882
Patent No. 6767895
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PatentIn version 3.0
SEQ ID NO 364
                                                                                                                TYPE: PRT
ORGANISM: Conus brunneus
US-09-894-882-364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 413
LENGTH: 35
TYPE: PRT
ORGANISM: Conus magus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-894-882-413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 72
US-09-894-882-119
                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-894-882-413
                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               엄
```

```
| APPLICANT: Watchings, Applications, Applicants, Shean, Grees, M. | Applicants, Shean, Grees, A. | Applicants, Shean, Grees, A. | Applicants, Applica
```

```
ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                  4; Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 52.9%; Score 63.5; DB 4; Length 36; Best Local Similarity 34.6%; Pred. No. 14; Matches 9; Conservative 10; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                  ; LOCATION: (1)..(36); OTHER INFORMATION: Xaa at residue 36 is Pro or hydroxy-Pro US-09-894-882-339
                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: University of Utah Research Foundation
                                                                                                                                                                                                                                                                                                                                                                                        Query Match 52.9%; Score 63.5; DB Best Local Similarity 34.6%; Pred. No. 14; Matches 9; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: 1. Superfeaming FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-10-27
PRIOR PILING DATE: 2000-11-08
PRIOR PRILING DATE: 2000-11-08
PRIOR PILING DATE: 2000-11-4
PRIOR PILING DATE: 2001-11-4
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-01-29
PRIOR FILING DATE: 2001-01-29
SEQ ID NOS: 506
SOFTWARE: Patentin version 3.0
SEQ ID NO 441
LENGTH: 36
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PATENTIN VERSION 3.0
; SEQ ID NO 339
; LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CXIXNOXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |::|:|:|:|:|csrigogcgob-spccgdmccHgolc 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 441, Application US/09894882
Patent No. 6767895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jimenez, Elsie C.
McIntosh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
                                                                                                                                                                                                 TYPE: PRT ORGANISM: Conus episcopatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cognetix, Inc.
Walker, Craig S.
Shetty, Reshma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Conus episcopatus
US-09-894-882-441
                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JS-09-894-882-441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 77
US-09-894-882-443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: PEPTIDE
LOCATION: (1)..(36)
OCHER INFORMATION: Xaa at residue 36 is Pro or hydroxy-Pro; Xaa at residue 23 is Tyr
OTHER INFORMATION: , 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho
OTHER INFORMATION: -Ty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 52.9%; Score 63.5; DB 4; Length 36; Best Local Similarity .38.5%; Pred. No. 14; Matches 10; Conservative 9; Mismatches 6; Indels
          Ourversity of Utah Research Foundation
Cognetix, Inc.
Malker, Craig S.
Shetty, Reshma
Jimenez, Elsie C.
Morlucoh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T: University of Utah Research Foundation
T: Cognetix, Inc.
T: Walker, Craig S.
T: Shetry, Reshma
T: Jimenez, Elsie C.
T: McIntosh, J. Michael
T: Olivera, Baldomero M.
T: Watkins, Maren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TILE OF INVENTION: 1-Superfamily Conotoxins
FILE REFERENCE: 214-218
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR APPLICATION NUMBER: US 60/245,581
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
                                                                                                                                                                                                                   APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
FILE REFERENCE: 2314-238
                                                                                                                                                                                                                                                                                            FILE REFERENCE: 2314-239
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-0-0-7
PRIOR FILING DATE: 2000-10-27
PRIOR PLING DATE: 2000-11-08
PRIOR PLING DATE: 2000-11-4
PRIOR PLING DATE: 2000-11-4
PRIOR PLING DATE: 2000-11-4
PRIOR FILING DATE: 2000-11-4
PRIOR FILING DATE: 2001-10-8
PRIOR FILING DATE: 2001-10-8
PRIOR FILING DATE: 2001-10-8
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PATENTIN VETSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 CSRIGOGCGOD-SDCCGDMCCXGOIC 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 339, Application US/09894882
Patent No. 6767895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Conus episcopatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jones, Robert M.
Shen, Greg S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-894-882-324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -09-894-882-339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

ï

```
;
                                                                                                                                                                                                         DB 4; Length 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 72;
                                                                                                                                                                                                                                                           Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: University of Utah Research Foundation APPLICANT: University of Utah Research Foundation APPLICANT: Walker, Inc. APPLICANT: Walker, Craig S. APPLICANT: Shetty, Reshma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Cartier, G. Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Shetty, kesume
APPLICANT: Jimnez, Elsie C.
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: Markins, Maren
APPLICANT: Markins, Maren
APPLICANT: Shen, Greg S.
ITILE OF INVENTION: I-Superfamily Conotoxins
FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT APPLICATION NUMBER: US 60/29
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR PLILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR SEQ ID NOS: 506
SOFTWARE: Patentin version 3.0
SEQ ID NO 338
LENGTH: 72
                                                                                                                                                                                                                                                        10; Mismatches
                                                                                                                                                                                                      Query Match 52.9%; Score 63.5; I
Best Local Similarity 34.6%; Pred. No. 26;
Matches 9; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
52.9%; Score 63.5; I
Best Local Similarity 34.6%; Pred. No. 26;
Matches 9; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                           1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                        1: |:|:|:|:|:|39 CSRIGQGCGQD-SDCCGDMCCYGQIC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 CSRIGQGCGQD-SDCCGDMCCHGQIC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 207, Application US/09749637A Patent No. 6762165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 338, Application US/09894882
Patent No. 6767895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cognetix, Inc.
Olivera, Baldomero M.
Cartier, G. Edward
Watkins, Maren
NUMBER OF SEQ ID NOS: 506
SOFTWARE: Patentin version 3.0
SEQ ID NO 323
LENGTH: 72
                                                                                                 TYPE: PRT
CORGANISM: Conus episcopatus
US-09-894-882-323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Conus episcopatus
US-09-894-882-338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-749-637A-207
                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-894-882-338
                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                             ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                               APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc. APPLICANT: Walker, Craig S. APPLICANT: Shetty, Reshma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: University of Utah Research Foundation
                                                                                                                                                                                                                                                                      APPLICANT: Gones, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR PELING DATE: 2000-11-08
PRIOR PELING DATE: 2000-11-08
PRIOR FILING DATE: 2001-11-09
PRIOR FILING DATE: 2001-11-09
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Melker, Craig S.
APPLICANT: Sherty, Reshma
APPLICANT: Mimenez, Elsie C.
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: Watkins, Marcin
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: 1. Shen, Greg S.
TITLE OF INVENTION: 1. Shen, Creg S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 52.9%; Score 63.5; I
Best Local Similarity 34.6%; Pred. No. 14;
Matches 9; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 2314-238

CURRENT APPLICATION NUMBER: US/09/894,882

CURRENT FILING DATE: 2001-06-29

PRIOR FILING DATE: 2000-06-30

PRIOR PELING DATE: 2000-06-30

PRIOR PELING DATE: 2000-10-27

PRIOR PELING DATE: 2000-10-27

PRIOR APPLICATION NUMBER: US 60/246,581

PRIOR PELING DATE: 2000-11-08

PRIOR PELING DATE: 2000-11-08

PRIOR PELING DATE: 2000-11-14

PRIOR PELING DATE: 2000-11-14

PRIOR PELING DATE: 2000-11-14

PRIOR PELING DATE: 2000-11-14

PRIOR PELING DATE: 2000-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 CSRIGQGCGQD-SDCCGDMCCHGQIC 27
Sequence 443, Application US/09894882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               // Sequence 323, Application US/09894882
// Patent No. 6767895
                                                                                                                                                                         Jimenez, Elsie C.
McIntosh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Conus episcopatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 78
US-09-894-882-323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBE: Pate
SOFTWARE: Pate
SEQ ID NO 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-894-882-443
                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
```

Gaps

;

```
Sequence 2, Application US/09214278
Fatent No. 6291210
FENERAL INFORMATION:
APPLICANT: Sakano, Seiji
APPLICANT: Itch, Akira
ITIZE OF INVENTION:
FILE REFERENCE: KP-8576
CURRENT APPLICATION NUMBER: US/09/214,278
CURRENT FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
LEWOTH: 1055
TYPE: RET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SAKANO, Seiji
APPLICANT: Itoh, Akira
ITILE OF INVENTION: DIFFRENTIATION-SUPPRESSIVE POLYPEPTIDE
ITILE REFERENCE: KP-8576
CURRENT PILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 09/214,278
PRIOR APPLICATION NUMBER: 09/214,278
NUMBER OF SEQ ID NOS: 32
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
LENGTH: 1055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52.5%; Score 63; DB 3; Length 1055; Alarity 23.1%; Pred. No. 3.18+02; Conservative 13; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1055;
                                                                                                                                                                                                                                                                                                                      Length 585;
                                                                                                                                                                                                                                                                                                           132.5%; Score 63; DB 4; Length 585 ilarity 30.8%; Pred. No. 1.8e+02; Conservative 10; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 52.5%; Score 63; DB 4; Length 105
Best Local Similarity 23.1%; Pred. No. 3.1e+02;
Matches 6; Conservative 13; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   380 GFAGPRCEHDLDDCAGRACANAGTCV 405
                                                                                                                                                                             LOCATION: (1)...(585)
CTHER INFORMATION: Xaa = Any Amino Acid
US-09-641-612-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : : : | : : | | | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 XIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 XIXNOXCXOXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 XIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-855-722-2
; Sequence 2, Application US/09855722
; Patent No. 663841
; GENERAL INPORMATION:
                                           TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
CRGANISM: Homo sapiens
US-09-855-722-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                        FEATURE:
NAME/KEY: VARIANT
          LENGTH: 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-214-278-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-214-278-2
                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-641-612-2

Sequence 2, Application US/09641612

Patent No. 6703221

GENERAL INPORMATION:

APPLICANT:

TILLE OF INVENTION: NOTCH RECEPTOR LIGANDS AND USES THEREOF

FILE REFERENCE: PPO-1602.002 / 200130.458

CURRENT APPLICATION NUMBER: US/09/641,612

CURRENT FILING DATE: 2000-08-17

NUMBER OF SEQ ID NOS: 10

SOCTOR SEQ ID NOS: 10

SOCTOR SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/09641612
| Patent No. 6703221
| GENERAL INFORMATION:
| APPLICANT: Vivien Chan et al.
| TITLE OF INVENTION: NOTCH RECEPTOR LIGANDS AND USES THEREOF
| FILE REPRENCE: PPO-1602.002 / 200130.498
| CURRENT APPLICATION NUMBER: US/09/641,612
| CURRENT PILING DATE: 1000-08-17
| NUMBER OF SEQ ID NOS: 10
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 76; 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.5%; Score 63; DB 4; Length 583 30.8%; Pred. No. 1.8e+02; tive 10; Mismatches 8; Indels
                                                                                  APPLICANT: LOSS. Robert M.
TITLE OF INVENTION: O-Superfamily Conotoxin Peptides
FILE REFERENCE: 2314-227
CURRENT APPLICATION NUMBER: US/09/749,637A
CURRENT FILING DATE: 2000-12-28
FRIOR PAPLICATION NUMBER: US/0/213,412
PRIOR APPLICATION NUMBER: US/0/219,440
PRIOR APPLICATION NUMBER: US/0/219,400
PRIOR APPLICATION NUMBER: US/0/219,263
PRIOR APPLICATION NUMBER: US/0/214,263
PRIOR PRILING DATE: 2000-06-26
PRIOR PELING DATE: 2000-06-26
PRIOR PELING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CXIXNQXCXQXLDDCCSXXCN-XXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | : ::|:|: | | | | | :: | : : : | : CNEAQEHCTQN-PDCCSESCNKFVGRCL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 63;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :::|::|||| ::|::||
378 GFAGPRCEHDLDDCAGRACANGGTCV 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
Hillyard, David R.
McIntosh, J. Michael
Layer, Richard T.
Jones, Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 35.73
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 52.5
Best Local Similarity 30.8
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Conus distans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-749-637A-207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 2
LENGTH: 583
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-641-612-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 82
US-09-641-612-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

ö

Gaps

;

```
538 GFTGTYCHENIDDCLGQPCRNGGTCI 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09566047 Patent No. 6703198 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Li, Linheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
       CORRESPONDENCE ADDRESS:
                                            Abbar-
STREET: 43.v.
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-882-046-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JS-09-566-047-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                 APPLICANT: Henrique, Domingos M.P.
APPLICANT: Henrique, Domingos M.P.
APPLICANT: Lewis, Julian H.
APPLICANT: Mari, Anna M.
APPLICANT: Mari, Anna M.
APPLICANT: Artavanis-Teakonas, Spyridon
APPLICANT: Artavan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.5%; Score 63; DB 2; Length 1065; 23.1%; Pred. No. 3.18+02; tive 13; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Li, Linheng
APPLICANT: Hood, Leroy
APPLICANT: Hood, Leroy
APPLICANT: Spinner, Nancy B.
APPLICANT: Spinner, Nancy B.
TITLE OF INVENTION: Human Jagged Polypeptide, Encoding
TITLE OF INVENTION: Mucleic Acids and Methods of Use
NUMBER OF SEQUENCES: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/400,159
FILING DATE: 07-MAR-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  457 GFTGTYCHENIDDCLGQPCRNGGTCI 482
601 GFTGTYCHENIDDCLGQPCRNGGTCI 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08882046
Patent No. 6136952
GENERAL INFORMATION:
APPLICANT: Li, Linheng
                                                                                                                                                                           Sequence 8, Application US/08400159
Patent No. 5869282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1065 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 23.17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-400-159-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-882-046-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
   쉽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hood, Leroy
Krantz, Ian D.
Spinner, Nancy B.
TITLE OF INVENTION methods of Diagnosing Alagille Syndrome
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 52.5%; Score 63; DB 3; Length 1148; Best Local Similarity 23.1%; Pred. No. 3.3e+02; Matches 6; Conservative 13; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Version #1.25
                                                                                                     COUNTRY: USA
ZIP: 92122
COMPUTER 18ADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,046
FILING DATE: 25-UN-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UW 2637
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 1148 amino acids
"VDF. amino acids
E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
FILING DATE: 05-May-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/882,046
FILING DATE: 25-JUN-1997
ATTORNEY/AGENT INFORMATION:
```

```
13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13; Mismatches
                                                                                                                         627 GFTGTYCHENIDDCLGQPCRNGGTCI 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : : : | : : : | | | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : : | : : : | : : : : | : : : | : : : | : : : : | : : : | : : : : | : : : | : : : : | : : : | : : : : | : : : : | : : : : | : : : : | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : | : : : : | : : : : | : : : 
                                                                         2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/09214278
Patent No. 6291210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/08882046
Patent No. 6136952
GENERAL INFORMATION:
APPLICANT: Li, Linheng
APPLICANT: Hood, Leroy
APPLICANT: Krantz, Ian D.
       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 23.1%
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
US-09-214-278-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 5
LENGTH: 1238
                                                                                                                                                                                                                                                                                        JS-09-214-278-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 92
US-08-882-046-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JS-09-855-722-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-855-722-5
       Matches
                                                                                                                                    g
                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09214278
; Patent No. 6291210
; GENERAL INFORMATION:
; APPLICANT: Sakano, Seiji
; APPLICANT: Icoh, Akira
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
; TITLE REFERENCE: KP-8576
; CURRENT APPLICATION NUMBER: US/09/214,278
; CURRENT FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 32
; SOFWARE: Patentin Ver. 2.1
; SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09855722
| Patent No. 6638741
| Patent No. 6638741
| APPLICANT: INFORMATION: Selji
| APPLICANT: Sakano, Selji
| TITLE OF INVENTION: DIFFERENTIATION-SUPFRESSIVE POLYPEPTIDE
| FILE REFERENCE: KP-8576
| CURRENT FILING DATE: 2001-05-16
| PRIOR FILING DATE: 1999-01-26
| NUMBER OF SEQ ID NOS: 32
| SOFTWARE: PatentIn Ver. 2.1
| SEQ ID NO 3
| LENGTH: 1212
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 52.5%; Score 63; DB 4; Length 1148; Best Local Similarity 23.1%; Pred. No. 3.3e+02; Matches 6; Conservative 13; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.5%; Score 63; DB 3; Length 1212; 23.1%; Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 63; DB 4; Pred. No. 3.5e+02;
REFERENCE/DOCKET NUMBER: P-UW 4164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 23.1%; Pred. No. 3.5e Matches 6; Conservative 13; Mismatches
                                                                                                                                                                                                                                                   ;
TOPOLOGY: linear
;
MOLECULE TYPE: protein
;
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-566-047-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   538 GFTGTYCHENIDDCLGQPCRNGGTCI 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (858) 535-9001
                                                                                                                         INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1148 amino acids
                                                                                                   (858) 535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.5%;
                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-722-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                   TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 88
US-09-214-278-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-214-278-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 89
US-09-855-722-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/09855722

Sequence 5, Application US/09855722

Sequence 10. 6638741

GENERAL INFORMATION:
APPLICANT: Sakano, Seiji
APPLICANT: Itch, Akira
TITLE OF INNENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
FILE REFERENCE: KP-6876
CURRENT APPLICATION NUMBER: US/09/855,722

CURRENT APPLICATION NUMBER: 09/214,278

PRIOR APPLICATION NUMBER: 09/214,278

PRIOR PILING DATE: 1999-01-26

NUMBER OF SEQ ID NOS: 32

SOFTWARE: Patentin Ver. 2.1

LENGTH: 1238
                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Sakano, Seiji
APPLICANT: Troh, Akira
TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
FILE REFERENCE: KP-8576
CURRENT APPLICATION NUMBER: US/09/214,278
CURRENT FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.5%; Score 63; DB 4; Length 1238; 23.1%; Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
52.5%; Score 63; DB 3; Length 123
Best Local Similarity 23.1%; Pred. No. 3.5e+02;
Matches 6; Conservative 13; Mismatches 7; Indels
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .7; Indels
```

```
2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ISh-Horowicz, David
APPLICANT: Henrique, Domingos M.P.
APPLICANT: Lewis, Julian H.
APPLICANT: Myat, Anna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/08611729A
Patent No. 6004924
GENERAL INFORMATION:
           FILING DATE: 25-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (212) 790-9090
(212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-611-729A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-611-729A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/09566047
Patent No. 6703198
GENERAL INFORMATION:
GENERAL INFORMATION:
Hood, Leroy
Krantz, Tan D.
Spinner, Nancy B.
TITLE OF INVENTION: Methods of Diagnosing Alagille Syndrome NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.5%; Score 63; DB 3; Length 1248; 23.1%; Pred. No. 3.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Indels
APPLICANT: Spinner, Nancy B.

TITLE OF INVENTION: Human Jagged Polypeptide, Encoding TITLE OF INVENTION: Nucleic Acids and Methods of Use NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS: ADDRESSE: Campbell & Flores LLP STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego STATE: Can Diego STATE: CUSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Diego
STATE: California
COUNTRY: USA
ZIE: 9122
COMPUTER READABLE FORM:
MEDIUM TYPE: FOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,046
FILING DATE: 25-UN-1997
CLASSIFICATION NUMBER: 31,815
ATORNEY/AGENT INFORMATION:
ARGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 31,815
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1248 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/09/566,047
FILING DATE: 05-May-2000
CLASSIPICATION: «UMKNOWN»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/882,046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            628 GFTGTYCHENIDDCMGQPCRNGGTCI 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 23.1
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-566-047-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-882-046-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Pleming, Robert J.
APPLICANT: Pleming, Robert J.
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Marn. Robert S.
APPLICANT: Gray, Grace E.
TITLE OF INVENTION: NUCLECTIDE AND PROTEIN SEQUENCES OF THE
TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 52.5%; Score 63; DB 4; Length 1248; Best Local Similarity 23.1%; Pred. No. 3.6e+02; Matches 6; Conservative 13; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/611,729A

FILING DATE: 06-MR-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 7326-037

TELECOMMUNICATION INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATTON NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UW 4164
TELEPHONE: (858) 535-9001
TELEPHONE: (858) 535-9001
TELEPAX: (658) 535-8949
INFORWATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1248 amino acids
                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-566-047-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       628 GFTGTYCHENIDDCMGQPCRNGGTCI 653
```

```
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-894-882-210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JS-09-894-882-433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ish-Horowicz, David
APPLICANT: Henrique, Domingos M.P.
APPLICANT: Henrique, Domingos M.P.
APPLICANT: Lewis, Julian H.
APPLICANT: Fleming, Robert J.
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICA
                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
Query Match 52.5%; Score 63; DB 3; Length 1257; Best Local Similarity 23.1%; Pred. No. 3.6e+02; Matches 6; Conservative 13; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 1257,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.5%; Score 63; DB 4; Length 125
23.1%; Pred. No. 3.6e+02;
tive 13; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: U.S.A.
ZIE: NO36-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: IN PPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: NEW PC compatible
COMPUTER: OF COMPUTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/611,729
FILING DATE: 06-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-037
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 869-9741/8864
TELEX: 66141 PENNIE
TELEX: 66141 PENNIE
INFORMATION FOR SEG ID NO: 8:
SEQUENCE CHARACTERISTICS:
TENNICH 1257 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                           : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : 
                                                                                                                                                                                                                                                                                                                        2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/09195524
Patent No. 6703489
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 23.19
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-195-524-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-195-524-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ģ
```

RESULT 96 US-09-894-882-433 ; Sequence 433, Application US/09894882

```
APPLICANT: Cognetix, Inc.
APPLICANT: Marker, Carig S.
APPLICANT: Marker, Carig S.
APPLICANT: Marker, Carig S.
APPLICANT: Minnersity Inc.
APPLICANT: Minnersity Resima
APPLICANT: Minnersity Re
```

ï

```
1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: University of Utah Research Foundation
        University of Utah Research Foundation
                                                                                                                                                                                                                APPLICANT: Watering, Marten
APPLICANT: Uones, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR PELICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR PLING DATE: 2000-11-08
PRIOR PLING DATE: 2000-11-08
PRIOR PLING DATE: 2000-11-14
PRIOR PLING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR PLING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR PLING DATE: 2001-01-29
NUMBER OF SEO ID NOS: 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SIGLEY, KEBRINGA
APPLICANT: MCINCOSh, J. Michael
APPLICANT: Olivera, Baldomero M.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
FILE REFERENCE: 2314-238
CURRENT FAPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR PILIAG DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR PLILING DATE: 2000-110-37
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FLLING DATE: 2000-11-14
PRIOR FLLING DATE: 2000-11-14
PRIOR PLLING DATE: 2000-11-14
PRIOR PLLING DATE: 2001-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 52.1%; Score 62.5; I
Best Local Similarity 33.3%; Pred. No. 31;
Matches 9; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 74, Application US/09894882
Patent No. 6767895
                                                                                                                Jimenez, Elsie C.
McIntosh, J. Michael
Olivera, Baldomero M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin version 3.0
SEQ ID NO 209
LENGTH: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin version 3.0 SEQ ID NO 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cognetix, Inc.
Walker, Craig S.
Shetty, Reshma
                                                                                                                                                                                                        Watkins, Maren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Conus lynceus
US-09-894-882-209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JS-09-894-882-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                NAME/KEY: PEPTIDE
LOCATION: (1)..(36)
OTHER INFORMATION: Xaa at residues 2 and 4 is Trp or bromo-Trp; Xaa at residue 25 is
OTHER INFORMATION: Tyr, 1251-Tyr, mono-lodo-Tyr, di-lodo-Tyr, O-sulpho-Tyr or O-pho
OTHER INFORMATION: spho-Ty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 36;
                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                        6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F. University of Utah Research Foundation
F. Cognetix, Inc.
F. Walker, Craig S.
F. Shetty, Reshma
Jimenez, Elsie C.
F. McInceh, J. Michael
Olivera, Baldomero M.
F. Watkins, Maren
                                                                                                                                                                                                                                                                                                                                                                52.1%; Score 62.5; I 37.0%; Pred. No. 17; tive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: I Superfamily Conotoxins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TILE REPERENCE: 1214-238

CURRENT APPLICATION NUMBER: US/09/894,882

CURRENT PILING DATE: 2001-06-29

PRIOR APPLICATION NUMBER: US 60/243,410

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-10-27

PRIOR FILING DATE: 2000-11-28

PRIOR FILING DATE: 2000-11-38

PRIOR FILING DATE: 2000-11-48

PRIOR FILING DATE: 2000-11-49

PRIOR FILING DATE: 2000-11-14

PRIOR FILING DATE: 2000-11-14

PRIOR FILING DATE: 2000-11-14

PRIOR FILING DATE: 2000-11-14

PRIOR FILING DATE: 2001-11-14

PRIOR FILING DATE: 2001-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.1%; Score 62.5; 33.3%; Pred. No. 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [:::|[:::| CFNAGVKCDNH-SDCCADTCCXDNTCV 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 CFNAGVKCDNH-SDCCADTCCYDNTCV 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-894-882-209
'Sequence 209, Application US/09894882
'Patent No. 6767895
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 404, Application US/09894882
SOFTWARE: Patentin version 3.0 SEQ ID NO 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jones, Robert M.
Shen, Greg S.
                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 37.0%
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 33.3*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Conus lynceus
US-09-894-882-404
                                                                                                                   ORGANISM: Conus lynceus
                                                                                                                                                                                                                                                                                                             US-09-894-882-210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JS-09-894-882-404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

```
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Conus striatus
US-09-894-882-74
```

Query Match 52.1%; Score 62.5; DB 4; Length 71; Best Local Similarity 33.3%; Pred. No. 31; Matches 9; Conservative 10; Mismatches 7; Indels

1;

1; Gaps

1 CXIXNOXCXQXLDDCCSXXCNXXXXXC 27 |: | | | : | | | : : | | | 39 CSFLGQGCGDH-SDCCWNMCCASEMCV 64

qq. ò

Search completed: April 18, 2005, 20:39:51 Job time : 32.5 secs

inis page blank (uspto)

Run

```
Sequence 258, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 268, App
Sequence 268, App
Sequence 27, Appli
Sequence 468, App
Sequence 12, Appl
Sequence 134, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 39, Appl
Sequence 39, Appl
Sequence 29, Appl
Sequence 470, Appl
Sequence 149, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Appli
Sequence 7, Appli
Sequence 109, Appl
Sequence 4, Appli
Sequence 4, Appli
Sequence 726, Appli
                                                                                                                                                                                                                                                                       114, Appl
18, Appl
18, Appl
23, Appl
4, Appl
4, Appl
10, Appl
116, Appl
116, Appl
116, Appl
116, Appl
117, Appl
119, Appl
119,
                                               Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                   Sequence
Sequence
Sequence
Sequence
                                          Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Seq
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence Sequence Sequence S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
2447
2447
2469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2555
2556
2556
2556
2556
2551
2531
2531
2531
    1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Appl
Appl
Appl
Appl
Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                           April 18, 2005, 20:29:42 ; Search time 91.5 Seconds (without alignments) 98.077 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6,
Sequence 7,
Sequence 9,
Sequence 10
Sequence 12
Sequence 12
Sequence 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Applications AA:*

1: /cgn2 6/ptodata/1/pubpaa/PCT_NEW_PUB_POP:*

2: /cgn2-6/ptodata/1/pubpaa/PCT_NEW_PUB_POP:*

3: /cgn2-6/ptodata/1/pubpaa/NGG_NEW_PUB_POP:*

4: /cgn2-6/ptodata/1/pubpaa/USOG_NEW_PUB_POP:*

5: /cgn2-6/ptodata/1/pubpaa/USOG_NEW_PUB_POP:*

6: /cgn2-6/ptodata/1/pubpaa/USOB_NEW_PUB_POP:*

7: /cgn2-6/ptodata/1/pubpaa/USOB_NEW_PUB_POP:*

8: /cgn2-6/ptodata/1/pubpaa/USOB_NEW_PUB_POP:*

9: /cgn2-6/ptodata/1/pubpaa/USOB_PUBCOMB_POP:*

10: /cgn2-6/ptodata/1/pubpaa/USOB_PUBCOMB_POP:*

11: /cgn2-6/ptodata/1/pubpaa/USOB_PUBCOMB_POP:*

11: /cgn2-6/ptodata/1/pubpaa/USOB_PUBCOMB_POP:*

13: /cgn2-6/ptodata/1/pubpaa/USOB_PUBCOMB_POP:*

14: /cgn2-6/ptodata/1/pubpaa/USIOB_PUBCOMB_POP:*

15: /cgn2-6/ptodata/1/pubpaa/USIOB_PUBCOMB_POP:*

16: /cgn2-6/ptodata/1/pubpaa/USIOD_PUBCOMB_POP:*

17: /cgn2-6/ptodata/1/pubpaa/USIOD_PUBCOMB_POP:*

18: /cgn2-6/ptodata/1/pubpaa/USIOD_PUBCOMB_POP:*

19: /cgn2-6/ptodata/1/pubpaa/USIOD_PUBCOMB_POP:*

19: /cgn2-6/ptodata/1/pubpaa/USIOD_PUBCOMB_POP:*

10: /cgn2-6/ptodata/1/pubpaa/USIOD_PUBCOMB_POP:*
                                                                                                                                                                                                                                                                                                                                                                                                                    1421835
                       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-352-254-1
US-10-352-254-3
US-10-352-254-5
US-10-352-254-6
US-10-352-254-7
US-10-352-254-8
US-10-352-254-9
US-10-352-254-10
US-10-352-254-11
US-10-352-254-12
US-10-352-254-13
US-10-352-254-13
US-10-352-254-13
                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                               120
1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                           1421835 seqs, 332370683 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 0%
Match 100%
first 100 summaries
                                                                                                        protein search, using sw model
                                                                                                                                                                                                                                                                                                             BLOSUM62DX
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                             length: 0
length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-627-685A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum M
Maximum M
Listing f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing:
                                                                                                                                                                                                                            Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM protein -
                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database
                                                                                                                                               ю
::
```

Result Š.

```
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (1)...(27)

OTHER INFORMATION: at residue 4 may be Pro or Hyp; Xaa at residue 9 and OTHER INFORMATION: at an abe Phe.Tyr. meta-Tyr. ortho-Tyr. nor-Tyr, orthorwation: mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, nor-Tyr, O-ther INFORMATION: O-phospho-Tyr, di-halo-Tyr, Trp (D or L), FBATURE:

NAME/KEY: PEPTIDE: LOCATION: (1)..(27)

OTHER INFORMATION: neo-Trp, halo-Trp (D or L) or any synthetic aromatic amino OTHER INFORMATION: acid; Xaa at residue 11 is His or halo-His
                                     Sequence 27, Appl
Sequence 27, Appl
Sequence 23, Appl
Sequence 57, Appl
Sequence 723, Appl
Sequence 168, Appl
Sequence 167, Appl
Sequence 167, Appl
Sequence 6999, Appl
Sequence 6999, Appl
Sequence 26, Appli
Sequence 26, Appli
Sequence 26, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-352-254-1

US-10-352-254-1

Sequence 1, Application US/10352254

Publication No. US20030224343A1

GENERAL INFORMATION:
APPLICANT: COGNELIX, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: APPLICANT: McIncoh, J. Michael
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REPERBNCE: 2314-254
CURRENT FILING DATE: 2003-01-28
FRICK APPLICATION NUMBER: US 60/352,219
FRIOR FILING DATE: 2002-01-29

NUMBER OF SEQ ID NOS: 28

SOFTWARE: PatentIn Ver. 2.0

LENGTH: 27

"WORD APPLICATION OF APPLICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
OCHER INFORMATION: Xaa at residue 2, 7, 18, 19, 22 and 25 may be Arg,
OCHER INFORMATION: An at residue, ornithine, Lys, N-methyl-Lys,
OCHER INFORMATION: N.N-dimethyl-Lys, N.N.N-trimethyl-Lys, any
OCHER INFORMATION: Synthetic Dasic amino acid, His or halo-His; Xaa
NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
S US-10-369-072-2

S US-10-190-115-27

US-10-10-115-27

US-10-765-727-23

T US-10-84-989-57

US-10-322-281-723

US-09-894-882-168

US-09-894-882-169

US-09-894-882-167

US-09-894-882-167

US-09-894-882-167

US-10-369-493-6999

US-10-369-493-6999

US-10-369-493-6999

US-10-369-072-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 120; DB 15;
100.0%; Pred. No. 4.7e-05;
live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
      115
117
117
118
118
118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27; Conservative
   2469
2471
2471
2471
2471
2503
36
36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity

    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0
    0</t
   Matches
```

1 CXIXNOXCXQXLDDCCSXXCNXXNXCV 27

ò

```
APPLICANT: Cogneix, Inc.
APPLICANT: Cogneix, Inc.
APPLICANT: Cogneix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: Pemberton-Goodman, Karen
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: Olivera, Baldomero M.
ITILE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 214-254
CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT APPLICATION NUMBER: US 60/352,219
PRIOR APPLICATION NUMBER: US 60/352,219
PRIOR PLING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Pemberton-Goodman, Karen
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
CURRENT APPLICATION NUMBER: US 60/352,254
CURRENT FILING DATE: 2003-01-29
PRIOR PILING DATE: 2003-01-29
PRIOR PLILOR DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 27
TENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 120; DB 15; Best Local Similarity 66.7%; Pred. No. 4.7e-05; Matches 18; Conservative 9; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 120; DB 15; Best Local Similarity 66.7%; Pred. No. 4.7e-05; Matches 18; Conservative 9; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CXIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CRIXNQKCFQHLDDCCSAKCNRFNKCV 27
                 Sequence 2, Application US/10352254
Publication No. US20030224343A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/10352254 Publication No. US20030224343A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     i TYPE: PRT
i ORGANISM: Conus purpurascens
i FBATURE:
i NAME/KEY: PEPTIDE
i LOCATION: (1)..(27)
i OTHER INFORMATION: Xaa is Hyp
US-10-352-254-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Conus purpurascens
FEATURE:
JS-10-352-254-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-352-254-3
```

```
Length 27;
                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                  ; Score 120; DB 15;
Pred. No. 4.7e-05;
9; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 120; D
Best Local Similarity 66.7%; Pred. No. 4.7e
Matches 18; Conservative 9; Mismatches
                                                                                         1 CXIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                              1 CAIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/10352254 Publication No. US20030224343A1
                Query Match
Best Local Similarity 66.7%; Matches 18; Conservative 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
OTHER INFORMATION: Xaa is Hyp
US-10-352-254-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Conus purpurascens
                                                                                                                     g
                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/1035254
; Sequence 6, Application US/1035254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Temple, Davis
; APPLICANT: Temple, Davis
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Allowere, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
: LENGTH: 27
                                                                                                                                                   Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 120; DB 15; Best Local Similarity 66.7%; Pred. No. 4.7e-05; Matches 18; Conservative 9; Mismatches 0;
1 CRIXNQKCFQHLDDCCSRACNRFNKCV 27
                                                                                                                           ; Sequence 5, Application US/10352254
; Publication No. US20030224343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (1)..(27)
CTHER INFORMATION: Xaa is Hyp
US-10-352-254-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
 ઠે
                                 셤
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/1035254;
Sequence 7, Application US/1035254;
Publication No. US20030224343A1
GENERAL INFORMATION:
APPLICANT: Cognetix, Inc.;
APPLICANT: University of Utah Research Foundation
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: McIntosh, J. Michael
APPLICANT: McInt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Pemberton-Goodman, Karen
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: Temple, Jamichael
APPLICANT: Temple, Jamichael
APPLICANT: Olivera, Baldomero M.
ITILE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
CURRENT FILING DATE: 2003-01-28
FRIOR APPLICATION NUMBER: US 60/352,254
CURRENT FILING DATE: 2003-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 27
Gaps
ö
```

```
Pred. No. 4.76
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                   1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                           1 CRIXNQACFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CRIXNQKCMQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CXIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.7%; Matches 18; Conservative 9,
                 SEQ ID NO 10
LENGTH: 27
TYPE: PRT
ORGANISM: Conus purpurascens
FEATURE:
NAME/KEY: PEPTIDE
                                                                                                                                                              ; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Conus purpurascens
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 66.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-352-254-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cognetix, Inc.

APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Jones, Robert M.
APPLICANT: Temple, Davis
APPLICANT: Temple, Javis Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT APPLICATION NUMBER: US/10/352,219
FRIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-352-254-10

| Sequence 10, Application US/1035254 |
| Sequence 10, Application US/1035254 |
| Sequence 10, Application US/1035254 |
| Sequence 10, Application No. US20030224343A1 |
| GENERAL INFORMATION: |
| APPLICANT: Cognetix, Inc. |
| APPLICANT: Pemberton-Goodman, Karen |
| APPLICANT: Temple, Davis |
| APPLICANT: Temple, Davis |
| APPLICANT: Olivera, Baldomero M. |
| APPLICANT: Olivera, Baldomero M. |
| TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants |
| FILE REFERENCE., 2314-254 |
| CURRENT APPLICATION NUMBER: US/10/352,254 |
| CURRENT FILING DATE: 2003-01-28 |
| PRIOR FILING DATE: 2002-01-29 |
| NUMBER OF SEQ ID NOS: 28 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                 DB 15; Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 120; DB 15; Length 27;
Best Local Similarity 66.7%; Pred. No. 4.7e-05;
Matches 18; Conservative 9; Mismatches 0; Indels (
                                                                                                                            Query Match
100.0%; Score 120; DB 15;
Best Local Similarity 66.7%; Pred. No. 4.7e-05;
Matches 18; Conservative 9; Mismatches 0;
                                                                                                                                                                                                                           1 CXIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                      1 CRIXNQKCFQHLDDCCSRKCNRFNACV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CXIXNOXCXOXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CKIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/10352254
Publication No. US20030224343A1
            ; NAME/KEY: PEPTIDE
; LOCATION: (1)...(27)
; O'THER INFORMATION: Xaa is Hyp
US-10-352-254-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

```
US-10-352-254-11

Sequence 11, Application US/10352254

Sequence 11, Application US/10352254

Publication No. US20030224343A1

GENERAL INFORMATION:

APPLICAMT: OGnetix, Inc.

APPLICAMT: University of Utah Research Foundation

APPLICAMT: University of Utah Research Foundation

APPLICAMT: Temple, Davis

APPLICAMT: Temple, Javis

APPLICAMT: McIntosh, J. Michael

APPLICAMT: McIntosh, J. Michael

APPLICAMT: McIntosh, J. Michael

APPLICAMT: Olivera, Baldomero M.

TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants

FILE REFERENCE: 2314-254

CURRENT APPLICATION NUMBER: US 60/352,254

CURRENT PILING DATE: 2002-01-29

NUMBER: OF SEQ ID NOS: 28

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 11

LENGTH: 27
                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: Dinversity of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Temple, Davis
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: McIntosh, J. Michael
; APPLICANT: OF INVENTION: Raplaomero M.
; TITLE OF INVENTION: Rappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
                                                         Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
  Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 27;
                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
Score 120; DB 15;
Pred. No. 4.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 120; DB 15;
66.7%; Pred. No. 4.7e-05;
tive 9; Mismatches 0;
```

```
Pag

APPLICANT: Temple, Davis
APPLICANT: McIntosh, J. Michael
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REPERENCE: 2314-254
CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT FILING DATE: 2003-01-28
PRIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
LENGTH: 27
TYPE: ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: Pemberton-Goodman, Karen
APPLICANT: Pemple, Davis
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: Onlivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
CURRENT PAPLICANTON NUMBER: US/10/352,254
CURRENT FILING DATE: 2003-01-28
PRIOR FILING DATE: 2002-01-29
PRIOR FILING DATE: 2002-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 120; DB 15; Length 27; 63.0%; Pred. No. 4.7e-05; cive 10; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 100.0%; Score 120; DB 15; Local Similarity 66.7%; Pred. No. 4.7e-05; Les 18; Conservative 9; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CRIXNOKCFOALDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CRIANQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24, Application US/10352254 . Publication No. US20030224343A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
US-10-627-685-1
Sequence 1, Application US/10627685; Publication No. US20040092447A1; GENERAL INFORMATION:
APPLICANT: Cornell-Bell, Ann H.; APPLICANT: Pemberton, Karen E.; APPLICANT: Temple Jr., Davis L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-14
                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Conus purpurascens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 24
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 63.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: PEPTIDE LOCATION: (1)..(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JS-10-352-254-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-352-254-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13, Application US/1035254

Publication No. US2003024343A1

GENERAL INFORMATION:

APPLICANT: Cognetix, Inc.

APPLICANT: University of Utah Research Foundation

APPLICANT: Pemberton-Goodman, Karen

APPLICANT: Temple, Davis

APPLICANT: Temple, Davis

APPLICANT: Temple, Davis

APPLICANT: Temple, Davis

APPLICANT: Jances, Jaldomero M.

TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants

FILE REFERENCE: 2314-254

CURRENT APPLICATION NUMBER: US/10/352,254

CURRENT FILING DATE: 2003-01-29

NUMBER OF SEQ ID NOS: 28

SOUTHWARE: PATENTIN VEY: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 120; DB 15; Length 27; 66.7%; Pred. No. 4.7e-05; tive 9; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 120; DB 15; Best Local Similarity 66.7%; Pred. No. 4.7e-05; Matches 18; Conservative 9; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation APPLICANT: Pemberton-Goodman, Karen APPLICANT: Jones, Robert M.
                                                                                                                CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 60/352,219
PRIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CRIXNQKCYQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CQIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CXIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/10352254; Publication No. US20030224343A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1)..(27)
COTHER INFORMATION: Xaa is Hypus-10-352-254-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (1)...(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-13
                                                                                                                                                                                                                                                                                                                       ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.7%
....hes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
US-10-352-254-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 13
LENGTH: 27
                                                                                                                                                                                                                                                                                                         IYPE: PRT
                                                                                                                                                                                                                                                                                                                                                    FEATURE:
```

g

ö

ò ď

```
Gaps
                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                       Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 27;
                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3. Application US/10627685

Publication No. US20040092447A1

GENERAL INFORMATION:
APPLICANT: Cornell. Bell, Ann H.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-FVIIA
CURRENT APPLICATION UNMBER: US/10/627,685
CURRENT FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3: SEQ ID NOS: 25
LENGER H. 27
                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 120; DB 15; Best Local Similarity 66.7%; Pred. No. 4.7e-05; Matches 18; Conservative 9; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 120; DB 15; Best Local Similarity 66.7%; Pred: No. 4.7e-05; Matches 18; Conservative 9; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                      1 CRIXNQKCFQHLDDCCSAKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                        1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CXIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/10627685; Publication No. US20040092447A1; GENERAL INPOWATION: APPLICANT: Cornell-Bell, Ann H.; APPLICANT: Temple Jr., Davis L.; APPLICANT: Layer, Richard T.; APPLICANT: McCabe, R. Tyler
                                                                                                                                                            , LOCATION: (1) ----;
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: PEPTIDE

: LOCATION: (1)..(27)

: OTHER INFORMATION: Xaa is Hyp
US-10-627-685-3
                                                                                                ORGANISM: Conus purpurascens
FRATURE:
LOCATION: (1)...(27)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Conus purpurascens
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-627-685-5
                        SEQ ID NO 2
LENGTH: 27
                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (1)...(27)

LOCATION: (1)...(27)

OTHER INFORMATION: Xaa at residue 2, 7, 18, 19, 22 and 25 may be Arg, OTHER INFORMATION: homoarginine, Lys, N-methyl-Lys, OTHER INFORMATION: N. N-dimethyl-Lys, N. N. N-trimethyl-Lys, any OTHER INFORMATION: synthetic basic amino acid, His or halo-His; Xaa at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DCATION: [1]..(27)

OTHER INFORMATION: residue 4 may be Prc or Hyp; Xaa at residue 9 and OTHER INFORMATION: and be Phe, Tyr, meta-Tyr, ortho-Tyr, nor-Tyr, OTHER INFORMATION: mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, OTHER INFORMATION: O-phospho-Tyr, nitro-Tyr, Trp (D or L), neo-Trp, FRATURE:
NAME/KEY: PEPTIDE:
NAME/KEY: PEPTIDE
OCHER INFORMATION: (1)..(27)

OTHER INFORMATION: acid; Xaa at residue 11 is His or halo-His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
     APPLICANT: McCabe, R. Tyler
APPLICANT: McCabe, R. Tyler
APPLICANT: Jones, Robert M.
APPLICANT: Cognetix, Inc.
TTILE OF INVENTION: Uses of Kappa-Conotcxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/10/627,685
CURRENT PILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/155,135
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGINE DATE: AUGUST OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: Jones, Robert M.
APPLICANT: Ognetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/10/66,837
PRIOR APPLICATION NUMBER: US/09/66,837
PRIOR APPLICATION NUMBER: US/09/21
PRIOR APPLICATION NUMBER: US/09/21
PRIOR APPLICATION NUMBER: US/09/21
PRIOR APPLICATION NUMBER: US/09/21
PRIOR APPLICATION NUMBER: US/00-09-21
PRIOR FILING DATE: 1999-09-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 120; DB 15;
100.0%; Pred. No. 4.7e-05;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/10627685
Publication No. US20040092447A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 16
US-10-627-685-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-627-685-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
```

g à

ô

1 CAIXNOKCFQHLDDCCSRKCNRFNKCV 27

셤

Jones, Robert M.

```
Sequence 7, Application US/10627685 Publication No. US20040092447A1 GENERAL INFORMATION:
                                                                                                                                                     APPLICANT: Cornell-Bell, Ann H
APPLICANT: Pemberton, Karen E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 120; DB 15; Length 27; Best Local Similarity 66.7%; Pred. No. 4.7e-05; Matches 18; Conservative 9; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 120; DB 15; Length 27; 66.7%; Pred. No. 4.7e-05; tive 9; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cornell.Bell, Ann H.
APPLICANT: Cornell.Bell, Ann H.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: McCabe, R. Tyler
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/10/627,685
APPLICANT: Coghetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
                                                      CURRENT APPLICATION NUMBER: US/10/627,685
CURRENT FILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-07-20
PRIOR PILING DATE: 2000-07-20
PRIOR PILING DATE: 2000-07-20
PRIOR PILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PARENTIN VET: 2.0
SSOFTWARE: PARENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR PILING DATE: 2000-07-20
PRIOR PILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 6
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 6, Application US/10627685; Publication No. US20040092447A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COCATION: (1)..(27)
COTHER INFORMATION: Xaa is Hyp
US-10-627-685-6
                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indela
APPLICANT: Demberton, Karen E.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Temple Jr., Davis L.
APPLICANT: McCabe, R. Tyler
APPLICANT: McCabe, R. Tyler
APPLICANT: Jones, Robert M.
APPLICANT: Jones, Johnson, Jones, Jones, Johnson, Jones, Jones, Johnson, Jones, Jones, Johnson, Jones, Jones, Johnson, Jones, Jones,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-627-685-8

Sequence 6, Application US/10627685

Publication No. US20040092447A1

GENERAL INFORMATION:

APPLICANT: Cornell-Bell, Ann H.

APPLICANT: Pemberton, Karen E.

APPLICANT: Temple Jr., Davis L.

APPLICANT: Mccabe, R. Tyler

APPLICANT: Mccabe, R. Tyler

APPLICANT: Gones, Robert M.

APPLICANT: Cognetix, Inc.

TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA

FILE REFERENCE: Kappa-PVIIA

CURRENT PLING DATE: 2003-07-28

PRIOR FILING DATE: 2000-07-21

PRIOR FILING DATE: 2000-07-21

PRIOR FILING DATE: 2000-07-21

PRIOR FILING DATE: 2000-07-20

NUMBER OF SEQ ID NOS: 25

NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 120; DB 15; Best Local Similarity 66.7%; Pred. No. 4.7e-05; Matches 18; Conservative 9; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CRIXNQKCAQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 8
LENGTH: 27
```

```
100.0%; Score 120; DB 15; ilarity 66.7%; Pred. No. 4.7e-05; Conservative 9; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Pemberton, Karen E.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: Jones, Robert M.
APPLICANT: Cognetix, Inc.
TILLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
PILE REFERENCE: Kappa-PVIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 120; I
Pred. No. 4.7e
9; Mismatches
           PRIOR APPLICATION NUMBER: 2003-07-28
PRIOR PLICATION NUMBER: US/09/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR PLILING DATE: 2000-09-21
PRIOR PLILING DATE: 2000-07-20
PRIOR FILING DATE: 2000-07-20
PRIOR PLILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 10
LENGTH: 27
TYPE: 100-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/627,685
CURRENT FILING DATE: 2003-07-28
PRIOR PRILOR APPLICATION NUMBER: US/09/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VET. 2.0
SSOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 11
LENGTH: 27
         CURRENT APPLICATION NUMBER: US/10/627,685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CRIXNQACFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CXIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRIXNOKCMOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/10627685
Publication No. US20040092447A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 66.7%;
Matches 18; Conservative 9
                                                                                                                                                                                                                                                                                                                                            NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
CHER INFORMATION: Xaa is Hyp
US-10-627-685-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTHER INFORMATION: Xaa is Hyp US-10-627-685-11
                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Conus purpurascens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: PEPTIDE LOCATION: (1)..(2
                                                                                                                                                                                                                                                                                                                         FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                      100.0%; Score 120; DB 15; Length 27; 66.7%; Pred. No. 4.7e-05; tive 9; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Pemberton, Karen E.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: Layer, R. Tyler
APPLICANT: McCabe, R. Tyler
APPLICANT: Gones, Robert M.
APPLICANT: Gones, Robert M.
APPLICANT: Gonel, Nobert M.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/09/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 120; DB 15;
Pred. No. 4.7e-05;
9; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Temple Jr., Davis L.
APPLICANT: McCabe, R. Tyler
APPLICANT: Jones, Robert M.
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
                                                                                                                                                                                                                                                  1 CXIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                            1 CRIXNQKCFQHLDDCCSRKCNRFNACV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:||||:||:||:||CKIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/10627685
Publication No. US20040092447A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 9, Application US/10627685; Publication No. US20040092447A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
66.7%; P
                                     NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
// OTHER INFORMATION: Xaa is Hyp
US-10-627-685-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-9
ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Conus purpurascens
                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 66.7
Matches 18; Conservative
                                                                                                                                                    Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 23
US-10-627-685-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
```

Gaps

ö

Indels

Length 27;

RESULT 25

ö

Length 27;

Indels

```
Gaps
                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 27;
                                                                                              Length 27;
                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Pemberton, Karen E.
APPLICANT: Pemple Jr., Davis L.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: Layer, Richard T.
APPLICANT: Gones, Robert M.
APPLICANT: Cognet, R. Tyler
APPLICANT: Gones, Robert M.
APPLICANT: Jones, Robert M.
APPLICANT: Jones, Robert M.
APPLICANT: NUMBER: US/10/627,685
CURRENT APPLICATION NUMBER: US/09/666,837
PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR APPLICATION NUMBER: US 60/155,135
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/155,135
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 14
LENGTH: 27
                                                                                              Query Match 100.0%; Score 120; DB 15; Best Local Similarity 66.7%; Pred. No. 4.7e-05; Matches 18; Conservative 9; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 120; DB 15; Best Local Similarity 66.7%; Pred. No. 4.7e-05; Matches 18; Conservative 9; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION UNBER: US/10/627,685
CURRENT FILING DATE: 2003-07-28
                                                                                                                                                                                                                         1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CXIXNOXCXOXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CRIXNQKCFQALDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                          1 CQIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                               US-10-627-685-14; Sequence 14, Application US/10627685; Publication No. US20040092447A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 24, Application US/10627685 Publication No. US20040092447A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cornell-Bell, Ann H. APPLICANT: Pemberton, Karen E. APPLICANT: Temple Jr., Davis L. APPLICANT: Layer, Richard T. APPLICANT: MCCabe, R. Tyler APPLICANT: Jones, Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-14
; OTHER INFORMATION: Xaa is Hyp US-10-627-685-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cognetix,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 120; DB 15; Length 27; Best Local Similarity 66.7%; Pred. No. 4.7e-05; Matches 18; Conservative 9; Mismatches 0; Indels
                                                                                                                 APPLICANT: Pemberton, Karen E.
APPLICANT: Pemple Jr., Davis L.
APPLICANT: Pemple Jr., Davis L.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: Gapt. R. Tyler
APPLICANT: Gones, Robert M.
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFREENCE: Kappa-PVIIA
CURRENT APPLICATION UNMBER: US/10/627,685
CURRENT APPLICATION UNMBER: US/09/666,837
FRIOR APPLICATION NUMBER: US 60/219,438
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR APPLICATION UNMBER: US 60/25,135
PRIOR APPLICATION UNMSER: US 60/25,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Femple JT., Davis L.
APPLICANT: Temple JT., Davis L.
APPLICANT: Temple JT., Davis L.
APPLICANT: Temple JT., Davis L.
APPLICANT: McCabe, R. Tyler
APPLICANT: Jones, Robert M.
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/10/666,837
FILOR APPLICATION NUMBER: US/09/666,837
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PALENTIN OFTE: 2000-07-20
SEQ ID NO 13
LENGTH: Z7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CRIXNQKCYQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13, Application US/10627685; Publication No. US20040092447A1; GENERAL INFORMATION:
                                   Sequence 12, Application US/10627685 Publication No. US20040092447A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cornell-Bell, Ann H. APPLICANT: Pemberton, Karen E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: PEPTIDE
CCATION: (1)..(27)
CTHER INFORMATION: Xaa is Hyp
US-10-627-685-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
                                                                                          GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

```
APPLICANT: Tognetix, Inc.

APPLICANT: University of Utah Research Foundation

APPLICANT: University of Utah Research Foundation

APPLICANT: Pemberton-Goodman, Karen

APPLICANT: Temple, Davis

APPLICANT: Temple, Davis

APPLICANT: Temple, Davis

APPLICANT: Temple, Davis

TITLE OF INVENTION: Kappa PVIIA-Related Conotoxins as Organ Protectants

TITLE OF INVENTION: Kappa PVIIA-Related Conotoxins as Organ Protectants

TITLE OF INVENTION: Kappa PVIIA-Related Conotoxins as Organ Protectants

CURRENT APPLICATION NUMBER: US/10/352,254

CURRENT FILING DATE: 2002-01-29

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 23

LENGTH: 27

TYPE: ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 97.5%; Score 117; DB 15; Length 27; Best Local Similarity 63.0%; Pred. No. 9.1e-05; Matches 17; Conservative 10; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 96.7%; Score 116; DB 15; Length 27; Best Local Similarity 65.4%; Pred. No. 0.00011; Matches 17; Conservative 9; Mismatches 0; Indels
    FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/10/627,685
CURRENT FILING DATE: 2003-07-28
FRIOR APPLICATION NUMBER: US 69/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 18
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CXIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CXIXNOXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 23, Application US/10627685; Publication No. US20040092447A1
                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (1)...(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
OTHER INFORMATION: Xaa is Hyp
                                                                                                                                                                                                                                                                                                                                              ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Conus purpurascens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-352-254-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-627-685-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: Demberton-Goodman, Karen
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conctoxins as Organ Protectants
FILE REFERENCE: 2314-254
CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT FILING DATE: 2003-01-29
PRIOR FILING DATE: 2003-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 18
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                               Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 27;
                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 120; DB 15; Best Local Similarity 63.0%; Pred. No. 4.7e-05; Matches 17; Conservative 10; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.5%; Score 117; DB 15;
63.0%; Pred. No. 9.1e-05;
cive 10; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: Mores, R. Dert M.
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
                                                                                                                                                                                                                                                                                                                                                                                      1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                      1 CRIANQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CRIXNQKCFQHLDDCCARKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                      PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/155,135
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 24
PRIOR APPLICATION NUMBER: US 60/219,438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 18, Application US/10352254; Publication No. US20030224343A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 18, Application US/10627685; Publication No. US20040092447A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cornell-Bell, Ann H. APPLICANT: Pemberton, Karen E. APPLICANT: Temple Jr., Davis L
                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Conus purpurascens
US-10-627-685-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 63.0°
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-627-685-18
                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

Gaps

; 0

ö

```
GENERAL INFORMATION:

APPLICANT: Cognetix, Inc.

APPLICANT: University of Utah Research Foundation

APPLICANT: University of Utah Research Foundation

APPLICANT: Pemberton-Goodman, Karen

APPLICANT: Pemberton-Goodman, Karen

APPLICANT: Temple, Davis

APPLICANT: McIntcoh, J. Michael

APPLICANT: McIntcoh, J. Michael

APPLICANT: McIntcoh, J. Michael

APPLICANT: Olivera, Baldomero M.

ITILE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants

ITILE OF INVENTION: Kappa-PVIIA-Related

CURRENT APPLICATION NUMBER: US/10/352,254

CURRENT FILING DATE: 2002-01-29

PRIOR PILING DATE: 2002-01-29

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin Ver. 2.0

LENGTH: 27

ORGANISM: Conus purpurascens

FEATURE:

NAME/KEY: PEPTIDE

LOCATTON: (1)..(27)

COTHER INPORMATION: Xaa is Hyp

US-10-352-254-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.8%; Score 115; DB 15; Length 27; 63.0%; Pred. No. 0.00014; tive 9; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Jones, Richard T.
APPLICANT: Jones, Robert M.
APPLICANT: Cognetix, Inc.
TILLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/627,685
CURRENT FILING DATE: 2003-07-28
PRIOR PILING DATE: 2003-07-21
PRIOR PILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR APLICATION NUMBER: US 60/155,135
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 4
                               1 CRAXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                       Sequence 20, Application US/10352254 Publication No. US20030224343A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/10627685 Publication No. US20040092447A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Conus purpurascens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 63.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-627-685-4
                                          셤
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: MCINTES, DO LIBER APPLICANT: MCINTES, DO LIBER APPLICANT: Olivera, Baldomero M. TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants FILE REFERENCE: 2314-254
CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT FILING DATE: 2003-01-28
PRIOR PAPLICATION NUMBER: US 60/352,219
PRIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 96.7%; Score 116; DB 15; Length 27; Best Local Similarity 65.4%; Pred. No. 0.00011; Matches 17; Conservative 9; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                             APPLICANT: Fembercon, Astein E., APPLICANT: Tempercon, Astein E., APPLICANT: Layer, Richard T., APPLICANT: Layer, Richard T., APPLICANT: McCabe, R. Tyler APPLICANT: Gones, Robert M., APPLICANT: Cognetix, Inc., TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA FILE REFERENCE: Kappa-PVIIA CURRENT APPLICATION NUMBER: US/10/627,685 CURRENT FILING DATE: 2003-07-28 PRIOR APPLICATION NUMBER: US/09/666,837 PRIOR FILING DATE: 2000-09-21 PRIOR FILING DATE: 2000-07-20 PRIOR FILING DATE: 1999-09-22 NUMBER OF SEQ ID NOS: 25 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/10352254
Publication No. US20030224343A1
GENERAL INFORMATION:
APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: Demberton-Goodman, Raren
APPLICANT: Jones, Robert M.
APPLICANT: Temple, Davis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.8%; Score 115; DB 15;
63.0%; Pred. No. 0.00014;
tive 9; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CXIXNOXCXOXLDDCCSXXCNXXNXC 26
       Cornell-Bell, Ann H. Pemberton, Karen E. Temnla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
JUNET INFORMATION: Xaa is Hyp. US-10-627-685-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 95.8
Best Local Similarity 63.0
Matches 17; Conservative
```

δ a

```
PRIOR APPLICATION NUMBER: US 60/352,219
PRIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22, Application US/10352254
Publication No. US20030224343A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16, Application US/10627685
Publication No. US20040092447A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Pemberton, Karen E.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: Jones, Robert M.
                                                                                                                                                                                                                NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
CTHER INFORMATION: Xaa is Hyp
US-10-352-254-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
CTHER INFORMATION: Xaa is Hyp
US-10-352-254-22
                                                                                                                                                                      ORGANISM: Conus purpurascens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 63.0°
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-627-685-16
                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Pemberton-Goodman, Karen
APPLICANT: Dones, Robert M.
APPLICANT: Jones, Robert M.
APPLICANT: Temple, Davis
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
APPLICANT: Olivera, Baldomero M.
FITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT FILING DATE: 2003-01-28
                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                    Score 115; DB 15; Length 27;
Pred. No. 0.00014;
9; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.8%; Score 115; DB 15; Length 27; 63.0%; Pred. No. 0.00014; live 9; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cognetix, Inc.

TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/10/627,685
CURRENT APPLICATION NUMBER: US/09/666,837
PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-20
PRIOR PILING DATE: 1999-09-22
NUMBER: PALING DATE: 1999-09-22
NUMBER: PALENTION NUMBER: US 60/155,135
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PALENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cognetix, Inc.
APPLICANT: Universalty of Utah Research Foundation APPLICANT: Pemberton-Goodman, Karen APPLICANT: Jones, Robert M.
                                                                                                                                                                                                              1 CXIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                           1 CRAXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20, Application US/10627685
Publication No. US20040092447A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16, Application US/10352254
Publication No. US20030224343A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Pemberton, Karen E.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Hayer, Richard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: Jones, Robert M.
                                                                                                               Ouery Match 95.8%;
Best Local Similarity 63.0%;
Matches 17; Conservative
                      ; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (1)..(27)
OTHER INFORMATION: Xaa is Hyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 17; Conserva
NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-627-685-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-352-254-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: Demberton-Goodman, Karen
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: McIntedsh, J. Michael
APPLICANT: McIntedsh, J. Michael
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT APPLICATION NUMBER: US 60/352,219
PRIOR APPLICATION NUMBER: US 60/352,219
PRIOR APPLICATION NUMBER: US 60/352,219
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 22
LENGTH: 27
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                              .;
0
95.0%; Score 114; DB 15; Length 27; 63.0%; Pred. No. 0.00018; ive 9; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

95.0%; Score 114, DB 15,
Best Local Similarity 63.0%; Pred. No. 0.00018;
Matches 17; Conservative 9; Mismatches 1;
                                                                                                                   1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                      1 CRIXNAKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CRIXNQKCFAHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
```

```
APPLICANT: Cognetix, Inc.

APPLICANT: Cognetix, Inc.

APPLICANT: University of Utah Research Foundation

APPLICANT: University of Utah Raren

APPLICANT: Temberton-Goodman, Karen

APPLICANT: Temple, Davis

APPLICANT: Temple, Davis

APPLICANT: Maintosh, J. Michael

APPLICANT: Maintosh, J. Michael

APPLICANT: Olivera, Baldomero M.

TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants

FILE REFERENCE: 2314-254

CURRENT FILING DATE: 2003-01-28

CURRENT FILING DATE: 2002-01-29

NUMBER OF SEQ ID NOS: 28

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 17

LENGTH: 27
                                                                                                                                                                        APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: Pemberton-Goodman, Karen
APPLICANT: Pemple, Davis
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
CURRENT PPLICANTION NUMBER: US/10/352,254
CURRENT PILING DATE: 2003-01-28
PRIOR FILING DATE: 2002-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 93.3%; Score 112; DB 15; Length 27; Best Local Similarity 63.0%; Pred. No. 0.00028; Matches 17; Conservative 9; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93.3%; Score 112; DB 15;
63.0%; Pred. No. 0.00028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CRIXNOKCFQHLDACCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17, Application US/10352254 Publication No. US20030224343A1 GENERAL INFORMATION:
                                                                                                    Sequence 15, Application US/10352254 Publication No. US20030224343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COCATION: (1)...(27)
COTHER INFORMATION: Xaa is Hyp
US-10-352-254-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Conus purpurascens
FEATURE:
NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 114; DB 15; Length 27; Pred. No. 0.00018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 114; DB 15; Length 27;
Pred. No. 0.00018;
9; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Pemberton, Karen E.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: Layer, Richard T.
APPLICANT: Layer, Richard T.
APPLICANT: Cognetix, Inc.
ITILE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/09/666,837
FILE REPERENCE: 2000-09-21
PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US 60/154,136
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTHARE: Patentin Ver. 2.0
SEQ ID NO SEQ ID NOS: 25
LENGTH: 27
APPLICANT: Cognetix, Inc.

TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/10/627,685
CURRENT FILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR PILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/19,438
PRIOR PILING DATE: 2000-07-20
PRIOR PLILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 16
SEQ ID NO 16
SEQ ID NO 16
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CRIXNAKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:||||:|||||CRIXNOKCFAHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22, Application US/10627685 Publication No. US20040092447A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 63.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , LUCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (1)...(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 63.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠ
```

```
APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT FILING DATE: 2003-01-28
PRIOR PILING DATE: 2003-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.0
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                 Gaps
                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 93.3%; Score 112; DB 15; Length 27; Best Local Similarity 63.0%; Pred. No. 0.00028; Matches 17; Conservative 9; Mismatches 1; Indels
                                                                                                                                                                                             Indels
                                                                                                            Score 112; DB 15;
Pred. No. 0.00028;
9; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: Jones, Robert M.
APPLICANT: Cognetix, Inc.
TILLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/627,685
CURRENT FILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-07-20
PRIOR PLICATION NUMBER: US 60/219,438
PRIOR PLILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/155,135
PRIOR FILING DATE: 1999-09-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                         1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                 1 CRIXNÓKCFOHLADCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15, Application US/10627685 Publication No. US20040092447A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 25, Application US/10352254 Publication No. US20030224343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUBLICAL INFORMATION:
APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Pemberton, Karen E.
; OTHER INFORMATION: Xaa is Hyp US-10-352-254-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (1)..(27)
OTHER INFORMATION: Xaa is Hyp
                                                                                                            Query Match 93.3%;
Best Local Similarity 63.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-352-254-25
                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cognetx, Inc.
APPLICANT: Cognetx, Inc.
APPLICANT: Cognetx, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Demberton-Goodman, Karen
APPLICANT: McInton, U. Michael
APPLICANT: McInton, U. Michael
APPLICANT: McInton, U. Michael
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REPERENCE: 2314-224
CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT FILING DATE: 2003-01-28
FRIOR APPLICATION NUMBER: US 60/352,219
FRIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SSOTWARE: PatentIn Ver. 2.0
SSOTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Jones, Robert M.
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: Michael
APPLICANT: Michael
APPLICANT: Michael
APPLICANT: Michael
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
CURRENT APPLICATION NUMBER: 105/10/352,254
CURRENT FILING DATE: 2003-01-28
        Gaps
        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 15; Length 27; 0.00028;
        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: Pemberton-Goodman, Karen
APPLICANT: Jones, Robert M.
    9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1) Score 112; 1) 1) 1) 12; 1) 12; 1) 12; 1) 12; 1) 12; 1) 12; 1) 12; 1) 12; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1] 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 13; 1) 
                                                                                1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CRIXNOKCFQHLDDCCSRKCNRFAKCV 27
                                                                                                                            1 CXIXNOXCXQXI,DDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/352,219
PRIOR FILING DATE: 2002-01-29
                                                                                                                                                                                                                                                                                                                                                 ; Sequence 19, Application US/10352254; Publication No. US20030224343A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21, Application US/10352254 Publication No. US20030224343A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Xaa is Hyp US-10-352-254-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT CORGANISM: CORGANISM: Cons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
LENGTH: 27
    17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: PEPTIDE LOCATION: (1)..(2
                                                                                                                                                                                                                                                                                                                 US-10-352-254-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            엄
                                                                                                                                                        a
a
                                                                                    ò
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 93.3%; Score 112; DB 15; Length 27; Best Local Similarity 63.0%; Pred. No. 0.00028; Matches 17; Conservative 9; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
APPLICANT: McCabe, R. Tyler
APPLICANT: Jones, Robert M.
APPLICANT: Cognetix, Inc.;
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION UNMBER: US/09/666,837
PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-07-20
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SECTIOR OF SEQ ID NOS: 25
LENGTHAR: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
93.3%; Score 112; DB 15;
Best Local Similarity 63.0%; Pred. No. 0.00028;
Matches 17; Conservative 9; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA FILE REFERENCE: Kappa-PVIIA CURRENT APPLICATION NUMBER: US/10/627,685 CURRENT FILING DATE: 2003-07-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US/0/66,837
PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR PILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR PILING DATE: 2000-07-20
PRIOR PLING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 21
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CRIXNOKCFOHLDDCCSRKCNRFAKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 21, Application US/10627685 Publication No. US20040092447A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Pemberton, Karen E.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: Jones, Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-21
                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cognetix, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                          Ouery Match 93.3%; Score 112;, DB 15; Length 27; Best Local Similarity 63.0%; Pred. No. 0.00028; Matches 17; Conservative 9; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 93.3%; Score 112; DB 15; Length 27; Best Local Similarity 63.0%; Pred. No. 0.00028; Matches 17; Conservative 9; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Temple Jr., Davis L.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: McCabe, R. Tyler
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Ubes of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/10/627,685
CURRENT FILING DATE: 2003-07-28
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                          1 CXIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                        1 CRIXNQKCFQHLDACCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CRIXNQKCFQHLDDCCSRKCARFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19, Application US/10627685; Publication No. US20040092447A1; GENERAL INFORMATION:
APPLICANT: Cornell-Bell, Ann H.; APPLICANT: Temple Jr., Davis L.; APPLICANT: Layer, Richard T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17, Application US/10627685
Publication No. US20040092447A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cornell-Bell, Ann H. APPLICANT: Pemberton, Karen E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: REPTIDE
LOCATION: (1)..(27)
COTHER INFORMATION: Xaa is Hyp
US-10-627-685-17
                                                                                                                                                                      NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
JUCHER INFORMATION: Xaa is Hyp
US-10-627-685-15
                                                                                                  TYPE: PRT ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Conus purpurascens
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-627-685-19
                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

```
Score 112; DB 15; Length 27;
Pred. No. 0.00028;
9; Mismatches 1; Indels
                                                                                                                                                                                         GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Cornell-Bell, Ann H.

APPLICANT: Pemberton, Karen E.

APPLICANT: Temple Jr., Davis I.

APPLICANT: McCabe, R. Tyler

APPLICANT: McCabe, R. Tyler

APPLICANT: Oones, Robert M.

APPLICANT: Cognetix, Inc.

TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA

TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA

CURRENT FILING DATE: 2000-09-20

PRIOR APPLICATION NUMBER: US 60/219,438

PRIOR APPLICATION NUMBER: US 60/219,438

PRIOR APPLICATION NUMBER: US 60/155,135

PRIOR FILING DATE: 2000-07-20

SROID NOS: 25

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntan, Marchiael
APPLICANT: Watkins, March
APPLICANT: Garrett, James E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Shon, Ki-Joon
APPLICANT: Shon, Ki-Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Cartier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
CURRENT PPLICATION NUMBER: US/09/910,082A
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SEQ ID NO 395
1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:|| |:|:|:|||||| |:||:||:||| CRIXAQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 395, Application US/09910082A; Publication No. US20030119731A1; GENERAL INFORMATION:
                                                                                                                                    ; Sequence 25, Application US/10627685; Publication No. US20040092447A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: (1)...(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 63.0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: PEPTIDE LOCATION: (1)..(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-910-082A-395
                                                                                                                   -10-627-685-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE
                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

```
Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                  Query Match 67.5%; Score 81; DB 10; Length 26; Best Local Similarity 34.6%; Pred. No. 0.28; Matches 9; Conservative 13; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 67.5%; Score 81; DB 16; Length 26; Best Local Similarity 34.6%; Pred. No. 0.28; Matches 9; Conservative 13; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIncosh, J. Michael
APPLICANT: McIncosh, J. Michael
APPLICANT: Markins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Shon, Ki-Joones E.
APPLICANT: Shon, Ki-Joones, Robert M.
APPLICANT: Jacobsen, Richard
APPLICANT: Gartier, G. Edward
TITLE OP INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Publication No. Control of GENERAL INCRMATION:
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Matkins, Maren
APPLICANT: Markins, Maren
APPLICANT: Garrett, James E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2014-01-29
CURRENT FILING DATE: 2004-01-29
PRIOR APPLICATION NUMBER: US 09/910,082
PRIOR FILING DATE: 2001-07-23
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2001-05-616
PRIOR FILING DATE: 2001-05-616
PRIOR FILING DATE: 2001-05-65,888
PRIOR FILING DATE: 2001-05-65
NUMBER OF SEQ ID NOS: 413
SOFTWARE: Patentin Version 3.0
SOFTWARE: 26
LENGTH: 26
                                                                                                                                                                                                                                                                             1 CKLKGOSCRRIMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                              1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | ::: |:|::: |||||::| :::|
1 CKLKGQSCRRTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Shon, Ki-Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Cartier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 257, Application US/09910082A Publication No. US20030119731A1
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 395, Application US/10765926
Publication No. US20040132663A1
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Conus striatus
US-09-910-082A-395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Conus striatus
US-10-765-926-395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-910-082A-257
                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
```

. 0

```
APPLICANT: Shon, Ki-Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Gartier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
CURRENT FILING DATE: 2001-07-23
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR APPLICATION NUMBER: US 60/265,888
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: PatentIn version 3.0
SEQ ID NO 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CKLKGQSCRRTMXDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S-10-765-926-258
Sequence 258, Application US/10765926
Publication No. US20040132663A1
GENERAL INFORMATION:
                                                 atkins, Maren
arrett, James E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10; Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 16; Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           General Invergention

APPLICANT: University of Utah Research Foundation

APPLICANT: Cognetix, Inc.

APPLICANT: Cognetix, Inc.

APPLICANT: Cognetix, Inc.

APPLICANT: McIntosh, J. Michael

APPLICANT: Matkins, Maren

APPLICANT: Markins, Maren

APPLICANT: Garrett, James E.

APPLICANT: Garrett, James E.

APPLICANT: Jacobsen, Richard

APPLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc. APPLICANT: Olivera, Baldomero M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 67.5%; Score 81; DB 10
Best Local Similarity 34.6%; Pred. No. 0.31;
Matches 9; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.5%; Score 81; DB 16
34.6%; Pred. No. 0.31;
Live 13; Mismatches
CURRENT APPLICATION NUMBER: US/09/910,082A CURRENT FILING DATE: 2001-07-23
                                  CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR FILING DATE: 2000-07-21
PRIOR PELING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: Patentin version 3.0
LENGTH: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 CKLKGQSCRRTMYDCCSGSCGRRGKC 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 55
US-09-910-082A-258
Sequence 258, Application US/09910082A
Publication No. US20030119731A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 257, Application US/10765926
; Publication No. US20040132663Al
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cognetix, Inc.
Olivera, Baldomero M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 34.69
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Conus striatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conus striatus
                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-910-082A-257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Cor
US-10-765-926-257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Pat.
SEQ ID NO 257
LENGTH: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 업
```

```
TYPE: PRT
ORGANISM:
CONDUSTANT
NORGANISM:
NAME/KEX: PEPTIDE
LOCATION: (1)...(26)
OTHER INFORMATION: Xaa at residue 13 is Tyr, 1251-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O
THEN INFORMATION: - sulpho-Tyr or O-phospho-Tyr
US-09-910-082A-258
                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Conus striatus
FRATURE:
NAME/KE: PEPTIDE
LOCATION: (1)..(26)
OTHER INFORMATION: Xaa at residue 13 is Tyr, 1251-Tyr, mono-iodo-Tyr,
OTHER INFORMATION: di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr.
                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                 Query Match 61.7%; Score 74; DB 10; Length 26; Best Local Similarity 34.6%; Pred. No. 1.3; Matches 9; Conservative 13; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Matkins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Shon, Ki-Joon
APPLICANT: Shon, Ki-Joon
APPLICANT: Jones, Robert M.
APPLICANT: Jones, Robert M.
APPLICANT: Cartier, G. Edward
ITILE OF INVENTION: Omega-Conopeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THILE REPERRNCE: 2314-241
CURRENT APPLICATION NUMBER: US/10/765,926
CURRENT FILING DATE: 2004-01-29
PRIOR APPLICATION NUMBER: US 09/910,082
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR APPLICATION NUMBER: US 60/265,888
PRIOR APPLICATION NUMBER: US 60/265,888
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SEQ ID NO 258
LENTH: 26
```

ö

34.6%; Pred. No. 1.4e+02; tive 12; Mismatches 5;

2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27

Tue Apr 19 09:12:33 2005

```
Best Local Similarity 34.6
Matches 9; Conservative
                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                              ö
                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Remaining Prior Application data removed - See File Wrapper or PALM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CANT: VOSS, Edward Z.

OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME REFERENCE: 21402-050 CIP
                                                                                                                 .
0
                                                  Query Match 61.7%; Score 74; DB 16; Length 26; Best Local Similarity . 34.6%; Pred. No. 1.3; Matches 9; Conservative 13; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 21402-050 CLF
CURRENT APPLICATION NUMBER: US/10/190,115
CURRENT FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: 60/303,168
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/368,996
                                                                                                                                                         1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/366,996
PRIOR FILING DATE: 2002-04-01
PRIOR PELING DATE: 2002-04-01
PRIOR PELING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2000-07-03
PRIOR PELING DATE: 2000-07-03
PRIOR PILING DATE: 2000-07-03
PRIOR PILING DATE: 2000-07-03
PRIOR PILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/216,585
PRIOR PILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/216,585
PRIOR APPLICATION NUMBER: 60/216,586
PRIOR PILING DATE: 2001-07-07
PRIOR PILING DATE: 2001-07-07
PRIOR PILING DATE: 2001-07-07
PRIOR PILING DATE: 2000-07-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shenoy, Suresh G.
Shimkets, Richard A.
Spaderna, Steven K.
Spytek, Kimberly A.
Szekeres, Edward S. Jr.
Taupler, Raymond J. Jr.
                                                                                                                                                                                                                                                                                                                                 Sequence 25, Application US/10190115
Publication No. US20030207394A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mezick, Amanda J.
Padigaru, Muralidhara
Patturajan, Meera
Ratelli, Luca
Shen, Lei
                                                                                                                                                                                                                                                                                                                                                                                                         Alsobrook, John P. II
Boldog, Ferenc L.
Burgess, Catherine E.
Casman, Stacie J.
Grosse, William M.
Gusev, Vladimir Y.
Ji, Weizhen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: CuraSeqList version 0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tchernev, Velizar T.
Zerhusen, Bryan D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pley, Denise M.
u, Xiaohong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-190-115-25
US-10-765-926-258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 25
LENGTH: 2524
```

```
APPLICANT: Shimkets, Richard
APPLICANT: Padigaru, Muzalidhara
TITILE OF INVENTION: No. US20040014081Alel Proteins and Nucleic Acids Encoding Same
FILE REPERENCE: 21402-050 CON2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/216,722
PRIOR FILING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-17
PRIOR PLING DATE: 2000-07-17
PRIOR PLING DATE: 2000-07-17
Remaining Prior Application data removed - See File Wrapper or PALM.
SUMBER OF SEC ID NOS: 100
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
60.0%; Score 72; DB 15; Length 2524;
Best Local Similarity 34.6%; Pred. No. 1.4e+02;
Matches 9; Conservative 12; Mismatches 5; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/369,072
CURRENT FILING DATE: 2003-02-18
PRIOR PRIORATION NUMBER: 10/174,372
PRIOR FILING DATE: 2002-06-17
PRIOR FILING DATE: 2001-07-03
PRIOR FILING DATE: 2001-07-03
PRIOR FILING DATE: 2000-07-03
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
248 GFSGQNCEENIDDCPSNNCRNGGTCV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 GFSGQNCEENIDDCPSNNCRNGGTCV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 XIXNOXCXQXLDDCCSXXCNXXXXX 27
                                                                                                                                                        Sequence 25, Application US/10369072
Publication No. US20040014081A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Burgess, Catherine E
                                                                                                                                                                                                                                           APPLICANT: Alsobrook II, John P
APPLICANT: Spaderna, Stephen K
APPLICANT: Tchernev, Velizar
APPLICANT: Liu, Xiaohong
APPLICANT: Shenoy, Suresh
APPLICANT: Spytek, Kimberly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Szerkeres, Edward S
Lepley, Denise M
                                                                                                                                                                                                                                                                                                                                                                                                               Zerhusen, Bryan
Patturajan, Meera
Taupier, Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rastelli, Luca
Grosse, William M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Xenopus laevis
US-10-369-072-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Pater
SEQ ID NO 25
LENGTH: 2524
```

RESULT 59

60.0%; Score 72; DB 15; Length 2524;

Query Match

```
APPLICANT: Miele, Lucio
TITLE OF INVENTION: METHOD AND REAGENTS FOR EPITHELIAL BARRIER FORMATION AND TREATMEN
TITLE OF INVENTION: MALIGNANT AND BENIGN SKIN DISORDERS BY MODULATING THE NOTCH PATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: misc_feature
LOCATION: (891).
OTHER INFORMATION: The 'Xaa' at location 891 stands for Gly, or Ala.
NAME/KEY: misc_feature
LOCATION: (1763)...(1763)
OTHER INFORMATION: The 'Xaa' at location 1763 stands for Gln, Arg, Pro, or Leu.
NAME/KEY: misc_feature
LOCATION: (1787)...(1787)
OTHER INFORMATION: The 'Xaa' at location 1787 stands for Thr, Ala, Pro, or Ser.
OTHER INFORMATION: Constitutively Active No. US20020151487Alch-1
                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                ; FEATURE:

: NAME/KEY: PEPTIDE

: LOCATION: (1)..(26)

: OTHER INFORMATION: Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr,

: OTHER INFORMATION: d1-iodo-Tyr, O -sulpho-Tyr or O-phospho-Tyr
                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 56.7%; Score 68; DB 9; Length 2444; Best Local Similarity 30.8%; Pred. No. 3.4e+02; Matches 8; Conservative 12; Mismatches 6; Indels
                                                                                                                                                                                                                                Length 26;
                                                                                                                                                                                                                                DB 16;
                                                                                                                                                                                                                             Query Match 58.3%; Score 70; DB 1
Best Local Similarity 34.6%; Pred. No. 3.2;
Matches 9; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 212583
CURRENT APPLICATION NUMBER: US/09/944,849
CURRENT FILING DATE: 2001-08-31
PRIOR FILING DATE: 2000-08-31
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 2444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248 GFTGQNCEENIDDCPGNNCKNGGACV 273
                                                                                                                                                                                                                                                                                                                                     1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                   1 CKLKGQSCRKTSXDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 469, Application US/10072012
Publication No. US20040033493A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09944849
Patent No. US20020151487A1
GENERAL INFORMATION:
APPLICANT: Nickoloff, Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Li, Li
Gangolli, Esha
Padigaru, Muralidhara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: TChernev, Velizar
APPLICANT: Spytek, Kimberly
APPLICANT: Zerhuenen, Bryan
APPLICANT: Patturajan, Meera
APPLICANT: Shimkete, Richard
TYPE: PRT
ORGANISM: Conus striatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JS-10-072-012-469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-944-849-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (1)..(26)
; OTHER INFORMATION: Xaa at residue 13 is Tyr, 1251-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
; OTHER INFORMATION: -sulpho-Tyr or O-phospho-Tyr
US-09-910-082A-268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.3%; Score 70; DB 10; Length 26; illarity 34.6%; Pred. No. 3.2; Conservative 12; Mismatches 5; Indels
                                                                                        APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Watkins, Maren
APPLICANT: Shor, Ki-Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Jones, Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: University of Utah Research Foundation APPLICANT: University of Utah Research Foundation APPLICANT: Olivers, Baldomero M. APPLICANT: Matkins, Maren APPLICANT: Watkins, Maren APPLICANT: Garrett, James E. APPLICANT: Shon, Ki-Joon APPLICANT: Jacobsen, Richard APPLICANT: Jacobsen, Richard APPLICANT: Jones, Robert M.
                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Omega-Conopeptides
TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
CURRENT APPLICATION NUMBER: US/09/910,082A
CURRENT FILING DATE: 2001-07-23
PRIOR PAPLICATION NUMBER: US 60/219,616
PRIOR PILING DATE: 2000-07-21
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/765,926
CURRENT FILING DATE: 2004-01-29
PRIOR PLILING DATE: 2004-01-29
PRIOR PLILING DATE: 2001-07-23
PRIOR PLILING DATE: 2000-07-21
PRIOR PLILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/265,888
PRIOR APPLICATION NUMBER: US 60/265,888
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: Patentin version 3.0
SERO ID NO 268
LENGTH: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cartier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
Sequence 268, Application US/09910082A Publication No. US20030119731A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 268, Application US/10765926; Publication No. US20040132663Al; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Conus striatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 9; Conserva
US-09-910-082A-268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 60
US-10-765-926-268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 268
LENGTH: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              엄
```

ઠે

```
APPLICANT: Gusev, Viadimir Y.
APPLICANT: Golman, Steven D.
APPLICANT: Wolenc, Adam R.
APPLICANT: Wolenc, Asam R.
APPLICANT: Wolenc, Asam R.
APPLICANT: Porta, Carol E. A
APPLICANT: Porta, Carol E. A
APPLICANT: Briese, William M.
APPLICANT: Briese, Daniel R.
APPLICANT: Briese, Doctor, 238
CURRENT FILING DATE: 2002-01-31
PRIOR FILING DATE: 2002-01-31
PRIOR PRIOR PLING DATE: 60/265,102
PRIOR PRIOR PLING DATE: 60/265,112
PRIOR PRIOR PLING DATE: 60/265,127
PRIOR PRIOR PLING DATE: 60/265,127
PRIOR PRIOR PLING DATE: 60/265,127
PRIOR PRIOR PLING DATE: 2001-01-31
PRIOR PRIOR PLING DATE: 2001-01-31
PRIOR PRIOR PLING DATE: 2001-01-31
PRIOR PLING DATE: 2001-02-06
PRIOR PLING DATE: 2001-02-07
PRIOR PLING DATE: 2001-0
                                                                                                                                                                                                                                                                                                                                                                                                                     Padigaru, Muralidhara
Anderson, David W.
Rastelli, Luca
Miller, Charles E.
Gerlach, Valerie
Taupier Jr. Raymond J.
Gusev, Vladimir Y.
                                                                                                                                                                                                                                                                   Patturajan, Meera
Shimkets, Richard
APPLICANT: Rassell', Luca en APPLICANT: Miller Charles En APPLICANT: Miller Charles En APPLICANT: Miller Charles En APPLICANT: Taupier Tr. Raymond J. APPLICANT: Taupier Tr. Raymond J. APPLICANT: Taupier Tr. Raymond J. APPLICANT: Colman, Stewen D. APPLICANT: Colman, Stewen D. APPLICANT: Pens, Carol E. APPLICANT: Pens, Carol E. APPLICANT: Pens, Carol E. APPLICANT: Pens, Carol E. APPLICANT: Display Deniel K. APPLICANT: Misger, Daniel K. APPLICANT: Risger, Daniel K. APPLICANT: Risger, Daniel K. APPLICANT: Risger, Carberine E. TITLE OP INVENTION NUMBER: 10/10/012.012

FRIDR APPLICANT: NUMBER: 10/265,102

FRIDR APPLICATION NUMBER: 60/265,514

FRIDR PILING DATE: 2001-01-31

FRIDR PILING DATE: 2001-02-02

FRIDR APPLICATION NUMBER: 60/265,395

FRIDR PILING DATE: 2001-02-02

FRIDR PILING DATE: 2001-02-02

FRIDR PILING DATE: 2001-02-02

FRIDR PILING DATE: 2001-02-02

FRIDR FILING DATE: 2001-02-03

FRIDR FILING DATE: 2001-03-03

FRIDR FILING DATE: 2001-03-03

FRIDR FILING DATE: 2001-03-03

FRIDR FILING DATE: 2001-03-03

FRIDR FILING DATE: 2001-03-03-03

FRIDR FILING DATE: 2001-03-03-03

FRIDR FILING DATE: 2001-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 30.8%; Pred. No. 3.4e+02;
Matches 8; Conservative 12; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Wherein Xaa is any amino acid. FEATURE:
NAME/KEY: VARIANT
LOCATION: (1763)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: VARIANT
LOCATION: (1787)
OTHER INFORMATION: Wherein Xaa is any amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (1763)
OTHER INFORMATION: Wherein Xaa is any amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: VARIANT
LOCATION: (891)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-072-012-469
```

```
ö
                                                                                                                                                                                                                                                                                                                56.7%; Score 68; DB 15; Length 2555; 30.8%; Pred. No. 3.5e+02; tive 12; Mismatches 6; Indels
TYPE: PRT
ORGANISM: Homo sapiens
PEATURE:
LOCATION: (890)
OTHER INFORMATION: Wherein Xaa is any amino acid.
FEATURE:
LOCATION: (1762)
                                                                                                                                                                       OTHER INFORMATION: Wherein Xaa is any amino acid.
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1786)
OTHER INFORMATION: Wherein Xaa is any amino acid.
US-10-072-012-468
                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 30.8:
Matches 8; Conservative
```

ö

RESULT 63 US-10-072-012-468 ; Sequence 468, Application US/10072012 ; Publication No. US20040033493A1

```
PRIOR FILING DATE: 2002-01-31

PRIOR FILING DATE: 2001-01-02-02

PRIOR FILING DATE: 2001-01-03-03

PRIOR FILING DATE: 2001-01-31

PRIOR FILING DATE: 2001-02-05

PRIOR FILING DATE: 2001-02-05

PRIOR FILING DATE: 2001-02-05

PRIOR PILING DATE: 2001-02-05

PRIOR PILING DATE: 2001-02-05

PRIOR PILING DATE: 2001-02-07

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 201-02-09

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPLICANT: Lepley, Denie M.

PPLICANT: Reger, Daniel K.

PPLICANT: Burgess, Catherine E.

PLICANT: Burgess, Catherine E.

TILE OF INVENTION: Proceins and Nucleic Acids Encoding Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 56.7%; Score 68; DB 15; L. Best Local Similarity 30.8%; Pred. No. 3.5e+02; Matches 8; Conservative 12; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248 GFTGQNCEENIDDCPGNNCKNGGACV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/072,012
CURRENT FILING DATE: 2002-01-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 467, Application US/10072012
Publication No. US20040033493A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rastelli, Luca
Miller, Charles E.
Gerlach, Valerie
Taupier Jr, Raymond J.
Gusev, Vladimir Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gangolli, Esha
Padigaru, Muralidhara
Anderson, David W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alsobrook II, John P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zerhusen, Bryan
Patturajan, Meera
Shimkets, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Colman, Steven D.
Wolenc, Adam R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Furtak, Katarzyna
Grossė, William M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carol E. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spytek, Kimberly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , ORGANISM: Homo sapiens
US-10-072-012-134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wolenc,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Zhang, Jie
APPLICANT: Wehrman, Tom
APPLICANT: Wehrman, Tom
APPLICANT: Wehrman, Tom
IIILE OF INVENTION: No. USCO040013657Alel Nucleic Acids and
IIILE OF INVENTION: Polypeptides
IIILE REFERENCE: 21272-029CIP2H-PCT
CURRENT APPLICATION NUMBER: US/10/294,006
CURRENT FILING DATE: 2002-11-12
PRIOR FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PL_Genes Version 2.0
SEQ ID NO 12

FENCENT SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 56.7%; Score 68; DB 15; Length 2556; Best Local Similarity 30.8%; Pred. No. 3.5e+02; Matches 8; Conservative 12; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CANT: Burgess, Catherine E. OF INVENTION: Proteins and Nucleic Acids Encoding Same
                                                                                                                  248 GFTGQNCEENIDDCPGNNCKNGGACV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248 GFTGQNCEENIDDCPGNNCKNGGACV 273
                                                                               2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/072,012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 XIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/10072012
o. US20040033493A1
                                                                                                                                                                                                                                                                                              ; Sequence 12, Application US/10294006
; Publication No. US20040013657A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gerlach, Valerie
Taupier Jr, Raymond J.
Gusev, Vladimir Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gangolli, Esha
Padigaru, Muralidhara
Anderson, David W.
Rastelli, Luca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alsobrook II, John P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Miller, Charles E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zerhusen, Bryan
Patturajan, Meera
Shimkets, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Colman, Steven D.
Wolenc, Adam R.
Pena, Carol E. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Furtak, Katarzyna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Grosse, William M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tchernev, Velizar
Spytek, Kimberly
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Asundi, Vinod
APPLICANT: Yang, Yonghong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lepley, Denise M
Rieger, Daniel K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 134, Ap
Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                              US-10-294-006-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-294-006-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPLICANT
                                                                                                                                        g
                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠ
```

ô

Gaps

```
Sequence 39, Application US/10764415B
; Publication No. US2005005903A1
; Publication No. US2005005903A1
; GENERAL INFORMATION:
; APPLICANT: Lorantis Ltd.
; TITLE OF INVENTION: Modulations of Notch signalling for use in Immunotherapy
; FILE REPERENCE: P011073US
; CURRENT APPLICATION NUMBER: US/10/764,415B
; CURRENT APPLICATION NUMBER: GB0118153.6
; PRIOR APPLICATION NUMBER: GB021923.6
; PRIOR PLING DATE: 2002-04-05
; PRIOR PILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: GB0212283.6
; PRIOR APPLICATION NUMBER: GB0212283.6
; PRIOR APPLICATION NUMBER: GB0212283.6
; PRIOR PILING DATE: 2002-05-28
; PRIOR FILING DATE: 2002-05-28
; PRIOR FILING DATE: 2002-05-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                 .
.
                                                                                              56.7%; Score 68; DB 17; Length 2556; allarity 30.8%; Pred. No. 3.5e+02; Conservative 12; Mismatches 6; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 56.7%; Score 68; DB 17; Length 25 Best Local Similarity 30.8%; Pred. No. 3.5e+02; Matches 8; Conservative 12; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ENIEND, FUNDANDEL CYRILLE PASCAL
APPLICANT: CHAMPION, BRIAN ROBERT
APPLICANT: CHAMPION, BRIAN ROBERT
APPLICANT: CHAMPION, BRIAN ROBERT
APPLICANT: RAGNO, SILVIA
APPLICANT: RAGNO, SILVIA
APPLICANT: TAGNO, SILVIA
APPLICANT: TOUNG, LESLEY LYNN
TITLE OF INVENTION: MEDICAL TREATMENT
FILE REFERENCE: 65452-2012
CURRENT FILING DATE: 2004-05-14
FRIOR APPLICATION NUMBER: DCT/GB02/05133
PRIOR FILING DATE: 2002-11-13
PRIOR FILING DATE: 2001-11-14
PRIOR PPLICATION NUMBER: GB 0127271.5
PRIOR PPLICATION NUMBER: GB 0220913.8
PRIOR PPLICATION NUMBER: GB 0220913.8
PRIOR APPLICATION NUMBER: GB 0220913.8
PRIOR PILING DATE: 2002-09-10
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PARCENTIN VOIL 3.2
SOFTWARE: PARCENTIN VOIL 3.2
                                                                                                                                                                                                                                                                                                248 GFTGQNCEENIDDCPGNNCKNGGACV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248 GFTGQNCEENIDDCPGNNCKNGGACV 273
                                                                                                                                                                                                                                                 2 XIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:

NAME/KEY: MOD RES

LOCATION: (89I)

OTHER INFORMATION: Variable amino acid
US-10-846-989-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 56, Application US/10846989
Publication No. US20050026831A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BODMER, MARK WILLIAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                      Query Match
Best Local Similarity
Matches 8; Conserv
                   US-10-765-727-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-764-415B-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 69
                                                                                                                                                                                                                                                     ઠ
                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 22, Application US/10765727
Publication No. US20050025751A1
GENERAL INFORMATION:
APPLICANT: BODMER, MARK WILLIAM
APPLICANT: BRIEND, EMMANUEL CYRILLE PASCAL
APPLICANT: CHAMPION, BRIAN ROBERT
APPLICANT: YOUNG, LESLEY LYNN
TITLE OF INVENTION: MODULATORS OF NOTCH SIGNALLING FOR USE IN IMMUNOTHERAPY
FILE REFERENCE: 674525-2010
               PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-31
PRIOR PLING DATE: 2001-01-31
PRIOR PLING DATE: 2001-01-31
PRIOR PLING DATE: 2001-01-31
PRIOR PLING DATE: 2001-01-31
PRIOR FILING DATE: 2001-02-02
PRIOR FILING DATE: 2001-02-02
PRIOR PLING DATE: 2001-02-02
PRIOR PLING DATE: 2001-02-07
PRIOR PLING DATE: 2001-02-08
PRIOR PLING DATE: 2001-02-08
PRIOR PLING DATE: 2001-02-08
PRIOR PLING DATE: 2011-02-08
PRIOR PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
56.7%; Score 68; DB 15; Length 2556;
Best Local Similarity 30.8%; Pred. No. 3.5e+02;
Matches 8; Conservative 12; Mismatches 6; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: VARIANT
; LOCATION: (891)
OTHER INFORMATION: Wherein Xaa is any amino acid.
US-10-072-012-467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION WUMBER: PCT/GB02/03426
PRIOR FILING DATE: 2005-07-25
PRIOR FILING DATE: 2005-07-25
PRIOR FILING DATE: 2005-07-25
PRIOR PELICATION NUMBER: GB 0207930.9
PRIOR PELICATION NUMBER: GB 0207930.9
PRIOR APPLICATION NUMBER: GB 0212282.8
PRIOR FILING DATE: 2002-05-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248 GFTGQNCEENIDDCPGNNCKNGGACV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/765,727
CURRENT FILING DATE: 2004-01-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 XIXNOXCXOXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (891)
OTHER INFORMATION: Variable amino acid
60/265,514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Post SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
```

```
; ORGANISM: Rattus norvegicus
US-10-369-072-29
                                                                                                                                                       US-10-190-115-29
                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME FILE REPERBUCE: 21402-050 CIP CURRENT APPLICATION NUMBER: US/10/190,115 CURRENT FILING DATE: 2003-02-10 PRIOR APPLICATION NUMBER: 60/303,168
                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                             Query Match 56.7%; Score 68; DB 17; Length 2556; Best Local Similarity 30.8%; Pred. No. 3.5e+02; Matches 8; Conservative 12; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                            248 GFTGQNCEENIDDCPGNNCKNGGACV 273
                                                                                                                                                                                                                                                                                                                                                     2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                  NAME/KEY: MISC FEATURE
COCATION: (891)...
COTHER INFORMATION: X is any amino acid
US-10-764-415B-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DR FILING DATE: 2001-07-05, DR FILING DATE: 2001-07-05

DR APPLICATION NUMBER: 60/368, 996

DR FILING DATE: 2002-04-01

DR APPLICATION NUMBER: 60/386, 816

DR FILING DATE: 2000-07-03

DR APPLICATION NUMBER: 60/215, 856

DR FILING DATE: 2000-07-03

DR APPLICATION NUMBER: 60/215, 856

DR FILING DATE: 2000-07-03

DR APPLICATION NUMBER: 60/215, 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 2000-07-03
APPLICATION UNDBER: 60/216,585,
FILING DATE: 2000-07-07
APPLICATION NUMBER: 60/216,586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2001-07-07
APPLICATION NUMBER: 60/216,722
FILING DATE: 2000-07-07
APPLICATION NUMBER: 60/218,622
FILING DATE: 2000-07-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 29, Application US/10190115; Publication No. US20030207394A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Alsobrook, John P. II
APPLICANT: Boldog, Ferenc L.
APPLICANT: Burgess, Catherine E.
APPLICANT: Casman, Stacie J.
APPLICANT: Grosse, William M.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Ji, Weizhen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spytek, Kimberly A.
Szekeres, Edward S. Jr
Taupier, Raymond J. Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Padigaru, Muralidhara
Patturajan, Meera
Rastelli, Luca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tchernev, Velizar T.
Zerhusen, Bryan D.
Voss, Edward Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      himkets, Richard A paderna, Steven K.
NUMBER OF SEQ ID NOS: 40,
SOFTWARE: Patentin version 3.0
SEQ ID NO 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lepley, Denise M.
Liu, Xiaohong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lezick, Amanda J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shenoy, Suresh G.
                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR
                                                                                                                                                                                                                                                                                                                                                       ઠે
```

```
| NUMBER OF SOLID NOS. 136
| SOFTWARE. CLEAGEGLIST VETSION 0.1
| SOFTWARE. SOFTWAR
```

```
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-31
PRIOR PILING DATE: 2001-01-31
PRIOR PELICATION NUMBER: 60/265,517
PRIOR PELING DATE: 2001-01-31
PRIOR PELING DATE: 2001-01-31
PRIOR PELING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,395
PRIOR APPLICATION NUMBER: 60/266,395
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR PELING DATE: 2001-02-05
PRIOR PELING DATE: 2001-02-05
PRIOR PELING DATE: 2001-02-05
PRIOR PELING DATE: 2001-02-05
PRIOR PELING DATE: 2001-02-07
PRIOR PELING DATE: 2001-02-08
PRIOR PELING DATE: 2001-02-08
PRIOR PELING DATE: 2001-02-08
PRIOR FILING DATE: 2001-02-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 55.8%; Score 67; DB 15; Length 2531; Best Local Similarity 30.8%; Pred. No. 4.38+02; Matches 8; Conservative 12; Mismatches 6; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Rieger, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-258
CURRENT APPLICATION NUMBER: US/10/072,012
                                                                                                   248 GFAGQNCEENVDDCPGNNCKNGGACV 273
                                                              2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 XIXNOXCXOXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                         Sequence 471, Application US/10072012
Publication No. US20040033493A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gerlach, Valerie
Taupier Jr, Raymond J.
Gusev, Vladimir Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gangolli, Esha
Padigaru, Muralidhara
Anderson, David W.
Rastelli, Luca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Miller, Charles E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zerhusen, Bryan
Patturajan, Meera
Shimkets, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Colman, Steven D. Wolenc, Adam R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Furtak, Katarzyna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rosse, William M
                                                                                                                                                                                                                                                                                                                                                                                                               Tchernev, Velizar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pena, Carol E. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Rattus norvegicus
US-10-072-012-471
                                                                                                                     g
                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              i Gerlach,
I Taupher Jr.
I Gusev, Vladimir 1.
IT: Colman, Steven D.
MT: Wolenc, Adam R.
ANT: Wolenc, Adam R.
ANT: Pena, Carol E.
Grosse, William M.
ICANT: Hepley, Dennise M.
ICANT: Rieger, Daniel M.
ICANT: Ling APPLICATION NUMBER: 60/265, 514
PRIOR FILING DATE: 2001-01-31
PRIOR PELING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/266, 767
PRIOR FILING DATE: 2001-02-02
PRIOR PELING DATE: 2001-02-02
PRIOR PELING DATE: 2001-02-02
PRIOR PELING DATE: 2001-02-03
PRIOR PELING DATE: 2001-02-04
PRIOR PELING DATE: 2001-02-07
PRIOR PELING DATE: 2001-02-08
PRIOR PELING DA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 1391
SOFTWARE: Patentin Ver. 2.1
                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
Query Match
55.8%; Score 67; DB 15; Length 2531;
Best Local Similarity 30.8%; Pred. No. 4.3e+02;
Matches 8; Conservative 12; Mismatches 6; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 55.8%; Score 67; DB 15; Length 2531; Best Local Similarity 30.8%; Pred. No. 4.3e+02; Matches 8; Conservative 12; Mismatches 6; Indels
                                                                                                                                                                                           248 GFAGONCEENVDDCPGNNCKNGGACV 273
                                                                                                                                           2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 470, Application US/10072012
Publication No. US20040033493A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gangolli, Esha
Padigaru, Muralidhara
Anderson, David W.
Rastelli, Luca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Miller, Charles E. Gerlach, Valerie Taupier Jr, Raymond J. Gusev, Vladimir Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zerhusen, Bryan
Patturajan, Meera
Shimkets, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Rattus norvegicus
US-10-072-012-470
                                                                                                                                                                                                                                                                                                                                                     US-10-072-012-470
                                                                                                                                                                                                             g
                                                                                                                                               à
```

ö

Gaps

g

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gray, Grace
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
VERTEBRATE DELTA GENE AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 94
                                                                                                                                                                                                                                                                                                              LOCATION: (1)...(29)
CTHER INFORMATION: Xaa at residue 4 and 7 is Pro or Hyp; Xaa at
OTHER INFORMATION: xeaidue 22 and 29 is Tyr, 1251-Tyr, mono-iodo-Tyr,
OTHER INFORMATION: di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
US-10-765-926-149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Myriad Genetics, Inc.
APPLICANT: Cimbora, Daniel M.
APPLICANT: Meichman, Karen
APPLICANT: Bartel, Paul L.
TITLE OF INVENTION: Protein-Protein Interactions
FILE REFERENCE: 2318-278-11
FILE REFERENCE: 2318-278-12
CURRENT APPLICATION NUMBER: US/10/024,599
CURRENT APPLICATION NUMBER: US 60/256,986
PRIOR APPLICATION NUMBER: US 60/256,986
PRIOR PILING DATE: 2001-12-21
PRIOR PILING DATE: 2001-12-21
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ish-Horowicz, David
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 55.0%; Score 66; DB 16
Best Local Similarity 38.5%; Pred. No. 8.7;
Matches 10; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 CVCVNGWSGDDCSENIDDCAFASCTPGSTCI 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CXIXN----QXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 25.8%; Pred. No. 46;
Matches 8; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , LOCATION: 1..176
; OTHER INFORMATION: Xaa is Gly or Cys
US-10-024-599-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/10024599 Publication No. US20020165352A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/09908322
Patent No. US20020107194A1
GENERAL INFORMATION:
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                           TYPE: PRT ORGANISM: Conus geographus FEATURE: NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: PEPTIDE
                                                                                                         SEQ ID NO 149
LENGTH: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JS-10-024-599-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-908-322-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: PEPTIDE
LOCATION: (1)..(29)
OTHER INFORMATION: Xaa at residue 4 and 7 is Pro or Hyp; Xaa at residue 22 and 29 is
OTHER INFORMATION: Tyr, 1251-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-pho
OTHER INFORMATION: spho-Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.0%; Score 66; DB 10; Length 29; 38.5%; Pred. No. 8.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: McIncosh, J. Michael
APPLICANT: Watkins, Maxen
APPLICANT: Watkins, Maxen
APPLICANT: Garrett, James E.
APPLICANT: Shon, Ki-Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jones, Robert M.
APPLICANT: Jones, Robert M.
APPLICANT: Jones, Robert M.
APPLICANT: Jones, Robert W.
APPLICANT: Jones, Robert M.
APPLICANT: Jones, Robert W.
APPLICANT: Jones, Robert W.
APPLICANT: Jones, Robert M.
APPLICANT: Jones, Robert M.
APPLICANT: Jones, Robert W.
APPLICANT: Jones W
                                                                                                                                                                                                                                                                         APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
COGNETIX, Inc.
APPLICANT: Olivers, Baldomero M.
APPLICANT: McIncoh, J. Michael
APPLICANT: Watkins, Maren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 2314-241

CURRENT APPLICATION NUMBER: US/09/910,082A

CURRENT APPLICATION NUMBER: US/09/910,082A

PRIOR APPLICATION NUMBER: US 60/219,616

PRIOR FILING DATE: 2000-07-21

PRIOR APPLICATION NUMBER: US 60/265,888

PRIOR APPLICATION NUMBER: US 60/265,888

PRIOR SEQ ID NOS: 413

SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 55.0%; Score bo; ub Best Local Similarity 38.5%; Pred. No. 8.7; Matches 10; Conservative 11; Mismatches
   248 GFAGGNCEENVDDCPGNNCKNGGACV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |: | ||:::: |||::: ||CKSXGTXCSRGMRDCCTSCLSXSNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Jones, Robert M.
APPLICANT: Cartier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
                                                                                                                                      Sequence 149, Application US/09910082A Publication No. US20030119731A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 149, Application US/10765926
; Publication No. US20040132663A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Garrett, James E.
Shon, Ki-Joon
Jacobsen, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Conus geographus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-910-082A-149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Pat
SEQ ID NO 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
```

ద ò

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.0%; Score 66; DB 10;
ilarity 32.0%; Pred. No. 1.7e+02;
Conservative 11; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Millennium Pharmaceuticals, Inc
APPLICANT: McCarthy, Sean
APPLICANT: Gearing, David
TITLE OF INVENTION: HUMAN DELIEA3 AND USES THEREOF
FILE REFERENCE: MBIO1997-002CP2M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.0%; Score 66; DB 14;
32.0%; Pred. No. 1.7e+02;
tive 11; Mismatches 6,
                      CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: ANIDET, Adriane M.
REGISTRATION NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 7326-122
TELEPHONE: 212-790-9090
TELEFAX: 212-796-9090
TELEFAX: 212-86-864
TELEFAX: 212-86-864
TELEFAX: 212-86-864
TELEFAX: 512-86-864
TELEFAX: 512-79-9090
TELEFAX: 512-79-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/417,719
CURRENT FILING DATE: 2003-04-17
PRIOR PILING DATE: 2003-04-17
PRIOR FILING DATE: 2000-05-09
PRIOR FILING DATE: 1999-06-11
PRIOR APPLICATION NUMBER: 08/872,855
PRIOR PILING DATE: 1999-06-11
PRIOR FILING DATE: 1999-06-11
PRIOR FILING DATE: 1997-04-04
NUMBER: OF SEQ ID NOS: 52
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36 GFSGRNCDDNLDDCTSFPCQNGGTC 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : ::|::||||||::|::|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 XIXNOXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 XIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 109, Application US/10042865; Publication No. US20040029216A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           LENGTH: 721 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/10417719
Publication No. US20030180784A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Padigaru, Muralidhara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 32.0°
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT .
ORGANISM: Xenopus Laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-042-865-109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-783-931-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-417-719-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-417-719-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gray, Grace
TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS
AND FRAGMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.0%; Score 66; DB 9; Length 721
32.0%; Pred. No. 1.7e+02;
tive 11; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/09783931
Publication No. US20030073620A1
GENERAL INFORMATION:
APPLICANT: 1Sh-Horowicz, David
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
                                                                                                                                                                                                 COMPUTER: 1BM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,322
FILING DATE: 17-Jul-2001
CLASSIFICATION: 
UNKNOWN>

                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION: CUMINIONIS

APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 18,872
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-69-9864
TELEFAX: 212-869-9864
TELEFAX: 212-869-9864
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
                      ADDRESSEE: Pennie & Edmonds LLP .
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/783,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-908-322-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : :: | | | | | :: | : : | 436 GFSGRNCDDNLDDCTSFPCQNGGTC 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 XIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 721 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                           COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 32.0%
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-783-931-5
```

à g

```
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shacks, Richard A.
APPLICANT: Spaderna, Steven K.
APPLICANT: Spytek, Theoria A.
APPLICANT: Szekere, Edward S. Jr.
APPLICANT: Taupier, Raymond J. Jr.
APPLICANT: Taupier, Raymond J. Jr.
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Carhusen, Bryan D.
APPLICANT: Voss, Edward Z.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME FILE REFERENCE: 21402-050 CIP
FILE REFERENCE: 21402-050 CIP
CURRENT APPLICATION NUMBER: US/10/190,115
                                  adigaru, Muralidhara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shenoy, Suresh
Spytek, Kimberly
Zerhusen, Bryan
Patturajan, Meera
Taupier, Raymond T
                                                           Patturajan, Meera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-190-115-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ellerman, Karen
APPLICANT: MacDougall, John
APPLICANT: Malyankar, Uriel M
APPLICANT: Milet, Isabele
APPLICANT: Milet, Isabele
APPLICANT: Saithson, Glennda
APPLICANT: Stone, David
APPLICANT: Stone, David
APPLICANT: Stone, David
TITLE OF INVENTION: Using the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 32.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 11; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TILLE REFERENCE: 21402-537
CURRENT APPLICATION NUMBER: US/10/042,865
CURRENT FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/260,417
PRIOR PILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-0
PRIOR FILING DATE: 2001-01-0
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/274,876
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/284,704
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36 GFSGRNCDDNLDDCTSFPCQNGGTC 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 XIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 81
US-10-190-115-4
US-10-190-115-4
Sequence 4, Application US/10190115
Fublication No. US20030207394A1
GENERAL INFORMATION:
APPLICANT Albobrook, John P. II
APPLICANT BOLdog, Ferenc L.
APPLICANT: Gaman, Stacie J.
APPLICANT: Gaman, Stacie J.
APPLICANT: Gamen, William M.
APPLICANT: Gueev, Vladimir Y.
APPLICANT: Gueev, Vladimir Y.
APPLICANT: Ji, Weizhen
                                                                                                                                                                                                                                                                                                              Boldog, Ference L
Grosse, William M
Alsobrook II, John P
Gerlach, Valerie L
Edinger, Shlomit R
Rothenberg, Mark E
                                                                                                    Zhong, Mei
Gangolli, Esha A
Burgess, Catherine E
Patturajan, Meera
Vernet, Corine A.M
                                                                                                                                                                                                                                            Tchernev, Velizar T
Miller, Charles E
Guo, Xiaojia
Bryan D
                               Casman, Stacie J
Shenoy, Suresh G
Spytek, Kimberly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lepley, Denise M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-042-865-109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 109
LENGTH: 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

```
ä
PRIOR PELING DATE: 2003-02-10
PRIOR PILING DATE: 2003-02-10
PRIOR PLING DATE: 2001-07-05
PRIOR PLING DATE: 2001-07-05
PRIOR PLICATION NUMBER: 60/386,996
PRIOR PLING DATE: 2002-06-07
PRIOR PLING DATE: 2002-06-07
PRIOR PLING DATE: 2000-07-03
PRIOR PLING DATE: 2000-07-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.0%; Score 66; DB 15; Length 1473; 25.8%; Pred. No. 3.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CXIXN----QXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 25.8%; Pred. No. 3.3e
Matches 8; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 82
US-10-369-072-4
; Sequence 4, Application US/10369072
; Publication No. US20040014081A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P
; APPLICANT: Spaderna, Stephen K
; APPLICANT: Tchernev, Velizar
, PPLICANT: Liu, Xiaohong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Grosse, William M
```

```
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REPERENCE: 21402-050 CIP
GURRENT PAPLICATION NUMBER: US/10/190,115
CURRENT PILING DATE: 2002-10
FRIOR APPLICATION NUMBER: 60/368,996
FRIOR APPLICATION NUMBER: 60/368,996
FRIOR APPLICATION NUMBER: 60/368,996
FRIOR PILING DATE: 2002-04-01
FRIOR PELING DATE: 2002-06-01
FRIOR FILING DATE: 2000-07-03
FRIOR PILING DATE: 2000-07-03
FRIOR PELING DATE: 2000-07-03
FRIOR APPLICATION NUMBER: 60/215,856
FRIOR PELING DATE: 2000-07-03
FRIOR PELING DATE: 2000-07-03
FRIOR PELING DATE: 2000-07-03
FRIOR PELING DATE: 2000-07-07
FRIOR FILING DATE: 2000-07-07
FRIOR FILING DATE: 2000-07-07
FRIOR FILING DATE: 2000-07-07
FRIOR FILING DATE: 2000-07-07
FRIOR PELING DATE: 2000-07-07
FRIOR PELING DATE: 2000-07-07
FRIOR APPLICATION NUMBER: 60/216,728
FRIOR PELING DATE: 2000-07-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.0%; Score 66; DB 15; Length 2447; illarity 29.0%; Pred. No. 5.3e+02; Conservative 15; Mismatches 3; Indels
                                                78 CVCVNGWSGDDCSENIDDCAFASCTPGSTCI 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        279 CVCVNGWSGLDCSENIDDCDTAACSPGSTCV 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CXIXN----OXCXOXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shenoy, Suresh G.
Shimkets, Richard A.
Spaderna, Steven K.
Spytek, Kimberly A.
Szekeres, Edward S. Jr.
Taupier, Raymond J. Jr.
                                                                                                                                                                                                                                         Sequence 28, Application US/10190115
Publication No. US20030207394A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Burgess, Catherine E. Casman, Stacie J. Grosse, William M. Gusev, Vladimir Y. Ji, Weizhen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mezick, Amanda J.
Padigaru, Muralidhara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CuraSeqList version 0.1
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Alsobrook, John P. II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tchernev, Velizar T.
Zerhusen, Bryan D.
Voss, Edward Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patturajan, Meera
Rastelli, Luca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lepley, Denise M.
Liu, Xiaohong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , ORGANISM: Homo sapiens
US-10-190-115-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shen, Lei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                 JS-10-190-115-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
APPLICANT: Szerkeres, Edward S
APPLICANT: Buejesy, Denise M
APPLICANT: Buejesy, Denise M
APPLICANT: Shen, Leajeley, Denise M
APPLICANT: Shen, Leajeley, Denise M
APPLICANT: Buegess, Catherine E
APPLICANT: Buegess, Catherine E
APPLICANT: Padigaru, Muralidhara
ITILE OF INVENTION NO. USZOQ40014081A1=1 Proteins and Nucleic Acids Encoding Same
ITILE OF INVENTION NO. USZOQ40014081A1=1 Proteins and Nucleic Acids Encoding Same
CURRENT APPLICATION NUMBER: US/10/369,072
CURRENT APPLICATION NUMBER: US/10/14/372
PRIOR APPLICATION NUMBER: G0/215,885
PRIOR FILING DATE: 2000-07-03
PRIOR PRILING DATE: 2000-07-03
PRIOR PRILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: G0/215,985
PRIOR FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: G0/216,586
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: G0/216,586
PRIOR FILING DATE: 2000-07-07
PRIOR PRILING DATE: 2000-07-17
PRIOR PRILING DATE: 2000-07-17
PRIOR PRING PRILING DATE: 2000-07-17
PRIOR PRING PRILING DATE: 2000-07-17
PRIOR PRING DATE: 2000-07-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 726, Application US/1032281
| Publication No. US20040126762A1
| GENERAL INPORMATION:
| APPLICANT: David W. Morris
| APPLICANT: Marc S. Malandro
| TITLE OF INVENTION: Novel Compositions and Methods in Cancer
| FILE REFERENCE: 52945201000
| CURRENT APPLICATION UNDBER: US/10/322,281
| NUMBER OF SEQ ID NOS: 866
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 55.0%; Score 66; DB 15; Length 1473; Best Local Similarity 25.8%; Pred, No. 3.3e+02; Matches 8; Conservative 14; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match , 55.0%; Score 66; DB 16; Length 2203; Best Local Similarity 25.8%; Pred. No. 4.8e+02; Matches 8; Conservative 14; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            324 CVCVNGWSGDDCSENIDDCAFASCTPGSICI 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CXIXN----OXCXOXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CXIXN----OXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 2203
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
US-10-369-072-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -10-322-281-726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-322-281-726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 요
```

;

```
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME FILL REFERENCE: 21402-050 CIP
OURRENT APPLICATION NUMBER: US/10/190,115
CURRENT APPLICATION NUMBER: US/10/190,115
CURRENT APPLICATION NUMBER: 60/36,96
PRIOR FILING DATE: 2001-07-05
PRIOR FILING DATE: 2002-04-01
PRIOR FILING DATE: 2002-04-01
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2000-07-03
PRIOR FILING DATE: 2000-07-03
PRIOR PLICATION NUMBER: 60/215,856
PRIOR PLICATION NUMBER: 60/215,856
PRIOR PLICATION NUMBER: 60/215,902
PRIOR PLICATION NUMBER: 60/216,586
PRIOR PLICATION NUMBER: 60/216,586
PRIOR PLING DATE: 2000-07-03
PRIOR PLING DATE: 2000-07-03
PRIOR PLING DATE: 2000-07-07
PRIOR PLING DATE: 2000-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 15; Length 2469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.0%; Score 66; DB 15; Lv
25.8%; Pred. No. 5.3e+02;
tive 14; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          323 CVCVNGWSGDDCSENIDDCAFGACTPGSTCI 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CXIXN----QXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/10369072; Sequence 2, Application No. US20040014081A1; GENERAL INFORMATION:
APPLICANT: Alsobrook II, John P; APPLICANT: Spaderna, Stephen K; APPLICANT: Tchernev, Velizar; APPLICANT: Shenoy, Suresh; APPLICANT: Shenoy, Suresh; APPLICANT: Speney, Suresh; APPLICANT: Schusen, Bryan
                                                                                                                                                                                                                                                                                                                                                      Shenoy, Suresh G.
Shimkets, Richard A.
Spaderna, Steven K.
Syytek, Kimberly A.
Szekeres, Edward S. Jr.
Taupier, Raymond J. Jr.
Tchernev, Velizar T.
Zerhusen, Bryan D.
Voss, Edward Z.
                                                                                                                                                                             Mezick, Amanda J.
Padigaru, Muralidhara
Grosse, William M. Gusev, Vladimir Y.
                                                                                                                                                                                                                                                Patturajan, Meera
Rastelli, Luca
                                                                                                             Lepley, Denise M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 25.8*
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-190-115-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 87
US-10-369-072-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: BLISBERS, CALIBETINE BARPLICANT: BLISBERS, CALIBETINE BAPPLICANT: Padigaru, Muralidhara
TITLE OF INVENTION: No. US20040014081Alel Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-050 CON2
CURRENT APPLICATION NUMBER: US/10/369,072
CURRENT FILING DATE: 2003-02-18
PRIOR PELING DATE: 2001-07-03
PRIOR FILING DATE: 2001-07-03
PRIOR FILING DATE: 2000-07-03
PRIOR PELING DATE: 2000-07-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEG ID NOS: 100

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 28

LENGTH: 2447

TYPE: PRT

ORCANISM: Takifugu rubripes

US-10-369-072-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55.0%; Score 66; DB 15; Length 2447; 29.0%; Pred. No. 5.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       279 CVCVNGWSGLDCSENIDDCDTAACSPGSTCV 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CXIXN----QXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 2, Application US/10190115; Publication No. US20030207394A1; GENERAL INFORMATION:
APPLICANT: Alsobrook, John P. II; APPLICANT: Boldog, Ferenc L.; APPLICANT: Burgess, Catherine E.; APPLICANT: Casman, Stacie J.
                                                            Sequence 28, Application US/10369072; Publication No. US20040014081A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rastelli, Luca
Grosse, William M
Szerkeres, Edward S
Lepley, Denise M
Shen, Lei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Burgess, Catherine E
                                                                                                                                                                         APPLICANT: Alsobrook II, John P
APPLICANT: Spaderna, Stephen K
APPLICANT: Thernev, Velizar
APPLICANT: Liu, Xiaohong
                                                                                                                                                                                                                                                                                                                Shenoy, Sureah
Spytek, Kimberly
Zerhusen, Bryan
Patturajan, Meera
Taupier, Raymond T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 29.0%
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 86
US-10-190-115-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
```

us-10-627-685a-1.rapb

```
APPLICANT: Burgess, Catherine E
APPLICANT: Shimkets, Richard
APPLICANT: Padigaru, Murahidhara
TITLE OF INVENTION: No. US20040014081Alel Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-050 CON2
                              APPLICANT: SEGRETES, Jr.
APPLICANT: Equation S. Jr.
APPLICANT: Equation V. Reymond J. Jr.
APPLICANT: Taupier, Reymond J. Jr.
APPLICANT: Technerov, Velizar T.
APPLICANT: Technerov, Velizar T.
APPLICANT: Edward Z.
TILL OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFREENCE: 1402-050 CIP
CURRENT APPLICATION NUMBER: 60/303,168
PRIOR APPLICATION NUMBER: 60/303,168
PRIOR APPLICATION NUMBER: 60/368,996
PRIOR APPLICATION NUMBER: 60/368,996
PRIOR APPLICATION NUMBER: 60/368,996
PRIOR APPLICATION NUMBER: 60/215,854
PRIOR FILING DATE: 2000-07-03
PRIOR FILING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Remaining Prior Application data removed - See File Wrapper or PALM, NUMBER OF SEQ ID NOS: 136
SSOFTWARE: CuraSeqList version 0.1
LENGTH: 2471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.0%; Score 66; DB 15; Length 24
25.8%; Pred. No. 5.3e+02;
tive 14; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CXIXN----OXCXOXLDDCCSXXCNXXNXCV 27
pytek, Kimberly A.
zekeres, Edward S. Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 27, Application US/10369072
Publication No. US20040014081A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patturajan, Meera
Taupjer, Kaymond T
Rastelli, Luca
Grosse, William M
Szerkeres, Edward S
Lepley, Denise M
Shen, Lei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spaderna, Stephen
Tchernev, Velizar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu, Xiaohong
Shenoy, Suresh
Spytek, Kimberly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 25.84
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zerhusen, Bryan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-190-115-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS-10-369-072-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                   APPLICANT: Shimkets, Richard
APPLICANT: Paddigaru, Muralidhara
TITLE OF INVENTION: No. US20040014081A1e1 Proteins and Nucleic Acids Encoding Same
CURRENT APPLICATION NUMBER: 10/174,372
PRIOR APPLICATION NUMBER: 10/174,372
PRIOR APPLICATION NUMBER: 60/218,854
PRIOR FILING DATE: 2000-07-03
PRIOR FILING DATE: 2000-07-03
PRIOR FILING DATE: 2000-07-03
PRIOR PELING DATE: 2000-07-03
PRIOR PELING DATE: 2000-07-03
PRIOR PELING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/216,585
PRIOR PELING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/216,585
PRIOR PILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/218,992
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 60/218,992
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - See File Wrapper or PALM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.0%; Score 66; DB 15; Length 24 25.8%; Pred. No. 5.3e+02; Live 14; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CXIXN----OXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 27, Application US/10190115
; Publication No. US20030207394A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boldog, Ferenc L.
Burgess, Catherine E.
Casman, Stacie J.
Grosse, William M.
Gusev, Vladimir Y.
Ji, Weizhen
Lepley, Denise M.
Liu, Xiaohong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mezick, Amanda J.
Padigaru, Muralidhara
Patturajan, "Meera
Rastelli, Luca
                              Grosse, William M
Szerkeres, Edward S
Lepley, Denise M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Alsobrook, John P. II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shenoy, Suresh G.
Shimkets, Richard A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 25.8%
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-072-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 2
LENGTH: 2469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-190-115-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠ
```

ï

```
Sequence 40, Application US/10764415B

Sequence 40, Application US/20050059093A1

GENERAL INFORMATION: US20050059093A1

GENERAL INFORMATION: US20050059093A1

TITLE OF INVENTION: Modulations of Notch signalling for use in Immunotherapy
FILE REFERENCE: PO11073U3

CURRENT APPLICATION NUMBER: US/10/764,415B

CURRENT PILING DATE: 2004-01-23

PRIOR APPLICATION NUMBER: GB0118153.6

PRIOR PILING DATE: 2002-04-05

PRIOR PILING DATE: 2002-04-05

PRIOR FILING DATE: 2002-05-28

PRIOR FILING DATE: 2002-05-28

NUMBER OF SEQ ID NOS: 40

SSOFTARE: PATCHING VATE: 2002-05-28

NUMBER OF SEQ ID NOS: 40

SSOFTARE: BATCHING VATE: 2002-05-38

LENGTH: 2471
             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
                   4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 66; DB 17; Length 2471;
Pred. No. 5.3e+02;
4; Mismatches 5; Indels 4
             Indels
             2
                                                                                                                                                                                                          |:::| ::::::|| |::::|| |::::|| |:::|| |:::|| |:::|| |:::|| |::::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      324 CVCVNGWSGDDCSENIDDCAFASCTPGSTCI 354
                                                                                                                                  1 CXIXN----QXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CXIXN----QXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 25.8%; Pred. No. 5.3e
Matches 8; Conservative 14; Mismatches
             14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTLE OF INVENTION: MEDICAL TREATMENT
FILE REFERENCE: 654525-2012
CURRENT APPLICATION NUMBER: US/10/846,989;
CURRENT FILING DATE: 2004-05-14
PRIOR PILING DATE: 2002-11-13
PRIOR FILING DATE: 2002-11-13
PRIOR FILING DATE: 2002-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2002-09-10
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PARCHEL SECONDER: 2002-09-10
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PARCHEL SECONDER: 2002-09-10
NUMBER OF SEQ ID NOS: 68
SOFTWARE: 2471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: BODMER, MARK WILLIAM
APPLICANT: BRIEND, EMMANUEL CYRILLE PASCAL
APPLICANT: CHAMPION, BRIAN ROBERT
APPLICANT: LENNARD, ANDREW CHRISTOPHER
APPLICANT: MCKENZIE, GRAHAME JAMES
APPLICANT: TGAGNO, SILVIA
APPLICANT: TGAL, TAMARA
APPLICANT: YOUNG, LESLEY LYNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 57, Application US/10846989
Publication No. US20050026831A1
             8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
JS-10-846-989-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-764-415B-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-764-415B-40
             Matches
                                                                                                                                                                                                                                           a
                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 23, Application US/10765727

Sequence 23, Application US/10765727

Publication No. US2005025751A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BIDDMER, WARK WILLIAM
APPLICANT: GHAMPION, BRIAN ROBERT
APPLICANT: CHAMPION, BRIAN ROBERT
CURRENT PELING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: GB 0118153.6
PRIOR FILING DATE: 2001-07-25
PRIOR FILING DATE: 2002-04-05
PRIOR FILING DATE: 2002-04-05
PRIOR PILING DATE: 2002-04-05
PRIOR FILING DATE: 2002-04-05
                                                                                                                                                                   PRIOR FILING DATE: 2002-06-107
PRIOR PILING DATE: 2002-06-107
PRIOR APPLICATION NUMBER: 09/898,994
PRIOR PILING DATE: 2001-07-03
PRIOR PILING DATE: 2000-07-03
PRIOR PILING DATE: 2000-07-03
PRIOR PILING DATE: 2000-07-03
PRIOR PILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/215,902
PRIOR APPLICATION NUMBER: 60/216,586
PRIOR PILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/216,586
PRIOR PILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/216,586
PRIOR APPLICATION NUMBER: 60/216,586
PRIOR APPLICATION NUMBER: 60/216,722
PRIOR APPLICATION NUMBER: 60/216,722
PRIOR PILING DATE: 2000-07-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 55.0%; Score 66; DB 15; Length 2471; Best Local Similarity 25.8%; Pred. No. 5.3e+02; Matches 8; Conservative 14; Mismatches 5; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.0%; Score 66; DB 17; Length 2471; 25.8%; Pred. No. 5.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1::|:::|:::|| 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 | 354 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CXIXN----QXCXQXLDDCCSXXCNXXNXCV 27
CURRENT APPLICATION NUMBER: US/10/369,072 CURRENT FILING DATE: 2003-02-18
                                                                                                                                  IOR APPLICATION NUMBER: 10/174,372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , ORGANISM: Drosophila melanogaster
US-10-369-072-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Ver. 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
US-10-765-727-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 90
US-10-765-727-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 2471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Post SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 27
```

셤 ઠે

ä

```
gamma-carboxy-Glu; Xaa at residues 18
c, mono-iodo-Tyr, di-iodo-Tyr, O-sulph
                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                               ï
                                                                                                                                                                                                          DB 9; Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 9; Length 36;
                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                      LOCATION: (1)..(36)
COTHER INFORMATION: Xaa at residue 10 is Glu or ga;
COTHER INFORMATION: , 23 and 36 is Tyr, 125I-Tyr, OTHER INFORMATION: o-Tyr or O-phospho-Ty
US-09-894-882-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc. APPLICANT: Walker, Craig S. APPLICANT: Shetty, Reshma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: McIntosh, J. Michael
                                                                                                                                                                                               Ouery Match
Best Local Similarity 44.4%; Pred. No. 12;
Matches 12; Conservative 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
IITLE OF INVENTION: I Superfamily Conotoxins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE KEREKENCE: 4.314-4.36
CURRENT PILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2001-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-10-27
PRIOR PILING DATE: 2000-11-08
PRIOR PILING DATE: 2000-11-08
PRIOR PELING DATE: 2000-11-08
PRIOR PELING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-01-29
PRIOR FILING DATE: 2001-01-29
SOFTWARE: PATENTING NUMBER: US 60/264,256
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PATENTIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 33.3%; Pred. No. 12;
Matches 9; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                     1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                         |::|:||::||CLSLGQRCXRH-SDCCGXLCCFXDKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 CLSLGQRCERH-SDCCGYLCCFYDKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CXIXNQXCXQXLDDCCSXXCNXXXXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 369, Application US/09894882
Patent No. US20020102607A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 167, Application US/09894882
Patent No. US20020102607A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jimenez, Elsie C.
McIntosh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ; ORGANISM: Conus betulinus US-09-894-882-369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 2314-238
                   NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 96
US-09-894-882-167
                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                         US-10-322-281-723

Sequence 723, Application US/10322281

Sequence 723, Application US/10322281

Sequence 723, US2040126762A1

SEMERAL INFORMATION:

APPLICANT: David W. Morris

APPLICANT: David W. Morris

TITLE OF INVENTION: Novel Compositions and Methods in Cancer

TITLE OF INVENTION: Novel Compositions and Methods in Cancer

FILE REPERENCE: 529452001000

CURRENT APPLICATION NUMBER: US/10/322,231

CURRENT FILING DATE: 2002-12-17

NUMBER OF SEQ ID NOS: 866

SOFTWAREE FASESEQ for Windows Version 4.0
     55.0%; Score 66; DB 17; Length 2471; 25.8%; Pred. No. 5.3e+02; tive 14; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 16; Length 2503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPLICANT: University of Utah Research Foundation PPLICANT: Cognetix, Inc.
PPLICANT: Walker, Craig S.
PPLICANT: Shetty, Reshma
PPLICANT: Jimenez, Elsie C.
PPLICANT: McIncosh, U. Michael
PPLICANT: Olivera, Baldomero M.
PPLICANT: Watkins, Maren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 55.0%; Score 66; DB 16; Best Local Similarity 25.8%; Pred. No. 5.4e+02; Matches 8; Conservative 14; Mismatches 5
                                                                                                                                          |:::|:
376 CVCVNGWSGDDCSENIDDCAYASCTPGSTCI 406
                                                                                                            1 CXIXN----QXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CXIXN----QXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: I-Superfamily Conotcxins FILE REFERENCE: 2314-238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRIOR AFFLICATION NUMBER: US 60/243,410
PRIOR PILING DATE: 2000-06-30
PRIOR PELING DATE: 2000-06-30
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PATCHIN VETSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 168, Application US/09894882
Patent No. US20020102607A1
GENERAL INFORMATION:
Query Match
Best Local Similarity 25.81
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jones, Robert M.
Shen, Greg S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Conus betulinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
CRGANISM: Mus musculus
US-10-322-281-723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 723
LENGTH: 2503
                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME FILE REFERENCE: 21402-050 CIP CURRENT APPLICATION NUMBER: US/10/190,115 CURRENT FILING DATE: 2003-02-10 PRIOR APPLICATION NUMBER: 60/303,168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 735;
                                         APPLICANT: Rich, inchings
APPLICANT: Essier-Lavigne, Marc
APPLICANT: Tessier-Lavigne, Marc
TTLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/10/289,776
CURRENT FILING DATE: 2002-11-06
PRIOR APPLICATION NUMBER: 60/065,544
PRIOR APPLICATION NUMBER: 60/081,057
PRIOR FILING DATE: 1999-04-07
NUMBER OF SEO ID NOS: 20
SOFTWARE: PatentIn Ver. 2.0
SEO ID NO 9
LENGTH: 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 54.2%; Score 65; DB 14; Best Local Similarity 26.9%; Pred. No. 2.2e+02; Matches 7; Conservative 13; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248 GFEGDYCEKNIDDCVNSKCENGGKCV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2002-04-01
PRIOR PELING DATE: 2002-04-01
PRIOR PLING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: 60/215,854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/368,996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 26, Application US/10190115
Publication No. US20030207394A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boldog, Ferenc L.
Burgess, Catherine B.
Casman, Stacie J.
Grosse, William M.
Gusev, Vladimir Y.
Ji, Weizhen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Caenorhabditis elegans US-10-289-776-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Padigaru, Muralidhara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spytek, Kimberly A. Szekeres, Edward S. J Taupier, Raymond J. J Toherney, Velizar T. Zerhusen, Bryan D. Voss, Edward Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shenoy, Suresh G.
Shimkets, Richard A
Spaderna, Steven K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lepley, Denise M.
Liu, Xiaohong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patturajan, Meera
Rastelli, Luca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mezick, Amanda J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6999, Application US/10369493
; Sequence 6999, Application US/10369493
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Gldman, Barry S.
; APPLICANT: Gldman, Barry S.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION NUMBER: US 60/360,039
; PRIOR PELLING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.2%; Score 65; DB 15; Length 601; 26.9%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 9; Length 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Indels
                                         APPLICANT: Gross, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: 1-Superfamily Conotoxins
FILE FERENCE: 214-236
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT APPLICATION NUMBER: US 60/29
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-08
PRIOR PLING DATE: 2000-11-08
PRIOR FILING DATE: 2001-01-08
PRIOR FILING DATE: 2001-01-08
PRIOR FILING DATE: 2001-01-14
PRIOR FILING DATE: 2001-01-14
PRIOR FILING DATE: 2001-01-19
PRIOR FILING DATE: 2001-01-19
PRIOR FILING DATE: 2001-01-19
PRIOR FILING DATE: 2001-01-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 54.6%; Score 65.5; E
Best Local Similarity 33.3%; Pred. No. 23;
Matches 9; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 GFEGDYCEKNIDDCVNSKCENGGKCV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application US/10289776 Publication No. US20030170727A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6999
Oliyera, Baldomero M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 26.9%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Conus betulinus
US-09-894-882-167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 167
LENGTH: 73
```

g

요

ઠે

4; Gaps

```
FRIOR APPLICATION NUMBER: 60/218, 622
FRIOR PELING DATE: 2000-07-17
FREMAINING PATE: 2000-07-17
FREMAINING PRIOR APPLICATION data removed - See File Wrapper or PALM.
SEQ ID NO 26
IENGTH: 2317
FYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
NAME/KEY: VARIANT
LOCATION: (440)
COCHION: (440)
COCHION: (440)
COCHION: (440)
COCHION: (440)
COCHION: (440)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 54.2%; Score 65; DB 15; Length 2317; Best Local Similarity 30.0%; Pred. No. 6.2e+02; Matches 9; Conservative 13; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 CVCVNGWTGESCSQNIDDCATAVCFHGATC 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CXIXN----OXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: April 18, 2005, 20:43:00 Job time : 93.5 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ITLE OF INVENTION: No. US20040014081A1el Proteins and Nucleic Acids Encoding Same LLE REFERENCE: 21402-050 CON2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
1 LOCATION: (440)
2 OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
1S-10-19-115-26
        PRIOR PILING DATE: 2000-07-03
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2001-07-07
PRIOR PILING DATE: 2001-07-07
PRIOR PILING DATE: 2001-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-17
PRIOR FILING DATE: 2000-07-17
PRIOR FILING DATE: 2000-07-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 136
SOFTWARE: CuraSequist version 0.1
LENGTH: 2317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

S4.2%; Score 65; DB 15; Length 2317;
Best Local Similarity 30.0%; Pred. No. 6.2e+02;
Matches 9; Conservative 13; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 CVCVNGWTGESCSQNIDDCATAVCFHGATC 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CXIXN----QXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/369,072
CURRENT FILING DATE: 2003-02-18
PRIOR FILING DATE: 2002-06-17
PRIOR FILING DATE: 2002-06-17
PRIOR FILING DATE: 2000-07-03
PRIOR PLICATION NUMBER: 09/898,994
PRIOR PLICATION NUMBER: 60/215,854
PRIOR FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/215,856
PRIOR PRIOR DATE: 2000-07-03
PRIOR PLILING DATE: 2000-07-03
PRIOR FILING DATE: 2000-07-03
PRIOR PLILING DATE: 2000-07-03
PRIOR FILING DATE: 2000-07-03
PRIOR FILING DATE: 2000-07-03
60/215,902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 26, Application US/10369072
Publication No. US20040014081A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ION NUMBER: 60/216,586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/216,722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burgess, Catherine E
Shimkets, Richard
Padigaru, Muralidhara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Alsobrook II, John P
APPLICANT: Spaderna, Stephen K
APPLICANT: Tchernev, Velizar
APPLICANT: Liu, Xiaohong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rastelli, Luca
Grosse, William M
Szerkeres, Edward.S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shenoy, Suresh
Spytek, Kimberly
Zerhusen, Bryan
Patturajan, Meera
Taupier, Raymond T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lepley, Denise M
Shen, Lei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 100
US-10-369-072-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

30 61,5 51.2 31 61 50.8 32 61 50.8	33 61 50.8 1	aconds 35 61 50.8 37 60 50.0 8) 38 60 50.0 1 updates/sec 39 60 50.0	60 50.0 60 50.0 60 50.0 59 49.2	59 49.2 59 49.2 59 49.2	59 .49.2	59 49.2	50 50 50 50 50 50 50 50 50 50 50 50 50 5	59.4 49.2 1 1 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	58 48.3	58 48.3 58 48.3 3 57 47.5	57 47.5	ave a 65 57 47.5 1 g printed, 66 56.5 47.1 1	68 56 46.7 69 56 46.7	56 46.7 56 46.7	PV 74 56 46.7	76 56 46.7	78 56 46.7 1	80 56 46.7 2	omo 82 55.5 46.2	83 55.5 46.2	1.04	87 55 45.8	etical prote 88 55 45.8 1 P40E10.4 [89 55 45.8 3	90 54.5 45.4	92 54.5 45.4	36 93 54.5 45.4 1 36 94 54.5 45.4 1	g prot pror-R 96 54.5 45.4 1	97 54.5 45.4	54 45.0	000
GenCore vergion 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd	OM protein - protein search, using sw model	Run on: April 18, 2005, 20:23:04 ; Search time 26.5 Si (without alignment) 98.032 Million cell	Title: US-10-627-685A-1 Perfect score: 120 Sequence: 1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27	ıble:	seqs, 96216763	Total number of hits satisfying chosen parameters:	Minimum DB seg length: 0 Maximum DB seg length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries	PIR_79:*	1: pir1:* 2: pir2:* 3. pir2:*	pirs:	Pred. No. is the number of results predicted by chance to h score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution.	MMUS	A Oue re Mat	120 100.0 27 2	72 60.0 2524 2	68 56.7 2555 2	67 55.8 293 2 67 55.8 2139 2	67 55.8 2437 2 67 55 8 2531 2	0 67 55.8 2531 2	12 66 55.0 1203 2 A49175	4 66 55.0 2703 1	5 65 54.2 601 2 6 65 54.2 601 2	7 65 54.2 1964 2 8 65 54.2 2318 2	65 54.2 2331 2	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	2 64 53.3 2352 2	63 52.5 43 2	6 63 52.5 1687 2	C C L L C 2 C 2

mu-agatoxin I - fu
omega-conotoxin MV
C-Delta-1 - chicke
secreted leucine-r
gene serrate prote
slit protein 2 pre
slit protein 2 pre
slit protein 1 protein
metallothioneln hypothetical prote
compaga-conotoxin MV
metallothioneln jagged protein hom
hypothetical prote
lintinsic factor-B
complement C3b/C4b
hypothetical prote
lintinsic factor-B
complement C3b/C4b
hypothetical prote
hypothetical prote
lintinsic factor-B
complement C3b/C4b
hypothetical prote
lintinsic factor-B
complement C3b/C4b
hypothetical prote
hypothetical prote
lintinsic factor-B
robustoxin - funne
hypothetical prote
hypothetical prote
lintinsic factor-B
robustoxin - funne
hypothetical prote
hypothetical prote
lintinsic factor-B
robustoxin - funne
hypothetical prote
hypothetical prote
lintinsic factor-B
robustoxin - funne
hypothetical prote
hypothetical prote
hypothetical prote
lintinsic factor-B
robustoxin - funne
hypothetical prote
hypothetical prote
hypothetical prote
lintinsic factor-B
robustoxin - funne
hypothetical prote
hypothetical prote
hypothetical prote
lintinsic factor-B
lintinsic

ALIGNMENTS

```
A:Status: preliminary: nucleic acid sequence not shown; not compared with conceptual transmolecule type: mRNA
A:Molecule type: mRNA
C:Superfamily: Notch protein; ankyrin repeat homology; EGF homology conceptual
C:Superfamily: Notch protein; ankyrin repeat homology; EGF homology conceptual
C:Molecule type: mRNA
C:Molecule type: m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: JH0699
A;Accession: JH0699
A;Accession: JL9699
A;Accession: JL9699
A;Accession: JL9699
A;Accession: JL9699
A;Accession: JL9699
A;Accession: JL9699
A;Cross-references: UNIPROT:P37300; GB:S40826; NID:g252126; PIDN:AAB22674.1; PID:g252127
B;Nemoto, N.; Kubo, S.; Yoshida, T.; Chino, N.; Kimura, T.; Sakakibara, S.; Kyogoku, Y.;
Biochem: Biophys. Res. Commun. 207, 695-700, 1995
B;Aritle: Solution structure of omega-conotoxin MVIIC determined by NMR.
A;Reference number: PC2380; MUID:95169113; PMID:7864862
A;Reference number: PC2380; MUID:95169113; PMID:778169
A;Reference number: A66297; PD8:10MN
B;Residues: 3-28 and a shookhaven Protein Data Bank, December 1994
A;Reference number: A66297; PD8:10MN
A;Contents: annotation; conformation by (1)H-NMR, residues 3-28
B;Farr-Jones, S.; Miljanich, G.P.; Nadasdi, L.; Ramachandran, J.; Basus, V.J.
J. Mol. Biol. 248, 106-124, 1995
A;Title: Solution structure of omega-conotoxin MVIIC, a high affinity of P-type calcium of A;Reference number: A58882; MUID:95248539; PMID:7731037
A;Contents: annotation; conformation by (1)H-NMR
A;Reference number: A58882; MUID:95248539; PMID:7731037
A;Contents: annotation; conformation by (1)H-NMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Superfamily: omega-conotoxin
C; Keywords: acetylcholine release inhibition; amidated carboxyl end; calcium channel inhıle; 3-28/Product: omega-conotoxin MVIIC #status experimental <MAT>
F;3-18,10-22,17-28/Disulfide bonds: #status experimental
F;28/Modified site: amidated carboxyl end (Cys) (amide in mature form from following glyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Conus magus (magus cone)
C;Date: 17-Apr-1993 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
C;Accession: JH0699; PC2380
R;Hillyard, D.R.; Monje, V.D.; Mintz, I.M.; Bean, B.P.; Nadasdi, L.; Ramachandran, J.; M
Neuron 9, 69-77, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          omega-conotoxin MVIIC precursor [validated] - cone shell (Conus magus) (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
Xotch protein - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 16-Aug-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ArTitle: A new conus peptide ligand for mammalian presynaptic Ca2+ channels. ArReference number: JH0699; MUID:92337922; PMID:1352986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 2524;
27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                              C;Accession: A35844
R;Coffman, C.; Harris, W.; Kintner, C.
Science 249, 1438-1441, 1990
A;Title: Xotch, The Xenopus homolog of Drosophila notch.
A;Reference number: A35844; MUID:90385285; PMID:2402639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          < AN4 >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
60.0%; Score 72; DB
Best Local Similarity 34.6%; Pred. No. 27;
Matches 9; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;1025-1056/Domain: Box homology F;1024-1956/Domain: ankyzin repeat homology F;1957-1959/Domain: ankyzin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;1991-2023/Domain: ankyrin repeat homology F;2024-2056/Domain: ankyrin repeat homology F;2057-2089/Domain: ankyrin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   248 GFSGQNCEENIDDCPSNNCRNGGTCV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Owega-conotoxin SVIB [validated] - cone shell (Conus striatus)

Okaga-conotoxin SVIB [validated] - cone shell (Conus striatus)

C; Species: Conus striatus (striated cono)

C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 15-Sep-2000

C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 15-Sep-2000

R; Ramilo, C.A.; Zafaralla, G.C.; Nadasdi, L.; Hammerland, L.G.; Yoshikami, D.; Gray, W.R

Biochemistry 31, 9919-9926, 1992

A; Reference number: A44379; MUID: 93003172; PMID: 1390774

A; Reference number: A44379; MUID: 93003172; PMID: 1390774

A; Residues: 1-26 *RAM.

A; Roberned sources: venom

A; Roberned source: venom

A; Roberned contextion; conformation by (1) H-NMR, residues 1-26

A; Rilles R. X.J; Thomas, L.; Lewis, R. J; Alewood, P. P; Craik, D.J.

A; Reference number: Asf649; PDB: 1MV

A; Contents: annotation; conformation by (1) H-NMR, residues 1-26

A; Thitle: A consensus structure for omega-conotoxins with different selectivities for vol A; Thitle: A consensus structure for omega-conotoxins with different selectivities for vol A; Thitle: A consensus structure for omega-conotoxins with different selectivities for vol A; Thitle: A consensus structure for omega-conotoxin such anidated carboxylend; acetylcholine release inhibition; amidated carboxylend; acetylcholine release inhibition; amidated carboxylend; scetylcholine release inhibition; amidated carboxylend; scetylcholine release inhibition; amidated carboxylend; calcium channel inh
F; 1-16, 8-20, 15-26/Disulfide bonds: #status predicted

E; Seperiments amidated carboxylend carboxylen
                                                                                                                                                                                                                                                                                                                            C;Accession: A58997
R;Terlau, H.; Shon, K.J.; Grilley, M.; Stocker, M.; Stuchmer, W.; Olivera, B.M.
R;Terlau, H.; Shon, K.J.; Grilley, M.; Stocker, M.; Stuchmer, W.; Olivera, B.M.
Nature 381, 1986
A;Title: Strategy for rapid immobilization of prey by a fish-hunting marine snail.
A;Reference number: A58997
A;Status: preliminary
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-27 <TER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A)Cross-references: UNIPROT:P56633
C;Comment: This conotoxin blocks conductance of the Shaker potassium channel.
C;Keywords: hydroxyproline; neurotoxin; venom
F;4/Modified site: 4-hydroxyproline (Pro) #status experimental
                                                                                                                        Kappa-conotoxin PVIIA - cone shell (Conus purpurascens)
N;Alternate names: fin-popping peptide
C;Species: Conus purpurascens (purple cone)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64.2%; Score 77; DB 2; Length 26; 34.6%; Pred. No. 0.43; ive 12; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 120; DB 2; 63.0%; Pred. No. 4.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 120; D
Best Local Similarity 63.0%; Pred. No. 4.3e
Matches 17; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CXIXNQXCXQXLDDCCSXXCNXXNXC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 34.6%
Matches 9; Conservative
```

ò В

à 원 us-10-627-685a-1.rpr

```
R;Tepass, U.; Theres, C.; Knust, E.
Cell 61, 787-799, 1990
A;Title: crumbs encodes an EGF-like protein expressed on apical membranes of Drosophila &
A;Reference number: A35672, MUID:90263104; PMID:2344615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:P10040; GB:M33753
A;Note: the authors translated the codon GGC for residue 1928 as Cys, and TAT for residu<sup>k</sup>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-2437 <BIE>
A, Cross-references: UNIPROT: P46530; EMBL: X69088; NID: 9433866; PIDN: CAA48831.1; PID: 943380
C, Superfamily: notch protein; ankyrin repeat homology; EGF homology
F;755-786/Domain: EGF homology <EGF1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R.Bierkamp, C.; Campos-Ortega, J.A.
Mech. Dov. 43, 87-100, 1993
A.Jitle: A zebrafish homologue of the Drosophila neurogenic gene Notch and its pattern
A.Reference number: S42612; MUID:94128602; PMID:8297791
                                                                                                                                                                                                             crumbs protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 21-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Brachydanio rerio (zebra fish)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S42612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 67; DB 2;
; Pred. No. 76;
13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;1915-1947/Domain: ankyrin repeat homology <AN1>F;1948-1980/Domain: ankyrin repeat homology <AN2>F;1982-2014/Domain: ankyrin repeat homology <AN3>F;2012-2047/Domain: ankyrin repeat homology <AN4>F;2018-2080/Domain: ankyrin repeat homology <AN5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CXIXN----QXCXQXLDDCCSXXCNXXNXC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cransmembrane protein precursor - zebra fish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.8%; Score 67; 28.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1826 GFEGOHCEQNIDECADOPCHNGGNC 1850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.8%; Score 67; 30.0%; Pred. No.
       164 GFEGQHCEQNIDECADQPCHNGGNC 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 XIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Gene: FlyBase:crb
A,Cross-references: FlyBase:FBgn0000368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;1878-1914/Domain: EGF homology <EGX2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;1023-1054/Domain: EGF homology <EGF> F;1185-1216/Domain: EGF homology <EGF2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Keywords: transmembrane protein
F;352-385/Domain: EGF homology <EGK1>
F;392-424/Domain: EGF homology <EGF1>
F;691-722/Domain: EGF homology <EGF>
F;767-799/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 28.0%
Best Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 30.09
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2139 <TEP>
                                                                                                                                                                                                                                                                                                                        C; Accession: A35672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: S42612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
G
                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 6
B126637
B126637
B126637
B126637
B126637
B1266369
B126637
B1266369
B126637
B1266369
B126637
B1266369
B126637
B1266369
B126637

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: A40043
R;Ellisen, L.W.; Bird, J.; West, D.C.; Soreng, A.L.; Reynolds, T.C.; Smith, S.D.; Sklar, Cell 66, 649-661, 1991
A;Title: TAN-1, the human homolog of the Drosophila Notch gene, is broken by chromosomal A;Reference number: A40043; MUID:91347367; PMID:1831692
                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                  A40043
notch protein homolog TAN-1 precursor - human
C;Species: Homo sapiens (man)
C;Dete: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 16-Aug-2004
                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reaidues: 1-2555 <ELL>
A;Cross-references: GB:M73980
C;Superfamily: Nortein; ankyrin repeat homology; EGF homology F:261-292/Domain: EGF homology <EGX1>
F;494-525/Domain: EGF homology <EGF1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 67; DB 2; Length 293; ; Pred. No. 18; 13; Mismatches 5; Indels
       Length 29;
                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
Query Match 57.5%; Score 69; DB 2; Best Local Similarity 30.8%; Pred. No. 2.5; Matches 8; Conservative 12; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           < 4N4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.7%; Score 68; DB 30.8%; Pred. No. 64; ive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;1927-1959/Domain: ankyrin repeat homology
F;1960-1992/Domain: ankyrin repeat homology
F;1994-2026/Domain: ankyrin repeat homology
F;2027-2059/Domain: ankyrin repeat homology
F;2060-2092/Domain: ankyrin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   248 GFTGQNCEENIDDCPGNNCKNGGACV 273
                                                                                                                                                                                       3 CKGKGAPCRKTMYDCCSGSCGRRGKC 28
                                                                                                                                               1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 XIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;997-1019/Domain: EGF homology <EGX2>
F;1149-1180/Domain: EGF homology <EGF>
F;1187-1218/Domain: EGF homology <EGF3
F;1233-1264/Domain: EGF homology <EGF3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: FlyBase: FBgn0000368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F:139-170/Domain: EGF homology <EGX1>
F:177-208/Domain: EGF homology <EGF1>
F:216-252/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 28.0%
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: A40043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Gene: FlyBase:crb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
```

ö

Gaps

ö

ö

ä

Gape

4

us-10-627-685a-1.rpr

Page

```
A;Experimental source: embryo
A;Note: sequence extracted from NCBI backbone (NCBIN:131246, NCBIP:131247)
C:Comment: This protein has many EGF repeats and lin-12[#1172]/Notch repeats.
C.Comment: This protein is one of the neurogenic proteins controlling the decision between
                                                                        ,1935-1937,'L',1938-1967,'I',1969-2044,'IE',2047-2052,'S',2054-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Omega-conotoxin GVIIB - cone shell (Conus geographus)
NyAlternate names: shaker peptide GVIIB
NyAlternate names: shaker peptide GVIIB
CiSpecies: Conus geographus (geography cone)
CiSpate: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004
CiAccession: B43620
R;Olivera, B.M.; Gray, W.R.; Zeikus, R.; McIntosh, J.M.; Varga, J.; Rivier, J.; de Santos Science 230, 1338-1343, 1985
A;Title: Peptide neurotoxins from fish-hunting cone snails.
A;Reference number: A43620; MUID: 86070213; PMID: 4071055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: omega-conotoxin
C;Keywords: acetylcholine release inhibition; calcium channel inhibitor; hydroxyproline;
F;1-16,8-19,15-26/bisulfide bonds: #status predicted
F;4,7/Modified site: 4-hydroxyproline (Pro) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                        2
repeat homology; EGF homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.0%; Score 66; DB 2; Length 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <AN3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.8%; Score 67; DB 30.8%; Pred. No. 78; iive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248 GFAGQNCEENVDDCPGNNCKNGGACV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;1917-1948/Domain: ankyrin repeat homology F;1949-1981/Domain: ankyrin repeat homology F;1983-2045/Domain: ankyrin repeat homology F;2016-2048/Domain: ankyrin repeat homology F;2049-2081/Domain: ankyrin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1233-1264/Domain: EGF homology <EGF4>
1352-1383/Domain: EGF homology <EG19>
1391-1425/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   987-1018/Domain: EGF homology <EG14>
                                                                                                                                                                                                                                                                                                                                                                                                   region of chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <EG13>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: UNIPROT: P05483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;607-638/Domain: EGF homology of F;682-713/Domain: EGF homology of F;75-788/Domain: EGF homology of F;75-64/Domain: EGF homology of F;873-904/Domain: EGF homology of F;911-942/Domain: EGF homology of F;949-980/Domain: EGF homology of F;949-980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 30.8<sup>3</sup>
Matches 8; Conservative
                             A;Molecule type: nucleic acid
A;Residues: 1865-1932,'RR',193
A;Experimental source: embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein A; Residues: 1-29 <0LI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ,1025-1056/Domain: EGF
Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                   A, Note: proximal reg;
C, Superfamily: Notch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1025-1056/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :1149-1180/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: B43620
                                                                                                                                                                                                                                                                                                                                                         A, Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :222-254/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       532-563/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'Domain:
                                                                                                                                                                                                                                                                                                                       A; Gene: notch-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B43620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A46019

Notch-1 protein - mouse

Signate names: motch protein

Signate: 22-8ep-1993 #sequence revision 18-Nov-1994 #text_change 16-Aug-2004

C;Accession: A46019; S25144; C49175; B46438; A46438; PHI569; S32109

C;Accession: A46019; A25-264, 1993

A;Title: Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of A;Reference number: A46019; MUID:93194170; PMID:8449489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Molecule type: nucleic acid
A,Residues: 1-2531 <DEL>
A,Coss-references: UNIPROT:Q01705, GB:Z11886; GB:S47228; NID:g288502; PIDN:CAA77941.1;
A,Cross-reference extracted from NGB1 backbone (NGBIP:127318)
R,Franco del Amo, F.; Smith, D.E.; Swiatek, P.J.; Gendron-Maguire, M.; Greenspan, R.J.; submitted to the EMBL Data Library, April 1992
A,Reference number: Sz5144
A,Accession: S25144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R,Kopan, R., Weintraub, H.
J. Cell Biol. 121, 631-641, 1993
A,Title: Mouse notch: expression in hair follicles correlates with cell fate determinati
A,Reference number: A46438; MUID:93252998; PMID:8486742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Lardelli, M.; Lendahl, U.
Exp. Cell Res. 204, 364-372, 1993
A;Title: Motch A and Motch B--two mouse Notch homologues coexpressed in a wide variety
A;Reference number: A49175; MUID:93178563; PMID:8440332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                             R;Weinmaster, G.; Roberts, V.J.; Lemke, G. Development 113, 199-205, 1991 Ariticle: A homolog of Drosophila Notch expressed during mammalian development. A;Reference number: S18188; MUID:92111383; PMID:1764995
                                                       Species: Rattus norvegicus (Norway rat)
Date: 19-Peb-1994 #sequence_revision 10-Nov-1995 #text_change 02-Aug-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1161-1547 <LAR>
A;Cross-references: EMBL:X68278; NID:g287987; PIDN:CAA48339.1; PID:g287988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                               A,Accession: S18188
A,Molecule type: mRNA
A,Residues: 1-253
A,Cross-references: EMBL:XS7405; NID:g57634; PID:g57635
G,Suberfamily: notch protein; ankyrin repeat homology; EGF homology
F;987-1018/Domain: EGF homology <EGF>
F;1025-1056/Domain: EGF homology <EGF>
F;1233-1264/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Experimental source: embryo
A;Note: sequence extracted from NCBI backbone (NCBIP:126159)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Molecule type: mRNA
A,Residues: 1551-2108,'Q',2110-2114,'ALF',2118-2170 <FRA>
A,Cross-references: EMBL:211886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Status: preliminary, nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55.8%; Scc. 30.8%; Pred. No .c. 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F.1917-1949/Domain: ankyrin repeat homology. F.1950-1982/Domain: ankyrin repeat homology. F.1984-2016/Domain: ankyrin repeat homology. F.2050-2082/Domain: ankyrin repeat homology. F.2050-2082/Domain: ankyrin repeat homology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          248 GFAGQNCEENVDDCPGNNCKNGGACV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 30.8
Matches 8; Conservative
                     notch protein homolog - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
                                                                                                                                    Accession: S18188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
```

ä

```
Nucleic Acids Res. 17, 6463-6471, 1989
A;Title: Hypervariability of simple sequences as a general source for polymorphic DNA max
A;Reference number: S09358; MUID:89385974; PMID:2780284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Molecule type: DNA
A;Residues: 2565-2551, QQQQ,,2552-2576,'E',2578-2604 <TAU>
A;Residues: 2565-2551, Yedvobnick, B.; Finnerty, V.G.; Artavanis-Tsakonas, S.
Cell 40, 55-62, 1985
A;Filte: ops a novel family of transcribed repeats shared by the Notch locus and other of
A;Reference number: A05267; MUID:85099329; PMID:2981631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: A24420
A;Molecule type: DNA
A;Residues: 1-2703 «XID>
A;Crost-references: UNIPROT:P07207; GB:K03508; NID:g157991; PIDN:AAA28725.1; PID:g157993
R;Wharton, K.A.; Johansen, K.M.; Xu, T.; Artavanis-Tsakonas, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-48,'I',50-118,'R',120-230,'I',232-256,'N',258-266,'A',268-872,'R',874-958,'
A;Note: the authors translated the codon ATC for residue 49 as Thr, ATT for residue 2044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                notch protein - fruit fly (Drosophila melanogaster)
NyAlternate names: neurogenic repetitive locus protein
C;Species: Drosophila melanogaster
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 16-Aug-2004
C;Accession: A4420; A24768; S09358; A05267
R;Kidd, S;, Kelley, M.R.; Young, M.W.
Mol. Cell. Biol. 6, 3094-3108, 1986
A;Reference number: A24420; MUID:87064624; PMID:3097517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;2017-2049/Domain: ankyrin repeat homology <AN3>
F;2050-2082/Domain: ankyrin repeat homology <AN4>
F;2050-2115/Domain: ankyrin repeat homology <AN5>
F;2083-2115/Domain: ankyrin repeat homology <AN5>
F;2538-2568/Region: glutamine-rich
F;2538-2568/Domain: neurogenic repetitive element #status predicted <OPA>
                                                                                                                                                                                                                                           4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: 8.96-9.36
A;Introns: 53/3; 84/3; 171/3; 240/3; 283/3; 2333/3; 2436/3; 2588/3
C;Superfamily: Notch protein; ankyrin repeat homology. EGF homology
C;Keywords: differentiation; tandem repeat; transmembrane protein
                                                                                                                                          Length 2471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 66; DB 1; Length 2703;
Pred. No. 1e+02;
                                                                                                                                                                                                                                      Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1746-1762/Domain: transmembrane #status predicted <TMM2>
1950-1982/Domain: ankyrin repeat homology <AN1>
1983-2015/Domain: ankyrin repeat homology <AN2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: A24768; MUID:86079539; PMID:3935325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           727-43/Domain: transmembrane #status predicted <TMM1>
7297-328/Domain: EGF homology <EGX1>
7580-561/Domain: EGF homology <EGF1>
7588-1019/Domain: EGF homology <EGX2>
71084-1019/Domain: EGF homology <EGX2>
71187-1218/Domain: EGF homology <EGX3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;1988-2004/Domain: transmembrane #status predicted
                                                                                                                                     Query Match 55.0%; Score 66; DB 2; Best Local Similarity 25.8%; Pred. No. 96; Matches 8; Conservative 14; Mismatches
             F;1976-2008/Domain: ankyrin repeat homology <AN4>F;2009-2041/Domain: ankyrin repeat homology <AN5>
                                                                                                                                                                                                                                                                                                                                                                            324 CVCVNGWSGDDCSENIDDCAFASCTPGSTCI 354
                                                                                                                                                                                                                                                                                                                         1 CXIXN----QXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecule type: DNA
;Residues: 2504-2576,'E',2578-2611 <WHA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: FlyBase: FBgn0004647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.0%;
29.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: A24768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: notch; opa
                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Note: sequence extracted from NCBI backbone (NCBIP:126158)
C;Comment: This protein has many EGF repeats and lin-12/Notch repeats.
C;Comment: This protein is one of the neurogenic proteins controlling the decision betwe C;Comment: This protein; ankyrin repeat homology; EGF homology
F;143-174/Domain: EGF homology eEGF1>
F;482-513/Domain: EGF homology eEGF1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-1203 <LAR>
A;Cross-references: UNIPROT:035516; EMBL:X68279; NID:g287989; PIDN:CAA48340.1; PID:g2879
                                                                                                                                                                                                                                                                                                                                                     RESULT 12

A49175

Motch B protein - mouse (fragment)
NyAlternate names: Notch homolog
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: A49175; PH1570; S32113
Exp. Cell Res. 204, 364–312, 1993
A;Title: Motch A and Motch B-two mouse Notch homologues coexpressed in a wide variety A;Reference number: A49175; MUID:93178563; PMID:8440332
A;Accession: A49175
A;Accession
                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
A49128
cell-fate determining gene Notch2 protein - rat
C.Species: Rattus norvegicus (Norway rat)
C.Species: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2004
C.Accession: A49128
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Molecule Type: mRNA
A, Residues: 1-2471 «WIL>
A, Cross-references: UNIPROT:090W30
A, Experimental source: Schwann cell
A, Note: sequence extracted from NCBI backbone (NCBIP:127811)
C, Superfamily: Notch protein; ankyrin repeat homology; EGF homology
F, 264-295, Domain: EGF homology «EGX1»
F, 799-800 / Domain: EGF homology «EGX2»
F, 1029-106 / Domain: EGF homology «EGX2»
F, 1029-106 / Domain: EGF homology «EGX3»
F, 1153-1184 / Domain: EGF homology «EGX3»
F, 1153-1184 / Domain: EGF homology «EGX3»
F, 1153-1184 / Domain: EGF homology «EGX3»
F, 1151-1122 / Domain: EGF homology «EGX3»
F, 1151-1122 / Domain: EGF homology «EGX3»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.
                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 1203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: A49128
A;Status: preliminary; not compared with conceptual translation
                                                           5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Riwelnmaster, G.; Roberts, V.J.; Lemke, G.
Development 116, 931-941, 1992
A;Title: Notch2: a second mammalian Notch gene.
A;Reference number: A49128; MUID:93202015; PMID:1295745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 CVCVNGWSGDDCSENIDDCAYASCTPGSTCI 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CXIXN----QXCXQXLDDCCSXXCNXXNXCV 27
Best Local Similarity 26.9%; Pred. No. 4.8; Matches 7; 11 Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 25.8%; Pred. No. 59; es 8; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 66;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;1876-1908/Domain: ankyrin repeat homology F;1909-1941/Domain: ankyrin repeat homology F;1943-1975/Domain: ankyrin repeat homology
                                                                                                                                                                                                 CKSPGTPCSRGMRDCCTSCLSYSNKC 26
                                                                                                                                              1 CXIXNQXCXQXLDDCCSXXCNXXNXC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;560-591/Domain: EGF homology «EGF»
F;674-705/Domain: EGF homology «EGX2»
F;712-743/Domain: EGF homology «EGF3»
F;836-867/Domain: EGF homology «EGF3»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loc
Matches
                                                                                                                                                                                                               g
                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

ઠ

```
A; Gene: notch4
A; Map position: 17
A; Introns: 22/1; 49/2; 148/1; 264/1; 305/1; 384/1; 436/1; 501/1; 539/1; 577/1; 618/1; 671
B; Introns: 22/1; 40/2; 1761/3
C; Superfamily: notch protein; ankyrin repeat homology; EGF homology
C; Keywords: receptor; signal transduction
F; 514-545/Domain: EGF homology < EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A Molecule type: mRNA
A;Residues: 1-2318 cLAR>
A;Cross-references: UNIPROT: Q61982; EMBL:X74760; NID: 9483580; PIDN: CAA52776.1; PID: 9483581
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
F;163-195/Domain: EGF homology cEGF>
F;474-505/Domain: EGF homology cEGF>
F;854-885/Domain: EGF homology cEGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Lardelli, M.; Dahlstrand, J.; Lendahl, U.
Mech. Dev. 46, 123-136, 1994
A;Title: The novel Notch homologue mouse Notch 3 lacks specific epidermal growth factor-1.
A;Reference number: 845306; MUID:95001556; PMID:7918097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-2321 <JOU1>
A;Cross-references: UNIPROT:Q9UM47; EMBL:U97669; NID:g2668591; PIDN:AAB91371.1; PID:g2668
R;Joutel, A.; Corpechot, C.; Ducros, A.; Vahedi, K.; Chabriat, H.; Mouton, P.; Alamowitch
          A, Description: Sequence of the mouse major histocompatibility locus class III region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-1964 <ROW>
A;Cross-references: UNIPROT:P31695; EMBL:AF030001; NID:g2564945; PID:g2564947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: 878549; $71825
C;Accession: 797849; $71825
SiJoutel, A.; Tournier-lasserve, E.
Submitted to the EMBL Data Library, April 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S45306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.1e+02;
                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <AN3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <AN4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 CVCVNGWTGESCSQNIDDCATAVCFHGATC 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54.2%; Score 65; DB 30.0%; Pred. No. 1.16;ive 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CXIXN----QXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.2%; Score 65; 33.3%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;1839-1871/Domain: ankyrin repeat homology F;1872-1904/Domain: ankyrin repeat homology F;1906-1934/Domain: ankyrin repeat homology F;1939-1971/Domain: ankyrin repeat homology F;1972-2004/Domain: ankyrin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  348 GCEENLDDCAAATCAPGSTCI 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 XCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                    Reference number: Z16543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Reference number: S78549
A, Accession: S78549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
Les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             notch 3 protein - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     notch3 protein - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
                                                                                 Accession: T09059
                                                                                                                                                                                                                                                                                      A, Gene: notch4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                       C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  878549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                      hypothetical protein F40E10.4 - Caenorhabditis elegans (fragment)
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T22025
R;Smye, R.
Rswye, R.
Rismye, R.
Rismye, R.
Rismye, R.
R;Smye, R.
R;Smye; Data Library, February 1996
R;Smye, R.
R;Smye; Data Library, February 1996
R;Smye; Data Library, February, February 1996
R;Smye; Data Library, February, February 1996
R;S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T09059
notch4 - mouse '
notch4 - mouse '
notch5 - mouse '
notch6 - mouse musculus 'house mouse)
C;Bacie: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09059
C;Accession: T09059
R;Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Sd
submitted to the EMBL Data Library, October 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C,Accession: D89711

K;anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog

A;Reference number: A75000; MUID:99069613; PMID:9851916

A;Note: see webaites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele

A;Notes: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A;Accession: D89711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q20204; GB:chr_X; PIDN:CAA93668.1; PID:g3877014; GSPDB:GN00d
              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein F40E10.4 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 601; 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 601;
          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
          ر.
د
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
       12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 46;
13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.2%; Score 65; 26.9%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 GFEGDYCEKNIDDCVNSKCENGGKCV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GFEGDYCEKNIDDCVNSKCENGGKCV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.2%; Score 65; 26.9%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                             822 TGQKCETNIDDCVTNPCGNGGTCI 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                   4 XNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 26.94
Matches 7; Conservative
   7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 26.5
Best Local 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-601 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position: X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: F40E10.4
A;Map position: X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 17
                                                                   à
                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
```

ö

Gaps

ö

```
A,Molecule type: DNA
X,Residues: 1-1372 <MURS.
A;Cross-references: UNIRROT:P91526; EMBL:U80815; PIDN:AAB37995.1; GSPDB:GN00022; CESP:W0;
A;Experimental source: strain Bristol N2; clone W02C12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 08-Sep-2002
C;Accession: T30201
C;Accession: T30201
Fibri, S.; Saitoh, T.; Matsumoco, M.; Makabe, K.W.; Nishida, H.
Dev. Genes Evol. 207, 371-380, 1997
A;Title: Notch homologue from Halocynthia roretzi is preferentially expressed in the cent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: UNIPROT:070244; EMBL:AF022247; NID:93834379; PIDN:AAC71661.1; PID:93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Journal CUBLLIN

'Same: CUBLLIN

'Superfamily: intrinsic factor-B12 receptor cubilin, EGF homology

'Superfamily: intrinsic factor-B12 receptor intestine; kidney; peripheral membrane

'1-20/Domain: signal sequence #status predicted <SIG>

'21-3623/Product: intrinsic factor-B12 receptor CUBILIN #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Accession: T08618

'Moestrup, S.K.; Kozyraki, R.; Kristiansen, M.; Kaysen, J.H.; Rasmussen, H.H.; Brault,

Biol. Chem. 273, 5235-5242, 1998

Title: The intrinsic factor-vitamin B12 receptor and target of teratogenic antibodies

'Reference number: 216459; MUID:98148073; PMID:9478979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2352 <HOR>
A;Cross-references: EMBL:AB001327; NID:d1204472; PID:d1026501; PIDN:BAA25571.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: Notch
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
53.3%; Score 64; DB 2; Length 2352;
Best Local Similarity 26.9%; Pred. No. 1.4e+02;
Matches 7; Conservative 13; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1372;
                                                                                                                                                                                                                                                                                                                                                                               A;Map position: 4
A;Introns: 29/1; 66/1; 774/2; 823/2; 1046/1; 1108/2; 1298/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Notch homolog protein - sea squirt (Halocynthia roretzi)
C;Species: Halocynthia roretzi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
99;
                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            intrinsic factor-B12 receptor CUBILIN precursor 3, Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.3%; Score 64; 25.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : ::|:|::|:|
95 TGENCDQNIDECAASPCQNDAKCI 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 XNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;133-164/Domain: EGF homology <EGF1>F;436-467/Domain: EGF homology <EGF>
            A, Reference number: Z20112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-3623 < MOE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                            A;Gene: CESP:W02C12.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: T30201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C, Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
x, M.M.; Weissenbach, J.; Bach, J.F.; Bousser, M.G.; Tournier-Lasserve, E.
Nature 383, 707-710, 1996
A;Title: Notch3 mutations in CADASIL, a hereditary adult-onset condition causing stroke
A;Reference number: S71825, MUD:97032728; PMID:8878478
A;Accession: S71825
A;Accession: DNA
A;Residues: 67-113;138-194;268-333, 'G', 335-346;536-613;716-765;1240-1279;1815-1888 <JOUZ
A;Accession: DNA
A;Accession: BMBL:U97669
A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 20
T31070
Cycleh homolog - sea urchin (Lytechinus variegatus)
Cycleh homolog - sea urchin (Lytechinus variegatus)
Cycleh homolog - sea urchin (Lytechinus variegatus)
Cybate: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000
CyAccession: T31070
RySherwood, D.R.; McClay, D.R.
Bevelopment 124, 3363-3374, 1997
A;Title: Identification and localization of a sea urchin Notch homologue: insights into A;Accession: T31070
A;Reference number: Z20966; MUID:97454256; PMID:9310331
A;Accession: T31070
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             causing a type of stroke and homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-2531 <SHE>
A;Cross-references: EMBL:AF000634; NID:g2570350; PID:g2570351; PIDN:AAB82088.1
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T2533
R;Murray, J; Wohldmann, P.
submitted to the EMBL Data Library, December 1996
A;Description: The sequence of C. elegans cosmid W02C12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 54.2%; Score 65; DB 2; Length 2531; Best Local Similarity 38.1%; Pred. No. 1.2e+02; Matches 8; Conservative 11; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Description: may be involved in pathogenesis of CADASIL, C; Superfamily: notch protein; ankyrin repeat homology; EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein W02C12.1 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 65; DB 2;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <AN5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              < AN4 >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 CVCVNGWTGESCSQNIDDCATAVCFHGATC 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CXIXN----QXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;1871-1993/Domain: ankyrin repeat homology
F;1905-1931/Domain: ankyrin repeat homology
F:1938-1970/Domain: ankyrin repeat homology
F;1971-2003/Domain: ankyrin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;123-155/Domain: BGF homology <EGX1>
F;166-194/Domain: BGF homology <EGF1>
F;240-271/Domain: BGF homology <EGX2>
F;318-349/Domain: BGF homology <EGF>
F;318-349/Domain: BGF homology <EGF>
F;853-884/Domain: BGF homology <EGF>
F;853-884/Domain: BGF homology <EGF3>
F;928-959/Domain: BGF homology <EGX3>
F;928-959/Domain: BGF homology <EGX3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 XCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;1838-1870/Domain: ankyrin repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.2%;
30.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Keywords: tandem ref
F;123-155/Domain: EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
```

ö

Gaps

ω

Page

```
A;Reaidues: 1-1687 <SEL>
A;Cross-references: UNIPROT:Q61204; EMBL:US7368; NID:g1336627; PID:g1336628; PIDN:AAB0133
A;Experimental source: strain C57BL/6J; clone DBI-1; whole embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Omega-conotoxin GVIIA - cone shell (Conus geographus)
NAlternate names: shaker peptide GVIIA
Cispecies: Conus geographus (geography cone)
Cispecies: L1-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004
Cipate: 11-Dec-1992 11-Dec-1992 #text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DELTA-11ke 1 - mouse
C;Species: Mus musculus (house mouse)
C;Decies: Mus musculus (house mouse)
C;Dete: 02-3u1-1996 #sequence_revision 02-3u1-1996 #text_change 09-Ju1-2004
C;Accession: I48324
R;Bettenhausen, B.; de Angelis, M.H.; Simon, D.; Guenet, J.L.; Gossler, A.
Development 121, 2407-2418, 1995
A;Accession: I48324
A;Title: Translent and restricted expression during mouse embryogenesis of D111, a murint A;Reference number: I48324, MuID:95401888; PMID:7671806
A;Accession: I48334
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-722 <RES>
A;Cross-references: UNIPROT:Q61483; EMBL:X80903; NID:g80655; PIDN:CAA56865.1; PID:g80655;
                                                                                                                                                                                                                                                                                                                                                               Risell, C.; Hoff III, H.B. submitted to the EMBL Data Library, May 1996
A; Description: Cloning of a novel mRNA regulated by the insulin like growth factor type A; Reference number: 220762
A; Accession: T30176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:P05483
C;Superfamily: omega-conotoxin
C;Keylerdamily: omega-conotoxin
C;Keylerdes: acetylcholine release inhibition; calcium channel inhibitor; hydroxyproline;
F;1-16,8-19,15-26/Disulfide bonds: #status predicted
F;4,7/Modified site: 4-hydroxyproline (Pro) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                          C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004 C;Accession: T30176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.5%; Score 63; DB 2; Length 168
26.9%; Pred. No. 1.4e+02;
tive 13; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Length 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 51.7%; Score 62; DB Best Local Similarity 26.9%; Pred. No. 11; Matches 7; Conservative 13; Mismatches
                    205 GFTGDNCETDIDECASAPCRNGGACV 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : : : | : : : | | | | : : : | | | 480 GFEGSTCERNIDDCPNHKCQNGGVCV 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                  EGF repeat transmembrane protein - mouse C; Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 26.7"
Best Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Accession: A43620
A,Molecule type: protein
A,Residues: 1-29 <OLI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
                                                                                                                                         RESULT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    임
                                                                                                                                                                                                                                                                                                                                                                                                               metallothionein - common bobwhite (fragmen:)
C;Species: Colinus virginianus (common bobwhite)
C;Species: Colinus virginianus (common bobwhite)
C;Species: Colinus virginianus (common bobwhite)
C;Accession: 83379; 81B174
B;Shartzer, K.L.; Kage, K.; Sobieski, R.J.; Andrews, G.K.
B;Shartzer, K.L.; Kage, K.; Sobieski, R.J.; Andrews, G.K.
A;Title: Evolution of avian metallothionein: DNA sequence analyses of the turkey metallothionein: Evolution of avian metallothionein: DNA sequence analyses of the turkey metallothionein: preliminary
A;Reference number: 33379
A;Restaus: preliminary
A;Molecule type: mRNA
A;Residues: 1-43 <SHA>
A;Cross-references: UNIPROT: P27087; EMBL: X62512; NID: 962751; PIDN: CAA44371.1; PID: 962752
C;Superfamily: metallothionein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A48836

HA8836

HAB836

HAB836

HAB836

HAB836

HAB836

HAB836

HAB836

HAB836

HAB836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;23-34,28-43,45-54,62-88,180-191,185-200,202-211,218-229,223-238,240-249,256-267,261-27
fide bonds: #status predicted
                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-570 <BIS>
A;Cross-references: UNIPROT:P49013; GB:L07045; NID:g310659; PID:g310660
A;Note: sequence extracted from NCBI backbone (NCBIN:132724, NCBIP:132725)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
            Length 3623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 570;
                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Length 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Indels
    53.3%; Score 64; DB 2; Ler
29.2%; Pred. No. 1.9e+02;
tive 13; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;1-18/Domain: signal sequence #status predicted <SIG>F;19-570/Product: fibropellin C #status predicted <FIB>F;19-54/Domain: EGF homology <EGI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.5%; Score 63; DB 2; 26.9%; Pred. No. 68; tive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 33.3%; Score 63; DB Similarity 33.3%; Pred. No. 12; 9; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;57-175/Domain: CIr/Cls repeat homology cCIR>
F;176-211/Domain: EGF homology cEG3>
F;214-249/Domain: EGF homology cEG3>
F;252-287/Domain: EGF homology cEG4>
F;290-325/Domain: EGF homology cEG5>
F;364-363/Domain: EGF homology cEG5>
F;364-401/Domain: EGF homology cEG7>
F;404-439/Domain: EGF homology cEG7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CXIXNOXCXOXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |::|:|:|:||
CKCKNCRCRSCRKSCCSCCPAGCNNCV 3.2
                                                                                                                                                                                                          425 SGONCTENINDCSSNPCLNGGTCI 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                         4 XNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 29.2%
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;442-570/Region: avidin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity'
les 7; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 9; Congerv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loc
Matches
                                                                                                                                                             ò
                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
```

σ

```
F;23-34, 28-43, 45-54,62-88,180-191,185-200,202-211,218-229,223-238,240-249,256-267,261-27,751-466,468-477,484-495)Districted Try 484-495/Districted Try 484-853,527-541,65-580,582-591,598-609,603-618,620-62,5489-504,506-515,522-533,527-542,544+553,560-571,565-580,582-591,598-609,603-618,620-62,08,810-819,826-837,811-846,848-857,864-875,869-884,886-895,902-913,907-922,924-933/Districted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: A32038
R;Skinner, W.S.; Adams, M.E.; Quistad, G.B.; Kataoka, H.; Cesarin, B.J.; Enderlin, F.E.; J. Biol. Chem. 264, 2150-2155, 1989
A;Title: Purification and characterization of two classes of neurotoxins from the funnel A;Reference number: A32038; MUID:89123282; PMID:2914898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Monje, V.D.; Haack, J.A.; Naisbitt, S.R.; Miljanich, G.; Ramachandran, J.; Nasdasdi, L. Neuropharmacology 32, 1141-1149, 1993
A;Title: A new Conus peptide ligand for Ca channel subtypes.
A;Reference number: A58537; MUID:94150815; PMID:8107968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession 458537
A;Accession 458537
A;Anolecule type: mRNA
A;Residues: 1-29 <MON>
A;Residues: 1-29 <MON>
A;Residues: UNIPROT:026350; GB:369322; NID:9545399; PIDN:AAB29902.1; PID:9545400
A;Cross-references: UNIPROT:026350; GB:369322; NID:9545399; PIDN:AAB29902.1; PID:9545400
A;Cross-references: UNIPROT:026350; GB:369322; NID:9545399; PIDN:AAB29902.1; PID:9545400
                                                                                                                                                                                                                                                    ,180-191,185-200,202-211,218-229,223-238,240-249,256-267,261-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ٦,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C,Species: Agelenopais aperta
C,Date: 31-Jul-1989 #sequence_revision 22-Jul-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.Species: Conus magus (magus cone)
C.Date: 27-Mar-1997 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  omega-conotoxin MVIID precursor - cone shell (Conus magus) (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C:Reywords: amidated carboxyl end; myotoxin; venom F;2-16,9-22,17-32,24-30/Disulfide bonds: #status predicted F;36/Modified site: amidated carboxyl end (Asn) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ٠.
ص
                                                                                                                                                                                                                                                                                                                                                                                                              Length 1064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 36;
                                                                                                                                                                                                                                                                                                                                                                        51.7%; Score 62; DB 2; Length Lug-
26.9%; Pred. No. 1.3e+02;
6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.8%; Score 61; DB 2; Length 29; 28.0%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;4-29/Product: omega-conotoxin MVIID #status predicted <MAT>F;4-19,11-23,18-28/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mu-agatoxin I - funnel-weaving spider (Agelenopsis aperta)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 26.9%; Pred. No. 1.3e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.2%; Score 61.5; C
26.7%; Pred. No. 15;
tive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |::|:|:|:|:
CVPENGHCRDWYDECCEGFYCSCRQPPKCI 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CXIXNQXCXQXLDDCCS---XXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205 GFTGRNCEIDIDECASDPCONGGACV 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 XIXNOXCXQXLDDCCSXXCNXXNXCV 27
F;674-705/Domain: EGF homology «EG15»
F;712-743/Domain: EGF homology «EG16»
F;780-781/Domain: EGF homology «EG17»
F;788-819/Domain: EGF homology «EG18»
F;826-857/Domain: EGF homology «EG19»
F;864-895/Domain: EGF homology «EG20»
F;902-933/Domain: EGF homology «EG20»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: A58537
                                                                                                                                                                                                                          F; 936-1064/Region:
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fibropellin Ia - sea urchin (Strongylocentrotus purpuratus)
NyAlternate names: epidermal growth factor homolog precursor
NyContains: alternatively spliced fibropellin Ib (EGFI)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 13-May-1992 #sequence revision 17-Sep-1997 #text_change 09-Jul-2004
A;Delgadillo-Reynoso, M.G.; Rollo, D.R.; Hursh, D.A.; Raff, R.A.
J. Mol. Evol. 29, 314-327, 1989
A;Fitle: Structural analysis of the uEGF gene in the sea urchin Strongylocentrotus purpu
A;Accession: A40136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Riturt, L.T.; Barker, W.C.

AskEB J. 3, 1760-1764, 1989

A;Title: 1980

A;Title: 1980

A;Title: 1980

A;Title: 1980

A;Reference number: A43131; MUID:89196806; PMID:2784773

A;Contents: annotation

C;Comment: EGF homology repeats 10-17 are spliced out in the short form (fibropellin Ib)

E;10-1064/Product: fibropellin I #status predicted <FIB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 'K',747-821,898-978 cDE3>
R;Hursh, D.A.; Andrews, M.E.; Raff, R.A.
Science 237, 1487-1490, 1987
A;Title: A sea urchin gene encodes a polypeptide homologous to epidermal growth factor.
A;Reference number: A29316; MUID:87319677; PMID:3498216
A;Accession: A29316
                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNÅ
A;Residues: 'S',280-481,786-1064 <HUR>
A;Cross-references: GB:M17421; NID:g161474; PIDN:AAA30050.1; PID:g552260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:P10079; GB:X17530; NID:g10225; PID:g667061
A;Accession: B40136
                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: C40136
A;Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Status: preliminary, not compared with conceptual translation
                                                                                                                                                                                                                          2; Length 722;
                                                                                                                                                                                                                                                                                       6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Molecule type: DNA
A,Residues: 181-251,329-370,'R',372-408,'RA',411-441
                                                                                                                                                                                                          DB ?
                                                                                                                                                                                                                                                                                    12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1r/Cls repeat homology <C1R>
C,Genetics:
A,Gene: Dlll C,Superfamily: delta-4 protein; EGF homology F;31-362/Domain: EGF homology <EGF2>F;446-477/Domain: EGF homology <EGF>F;484-515/Domain: EGF homology <EGF>
                                                                                                                                                                                                                          51.7%; Score 62; 28.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                     : ::|:::|| |::| ::|
433 GFSGRYCEDNVDDCASSPCANGGIC 457
                                                                                                                                                                                                                                                                                                                                              2 XIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-54/Domain: EGF homology <EG01>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGF homology < EGF homology <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   homology
homology
homology
homology
homology
homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fibrational Stransform File Promology File 249/Domain: EGF homology File 249/Domain: EGF homology File 277/Domain: EGF homology
                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-114 < DEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;294-325/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;636-667/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;446-477/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                     ð
```

```
R;Thomas, U.; Speicher, S.A.; Knust, E.
Development 111, 749-761, 1991
A:Title: The Drosophila gene Serrate encodes an EGF-like transmembrane protein with a com
A;Reference number: S16148; MUID:91347903; PMID:1840519
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-1351, 'T',1353-1408 <THO2>
A; Cross-references: EMBL:X56811; NID:g8563; PID:g8564
R; Fleming A. J.; Scottgale, T.N.; Diederich, R.J.; Artavanis-Tsakonas, S.
Genes Dev. 4, 2188-2201, 1990
A; Title: The gene Serrate encodes a putative EGF-like transmembrane protein essential folla, Reference number: A36666; MUID:91099666; PMID:2125287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;1222-1246/Domain: transmembrane #status predicted <TM1>
F;1247-1408/Domain: intracellular #status predicted <INT>
F;152,196,247,331,412,452,558,739,965,977,1004,1030,1150/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         slit protein 2 precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Apr. 1991 #sequence_revision 30-Apr. 1991 #text_change 02-Aug-2002
C;Accession: B36665
R;Rothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.
Genes Dev. 4, 2169-2187, 1990
A;Title: allit: an extracellular protein necessary for development of midline glia and con A;Reference number: A36665; MUID:91099665; PMID:2176636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;1-84/Domain: signal sequence #status predicted <SIG>
;85-121408/Product: gene serrate protein #status predicted <MAT>
;85-1211/Domain: extracellular #status predicted <EXT>
;283-316/Domain: EGF homology <EGG01>
;319-348/Domain: EGF homology <EG02>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.8%; Score 61; DB 2; Length 1408;
23.1%; Pred. No. 1.9e+02;
ive 14; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-15,20-26,'A',28-1408 <FLE>
A;Cross_references: GB:M35759; NID:g158605; PID:g158606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #status atypical <EG04>
                                                                                                                                                                                                                                                                                                          R;Thomas, U. submitted to the EMBL Data Library, November 1990 A;Reference number: $16878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F homology <EGG3>
F homology &EGG3>
F homology &EGG0S>
F homology &EGG0S>
F homology &EGG0S>
F homology &EGG0S>
F homology <EGG0S>
F homology <EGG0S>
F homology <EGG0S>
F homology <EGG0S>
                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-1408 <THO1>
A;Cross-references: UNIPROT:P18168; EMBL:X56811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Keywords: glycoprotein; transmembrane protein;1-84/Domain: signal sequence #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: FlyBase: FBgn0004197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        homology <EG11>
homology <EG12>
homology <EG13>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cysteine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /Domain: EGF homology
/Domain: EGF homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 23.19
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1469 <ROT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGF
EGF
                                                                                                                                                              A; Accession: S16148
                                                                                                                                                                                                                                                                                                                                                                                                                          ;Accession: S16878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: A36666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene: FlyBase:Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    395-488/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :883-914/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       495-526/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          533-608/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5-645/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7-796/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            803-834/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               841-876/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         355-388/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            652-683/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  690-720/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                          C.Species: Gallus gallus (chicken)
C;Species: 13.69p-1996 #sequence_revision 13.5ep-1996 #text_change 09-Jul-2004
C;Accession: 150719
Nature 375, 787-790, 1995
A;Tile: Expression of a Delta homologue in prospective neurons in the chick.
A;Reference number: 150719, MUID:95319507; PMID:7556411
A;Reference number: 150719
A;Retus: preliminary; translated from GB/EMBL/DDBJ
A;Retus: preliminary; translated from GB/EMBL/DDBJ
A;Retus: preliminary; translated from GB/EMBL:026590; NID:G882411; PIDN:AAC59689.1; PID:G8824
C;Superfamily: delta 4 procein; EGF homology <EGX1>
F;293-3370/Domain: EGF homology <EGX1>
F;393-370/Domain: EGF homology <EGX2>
F;416-447/Domain: EGF homology <EGX2>
F;492-523/Domain: EGF homology <EGF3>
F;492-523/Domain: EGF homology <EGF3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cyaccosion: T42626
R:Holmes, G.P.; Negus, K.; Burridge, L.; Raman, S.; Algar, E.; Yamada, T.; Little, M.H.
RR:Holmes, G.P.; Negus, K.; Burridge, L.; Raman, S.; Algar, E.; Yamada, T.; Little, M.H.
Mech. 79, 57-72, 1998
A;Title: Distinct but overlapping expression patterns of two vertebrate slit homologs im
A;Reference number: 222177; MUID:99279238; PMID:10349621
A;Accession: T42626
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          secreted leucine-rich repeat-containing protein SLIT2 - mouse (fragment) N;Alternate names: neurogenic extracellular slit protein C;Species: Mus musculus (house mouse) C;Decies: Mus musculus (house mouse) C;Dete: 11-7an-2000 #sequence_revision 11-Jan-2000 #sequence_revision 11-J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene serrate protein precursor - fruit fly (Drosophila melanogaster)
C'Species: Drosophila melanogaster
C'Date: 31-Dec-1991 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C'Accession: S16148; S16878; As6666
           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.8%; Score 61; DB 2; Length 1025; 26.9%; Pred. No. 1.5e+02; Live 13; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 728;
           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.8%; Score 61; DB 2; I 28.0%; Pred. No. 1.2e+02; iive 12; Mismatches 6;
   13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : ::|: ::|| ::|| 485 GFEGENCEVNIDDCEDNDCENNSTCV 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                         1 CXIXNQXCXQXLDDCCSXXCNXXNX 25
                                                                                                            4 CQGRGASCRKTMYNCCSGSCNRGRC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 XIXNOXCXQXLDDCCSXXCNXXNXC 26
   7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 50.8
Best Local Similarity 26.9
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 34 S16148
                                                                                                                                                                                                                                                    RESULT 32
                                                                     ò
                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

```
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Rosicules: 1-354 <WIL>
A;Cross-references: UNIPROT:Q9XV21; EMBL:Z81540; PIDN:CAB04398.1; GSPDB:GN00023; CESP:F4
A;Experimental source: clone F46B3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neurogenic protein Delta precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Jrosophila melanogaster
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 02-Aug-2002
C;Accession: All246
R;Kopczynski, C.C.; Alton, A.K.; Fechtel, K.; Kooh, P.J.; Muskavitch, M.A.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein F46B3.9 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                 F;197-22.0 Domain: leucine-iricin alpha-2-glycoptocelli repeat indicated years. P;197-22.0 Domain: proteoglycan amino-terminal homology <PAN42.
F;288-313/Domain: proteoglycan amino-terminal homology <PAN42.
F;283-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR F;31-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR F;31-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR F;419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR F;419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR F;419-442/Domain: proteoglycan carboxyl terminal homology <PAN43.
F;512-537/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRI F;526-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRI F;526-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRI F;526-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRI F;520-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRI F;761-695/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRI F;761-695/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRI F;761-695/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRI F;761-894/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRI F;761-894/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRI F;761-894/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRI F;791-814/Domain: leuci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Map position: 5
A;Introns: 23/1; 55/1; 82/1; 112/1; 142/1; 170/1; 193/1; 223/1; 299/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                            leucine-rich alpha-2-glycoprotein repeat homology
leucine-rich alpha-2-glycoprotein repeat homology
leucine-rich alpha-2-glycoprotein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.8%; Score 61; DB 2; Length 1480; ilarity 26.9%; Pred. No. 2e+02; Conservative 12; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;846-890/Domain: proteoglycan carboxyl-terminal homology <PCS4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Ainscough, R. submitted to the EMBL Data Library, November 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Pred. No. 94;
13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CXIXN--QXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1055 GFHGTNCTDNIDDCQNHMCQNGGTCV 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.0%; Score 60; 28.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;1028-1061/Domain: EGF homology <EGF5
F;1068-1099/Domain: EGF homology <EGF2
F;1115-1148/Domain: EGF homology <EGF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 28.6'
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: Z19541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Gene: CESP:F46B3.9
                                                                                                                       7,197-220/Domain: 1
7,228-272/Domain: p
7,288-313/Domain: p
7,323-346/Domain: 1
7,371-394/Domain: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A31246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 36
A36665
Balit protein 1 precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 02-Aug-2002
C;Accession: A36665, A1640; Si3523
R;Rothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Teakonas, S.
Genes Dev. 4, 2169-2187, 1990
A;Title: slit: an extracellular protein necessary for development of midline glia and cd
A;Reference number: A36665; MUD:91099665; FMID:2176636
A;Accession: A36665
A;Status: preliminary
A;Molecule Type: mRNA
A;Residues: 1-1480 - ROT>
A;Cross-references: GB:X53959; NID:g8614; PIDN:CAA37910.1; PID:g8615
A;Cross-references: GB:X53959; NID:g8614; PIDN:CAA37910.1; PID:g8615
A;Cross-references: GB:X53959; NID:g8614; PIDN:CAA37910.1; PID:g8615
A;Cross-references: GB:X53959; NID:g8614; PIDN:A37910.1; PID:g8615
A;Title: slit: An EGF-homologous locus of D. melanogaster involved in the development of A;Reference number: A31640; MUID:g9077533; PMID:3144436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein C;Reywords: alternative splicing; growth factor F;66-91/Domain: proteoglycan amino-terminal homology <PAH1> F;66-91/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
                                                                                                                                                                       homology; leucine-rich alpha-2-glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <LR12>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <LR13>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <LR14>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <LRR8>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <LRR9>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <LR10>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <LR16>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                          A/Cuene: FlyBase: PBgn0003425
C; Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-;
Fé6-91/Domain: proteoglycan amino-terminal homology challs.
Fé6-91/Domain: proteoglycan amino-terminal homology clrRR.
F;101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR.
F;105-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR.
F;13-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR.
F;13-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR.
F;13-196/Domain: proteoglycan carboxyl-terminal homology cRR1.
F;228-272/Domain: proteoglycan amino-terminal homology cRR1.
F;33-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR.
F;349-445/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR.
F;371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLRR.
F;395-418/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLR1.
F;419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLR1.
F;51-537/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLR1.
F;51-537/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLR1.
F;51-537/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLR1.
F;520-643/Domain: proteoglycan carboxyl-terminal homology cRN1.
F;51-596/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLR1.
F;61-730/Domain: proteoglycan carboxyl-terminal homology cRN1.
F;74-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLR1.
F;74-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLR1.
F;74-700/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLR1.
F;74-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLR1.
F;76-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLR1.
F;76-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology cLR1.
F;76-790/Domain: EGF homology cEGF>
F;1028-1069/Pomain: EGF homology cEGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 1469; 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: A31640
A;Molecule type: DNA
A;Residues: 881-1182, 'G',1185-1404, 'GT',1463-1464, 'YHA' <RO2>
A;Cross-references: GB:M23543; NID:g340939; PID:g514357
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1055 GFHGTNCTDNIDDCQNHMCQNGGTCV 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 61;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: FlyBase: FBgn0003425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 26.3%
Best Local 7; Conservative
A;Cross-references: GB:X53959
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: FlyBase:sli
```

ઠ 셤 ö

```
EMBO J. 6, 761-766, 1987
A;Title: EGF homologous sequences encoded in the genome of Drosophila melanogaster, and t
A;Reference number: A91081; MUID:87218537; PMID:3107986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: A32901
R;Yochem, J.; Greenwald, I.
Cell S8, 553-563, 1989
A;Title: glp-1 and lin-12, genes implicated in distinct cell-cell interactions in Caenoril A;Reference number: A32901; MUID:89336787; PMID:2758466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CyAccession: E89753
R; anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A; Title: Georgian sequence of the nematode C. elegans: a platform for investigating biology|
A; Fitle: Georgian sequence of the nematode C. elegans: a platform for investigating biology|
A; Reference number: A75000; MUID: 99069613; PMID: 9851916
A; Reference number: A75000; MUID: 99069613; PMID: 9851916
A; Note: see websites genome. wustl. edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/ A; Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule: type: DNA
A;Molecule type: DNA
A;Molec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A/Gene: Delta, Dl
A/Gross-references: PlyBase:FBgn0000463
A/Cross-references: PlyBase:FBgn0000463
C/Superfamily: neurogenic protein
C/Superfamily: neurogenic protein
P/1-18/Domain: signal sequence #status predicted <SIG>
F/19-88/Product: neurogenic repetitive locus delta protein #status predicted <MAT>
F/457-488/Domain: EGF homology <EGF1>
F/533-564/Domain: EGF homology <EGF2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glp1 protein precursor - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Dec.1989 #sequence_revision 04-Sep-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein F11C7.4 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 422-436,'ET',439-458,'A',460-489,'T',491-621 <KNU>
A;Cross-references: GB:X05140; NID:97851; PIDN:CAA28786.1; PID:9929563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
50.0%; Score 60; DB 2; 1
Best Local Similarity 23.1%; Pred. No. 1.7e+02;
Matches 6; Conservative 12; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.0%; Score 60; DB 2; 25.8%; Pred. No. 2.2e+02; ive 13; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;1074-1106/Domain: ankyrin repeat homology <AN2> F;1107-1139/Domain: ankyrin repeat homology <AN3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | ::| | ::::| | 1.0 | 140 CICNNGYGGSYCEEGIDHCAQNECAEGSTCV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CXIXN----QXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;961-993/Domain: ankyrin repeat homology <AN1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 XIXNQXCXQXLDDCCSXXCNXXNXCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genes Dev. 2, 1723-1735, 1988
A;Title: Delta, a Drosophila neurogenic gene, is transcriptionally complex and encodes & A;Reference number: A31246
A;Reference number: A31246
A;Rocession: A;R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 39
S19087
gene Delta protein precursor - fruit fly (Drosophila melanogaster)
G.Species: Drosophila melanogaster
C.Species: Drosophila melanogaster
C.Bate: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C.Accession: S19087
R.Muskavitch M.A.T.
Submitted to the BMBL Data Library, June 1991
A.Reference number: S19087
A.Reference number: S19087
A.Status: preliminary
A.Status: preliminary
A.Status: Jreliminary
A.Stetus: Steliminary
A.Stetus: Steliminary
A.Stetus: Dresiminary
A.St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.0%; Score 60; DB 2; Length 832; 23.1%; Pred. No. 1.7e+02; ive 12; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.0%; Score 60; DB 2; Length 833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references. FlyBase:FBgn0000463
C;Superfamily: neurogenic protein delta; EGF homology
F;335-371/Domain: EGF homology «EGX1»
F;378-415/Domain: EGF homology «EGX1»
F;457-488/Domain: EGF homology «EGF»
F;533-564/Domain: EGF homology «EGF»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : : : | | | : : | : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : : : | | | : : | : | : 444 GFSGTRCETNIDDCLGHQCENGGTCI 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 23.11
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 23.19
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
```

ij

13

us-10-627-685a-1.rpr

```
10; Mismatches
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-43 < SHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: S33378
    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 46
                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 44

$33382
metallothionein - ring-necked pheasant (fragment)

$(5,5pecies: Phasianus colchicus (ring-necked pheasant)

$(5,5pecies: Phasianus colchicus (ring-necked pheasant)

$(5,5pecies: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999

$(5,5pecies: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999

$(6,5pecies: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999

$(7,5pecies: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999

$(7,5pecies: 13-Jan-1995 #sequence_revision 13-Jan-1999 #text_change 20-Aug-1999

$(7,5pecies: 13-Jan-1999 #text_change 20-Aug-1999)

$(7,5pecies: 13-Jan-1999 #text_change 20-Aug-1999)

$(7,5pecies: 13-Jan-1999 #text_change 20-Aug-1999)

$(7,5pecies: 13-Jan-1995 #text_change 20-Aug-1999)

$(7,5pecies: 13-Jan-1999 #text_change 20-Aug-1999)

$(7,5pecies: 13-Jan-1999)

$(7,5pecies: 13-Jan-1999)

$(7,5pecies: 13-Jan-1999)

$(7,5pecies: 13-Jan-1999)

$(7,5pecies: 13-Jan-199)

$(7,5pecies: 13-Jan-1999)

                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1722 <STO>
A;Cross-references: UNIPROT:Q19350; GB:chr_X; PIDN:AAC69012.1; PID:g1125776; GSPDB:GN006
C;Genetics:
A;Gene: F11C7.4
A;Map position: X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: A new conus peptide ligand for mammalian presynaptic Ca2+ channels.

A;Reference number: JH0699; MUID:92337922; PMID:1352986

A;Accession: JH0701

A;Accession: JH0701

A;Residues: nucleic acid sequence not shown

A;Residues: L-25 cHIL.

A;Residues: L-25 cHIL.

A;Residues: L-25 cHIL.

A;Cross-references: UNIPROT:PD5485

B;Olivera, B.M.; Cruz, L.J.; de Santos, V.; LeCheminant, G.W.; Griffin, D.; Zeikus, R.;

B;Olivera, B.M.; Cruz, L-30; de Santos, V.; LeCheminant, G.W.; Griffin, D.; Zeikus, R.;

A;Title: Neuronal calcium channel antagonists. Discrimination between calcium channel su

A;Reference number: A34115; MUID:87299637; PMID:2441741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: protein
A,Residues: 1-25 <OLI>
S,Superfamily: omega-conotoxin
C;Keywords: acetylcholine release inhibition; amidated carboxyl end; calcium channel inh
F;1-16,8-20,15-25/Disulfide bonds: #status predicted
F;25/Modified site: amidated carboxyl end (Cys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    omega-conotoxin MVIIB - cone shell (Conus magus)
C;Species: Conus magus (magus cone)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: JH0701; B34115
R;Hillyard, D.R.; Monje, V.D.; Mintz, I.M.; Bean, B.P.; Nadasdi, L.; Ramachandran, J.; Neuron 9, 69-77, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                      ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X62510; NID:g64214; PIDN:CAA44369.1; PID:g64215
C;Superfamily: metallothionein
                                                                                                                                                                                                                                                                                                                                                                                                                                      4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                 Length 1722,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 59; DB 2; Length 43; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                              7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Indels
                                                                                                                                                                                                                                                                                                                                                 50.0%; Score 60; DB 2; 1 26.7%; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1391 CNCDNNWRGAHCQHQMDTCLDFPCNNDGVC 1420
                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CXIXNQ----XCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 59;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | : : : | | | | : : : | | | : : : | CKGKGASCHRTSYDCCTGSCNRGKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CXIXNQXCXQXLDDCCSXXCNXXNX 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 28.0% Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-43 <SHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: B34115
A; Accession: E89753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
```

Best Local Similarity

```
metallothionein - common bobwhite (fragment)
C;Species: Colinus virginianus (common bobwhite)
C;Species: Colinus virginianus (common bobwhite)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: 333378; S18173
R;Shartzer, K.L.; Kage, K.; Sobieski, R.J.; Andrews, G.K.
A;Artzer, K.L.; Kage, Z52-262, 1993
A;Title: Bvolution of avian metallothionein: DNA sequence analyses of the turkey metallo A;Reference number: S33378; MUID:93247066; PMID:84883164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RiAhrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F. Virology 229, 381-339, 1997
A;Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis A;Reference number: Z17011; MUID:97271300; PMID:9126251
A;Accession: T10405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:P27086; EMBL:X62511; NID:g62749; PIDN:CAA44370.1; PID:g62750
C;Superfamily: metallothionein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conocoxin homolog - Autographa californica nuclear polyhedrosis virus
C;Species: Autographa californica nuclear polyhedrosis virus, AcMNPV
A;Note: dsDNA virus
C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004
C;Dates: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004
C;Accession: C72855; A44003
R;Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
Virology 202, 586-605, 1994
A;Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.
A;Reference number: A72850; MUID:94303173; PMID:8030224
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C,Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OpMNPV
C,Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conotoxin-like protein 1 - Orgyia pseudotsugata nuclear polyhedrosis virus
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indela
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Cross-references: EMBL: U75930; NID: 92934903; PID: 91911382
   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-53 <AHR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 49.2%; Score 59; DB 2; Local Similarity 32.1%; Pred. No. 32; les 9; Conservative 13; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 30.8%; Pred. No. 28;
Matches 8; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CXIXNOXCXQXLDDCCSXXCN-XXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                       |::|:|:|:|:|CKCKNCRCRCRCRCCRCCRAGCNNC 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-53 <AYR>
```

```
A;Introns: 11/1; 33/1
C;Superfamily: metallothionein
                                                                                                                                                                                                                          A;Accession: A28113
A;Molecule type: protein
A;Residues: 1-63 <MCC>
A;Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 metallothionein - turkey
                                                                   A; Accession: JQ0030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                        C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
Conditional like protein - Lymantria dispar nuclear polyhedrosis virus
C; Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV
C; Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C; Accession: T30499
R; Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohr A; Ticle: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria of A; Reference number: Z20836; MUD:99124785; PMID:987315
A; Accession: T30499
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-53 < KUZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type:~mRNA
A;Residues: 1-63 <WEI>
A;Residues: 1-63 <WEI>
A;Cross-references: EMBL:X06749; NID:g63617; PIDN:CAA29924.1; PID:g63618
A;Notes: part of this sequence, including the amino end of the mature protein, was confir
R;Fernando, L.P.; Andrews, G.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: UNIPROT: P09576
A; Cross-references: UNIPROT: P09576
R; Wei, D.; Andrews, G.K.
Nucleic Acids Res. 16, 537-553, 1988
A; Title: Molecular cloning of chicken metallothionein. Deduction of the complete amino A; Reference number: S01750; MUID: 88124253; PMID: 3340548
                                                                                                                                                                                                                                                                                                                                                              ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA958

metallothionein - chicken

C;Species: Gallus gallus (chicken)

C;Species: Gallus gallus (chicken)

C;Species: 13-Jul-1990 #sequence revision 13-Jul-1990 #text_change 09-Jul-2004

C;Accession: A34958; SO1750; JQ0030; A28113

G;Accession: A34958; Andrews, G.K.

J; Nutr. 119, 309-318, 1989

A;Title: Structure and expression of chicken metallothionein.

A;Reference number: A34958; MulD:89141100; EMID:2645390

A;Status: preliminary; not compared with conceptual translation

A;Molecule rype: mRNA

A;Residues: 1-63 - FER.>
                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                           3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:Q9YMH9; EMBL:AF081810; PIDN:AAC70335.1
                                                                                                                                                                                                                                                                                                      of Similarity 32.1%; Score 59; DB 2; Length 53; Similarity 32.1%; Pred. No. 32; 9; Conservative 13; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 59; DB 2;
; Pred. No. 32;
13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                             1 CXIXNQXCXQXLDDCCSXXCN-XXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CXIXNQXCXQXLDDCCSXXCN-XXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 32.1%;
Matches 9; Conservative 1
                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ਨੇ
```

```
C:Comment: Metallothioneins are a class of cysteine-rich, heavy-metal-binding proteins pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Melegris gallopavo (common turkey)
C;Species: Malegris gallopavo (common turkey)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S33381; S33380; Si8180
R;Shartzer, K.L.; Kage, K.; Sobieski, R.J.; Andrews, G.K.
J. Mol. Bvol. 36, 255-262, 1993
A;Title: Evolution of avian metallothionein: DNA sequence analyses of the turkey metallot
A;Reference number: S33378; MUID:93247066; PMID:8483164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A34620
metallothionein - duck
metallothionein - duck
c;Species: Anas plaryrhynchos (domestic duck)
C;Species: Anas plaryrhynchos (domestic duck)
C;Species: 22-Jun-1990 #sequence revision 22-Jun-1990 #text_change 09-Jul-2004
C;Accession: A34620; B34620; B3154; JC5095
R;Lih, Lr.Y. Huang, P.C.
Biochem. Biophys. Res. Commun. 168, 182-187, 1990
A;Title: Complete homology in metallothionein from two genera of ducks and their hybrids.
A;Reference number: A34620; MUID:90226357; PMID:2327997
A;Accession: A34620
                                                                                         A; Molecule type: DNA
A; Residues: 1-63 <FE2>
R; McCormick, C.C.; Fullmer, C.S.; Garvey, J.S.
Proc. Natl. Acad. Sci. U.S.A. 85, 309-313, 1988
A; Title: Amino acid sequence and comparative antigenicity of chicken metallothionein.
A; Reference number: A28113; MUID:88124831; PMID:2448773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
A/Title: Cloning and expression of an avian metallothionein-encoding gene. A/Reference number: JQ0030; MUID:90034180; PMID:2806910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A Reference number: S33378; MUID: 93247066; PMID: 8483164
A Accession: S33381
A A Accession: S3381
A A Residues: 1-63.cSHA>
A Residues: 1-63.cSHA>
A Rossidues: 103380
A Molecule type: mRNA
A Residues: 15-57 cSH2>
A Residues: 15-57 cSH2>
A Cross-references: EMBL: X62514; NID: 964090; PIDN: CAA44372.1; PID: 964091
C Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Introns: 11/1; 33/1
C;Superfamily: metallothionein
F;1-63/Product: metallothionein #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 30.8%; Score 59; DB 2; Similarity 30.8%; Pred. No. 36; 8; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match
Local Similarity 30.8%; Pred. No. 36;
es 8; Conservative 10; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 CKCKNCRCRSCRKSCCSCCPAGCNNC 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CXIXNOXCXOXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CXIXNQXCXQXLDDCCSXXCNXXNXC
```

```
C;Accession: S28764
R;Rauch, U.; Karthikeyan, L.; Maurel, P.; Margolis, R.U.; Margolis, R.K.
B;Biol. Chem. 257, 19536-19547, 1992
A;Title: Cloning and primary structure of neurocan, a developmentally regulated, aggregat A;Reference number: S28764; MUID:92406907; PMID:1326557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: T04215

T; Brandt, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, submitted to the Protein Sequence Database, March 1999
A;Reference number: Z15261
A;Accession: T04215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;1156-1212/Domain: complement factor H repeat homology <FHD>
F;121,339,737,147,164/Binding site: carbohydrate (ABN) (covalent) #status predicted
F;372,410/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted
F;944/Binding site: chondroitin sulfate (Ser) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                       hypothetical protein T5C23.110 - Arabidopsis thaliana
C,Species: Arabidopsis thaliana (mouse-ear cress)
C,Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Species: Rattus norvegicus (Norway rat)
;Date: 22-Nov-1993 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49.2%; Score 59; DB 2; Length 1257; 25.0%; Pred. No. 2.7e+02; ive 12; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-419 <BEV>
A;Cross-references: UNIPROT:Q9T0D5; EMBL:AL049500
A;Experimental source: cultivar Columbia; BAC clone T5C23
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

49.2%; Score 59; DB 2; Le.
Best Local Similarity 28.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 12; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

49.2%; Score 59; Du
Best Local Similarity 25.0%; Pred. No. 2.7e
Matches 6; Conservative 12; Mismatches
                                               20 CKCKNCRCRSCRKSCCSCCPAGCNNC 45
              1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               353 CKIDNAWLLMILQECCICLCEYEDG 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :::[:::|| ::||:::||
980 AGENCEIDIDDCLCSPCENGGTCI 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CXIXNOXCXQXLDDCCSXXCNXXNX 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 XNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Map position: 4
A,Introns: 200/2; 241/2; 285/3
A,Note: T5C23.110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neurocan precursor - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neurocan - mouse
                                                                                                                                                    RESULT 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 55
                                                              g
              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
A;Residues: 1-63 <LIN>
A;Cross-references: UNIPROT:P09576
A;Cross-references: UNIPROT:P09576
A;Experimental source: Anas platyrhynchos (domestic duck)
A;Accession: B34620
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-63 <LIZ->
A;Experimental source: Anas platyrhynchos x Cairina moschata (domestic duck x muscovy du A;Residues: 1-63 <LIZ->
A;Experimental source: Anas platyrhynchos y Cairina moschata (domestic duck x muscovy du B;Lin, L.Y.; Liu, L.F.; Tam, M.F.; Huang, P.C.; Vestling, M.; Fenselau, C.
Biochim. Blophys. Acta 1041, 31-35, 1990
A;Title: Primary sequence of duck metallothionein.
A;Reference number: S13154; MUID:91027866; PMID:2223844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genera of ducks and their hybrids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Rosidues: 1-63 <LEE>
A;Cross-references: GB:U34231; NID:g1000299; PIDN:AAC60048.1; PID:g1000300
A;Experimental source: strain tsai ya duck
C;Comment: This protein has a high metal binding capacity and sulfur content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:U34230; NID:g1000297; PIDN:AAC60047.1; PID:g1000298 C;Comment: This protein has a high metal binding capacity and sulfur content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Cairina moschāta (muscovy duck)
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004
C;Accession: C34620; JC5094
R;Lin, L.Y.; Huang, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Structure and expression of metallothionein gene in ducks. A;Reference number: JC5094; MUID:97075914; PMID:8918237 A;Accession: JC5095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Title: Structure and expression of metallothionein gene in ducks.
A,Reference number: JC5094, MUID:97075914, PMID:8918237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49.2%; Score 59; DB 2; Length 63; 30.8%; Pred. No. 36; stive 10; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Length 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: protein
A;Residues: 1-63 «L13»
R;Lee, Y.J.; Chen, Y.P.; Wang, S.H.; Chow, W.Y.; Lin, L.Y.
Gene 176, 85-92, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:P09576
R;Lee, Y.J.; Chen, Y.P.; Wang, S.H.; Chow, W.Y.; Lin, L.Y.
Gene 176, 85-92, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem. Biophys. Res. Commun. 168, 182-187, 1990
A;Title: Complete homology in metallothionein from two casterence number: A34620; MUID:90226357; PMID:2327997
A;Accession: C34620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49.2%; Score 59; DB 30.8%; Pred. No. 36; cive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 CKCKNCRCRSCRKSCCSCCPAGCNNC 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Introns: 11/1; 33/1
C;Superfamily: metallothionein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 52
C34620
metallothionein - muscovy duck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Superfamily: metallothionein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 30.8
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 30.8
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein A; Residues: 1-63 <LIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-63 < LEE>
                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Introns: 11/1; 33/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                A; Accession: S13154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: JC5094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

```
A/Title: Relationships between the gene and protein structure in human complement compone
A/Reference number: IS2400; MUID:89118250; PMID:3219351
                                                                                                                                                    A; Accession: I52400
A; Status: translated from GB/EMBL/DDBJ
C;Species: Mus musculus (house mouse)
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: $52781
R;Rauch, U.; Forsberg, N.; Kulbe, G.; Arnoid-Ammer, I.; Faessler, R.
submitted to the EMBL Data Library, February 1995
A;Reference number: $52781
A;Recession: Amino acid sequence of mouse neurocan and brevican and their different ex
A;Recession: S5781
A;Recession: S5781
A;Recession: S5781
A;Recession: S5781
A;Residues: preliminary
A;Molecule Lype: mRNA
A;Residues: 1-1668 cRAU>
A;Cross-references: UNIPROT: P55066; EMBL: X84727; NID: 9758629; PIDN: CAA59216.1; PID: 97586
C;Superfamily: aggrecan; C-type lectin homology cINK1>
F;76-253/Domain: link protein repeat homology <LNK1>
F;274-355/Domain: Link protein repeat homology <LNK2>
F;964-995/Domain: EGF homology <EGF>
F;1040-1160/Domain: C-type lectin homology <LNE>
F;1167-1223/Domain: C-type lectin homology <LNE>
F;1167-1223/Domain: Complement factor H repeat homology <FHD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein F42CS.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16342
R;Du, Z.
R;Du, Z.
R;Du, Z.
R;Du, Z.
R;Du, Z.
R;Du, Z.
A;Reference number: Z18497
A;Golecule type: DNA
A;Residues: 1-250 <DUZ>
A;Residues: 1-250 <DUZ>
A;Residues: 1-250 <DUZ>
A;Golecule type: DNA
A;Golecule type: DNA
A;Residues: 1-250 <DUZ>
A;Golecule type: DNA
A;Residues: 1-250 <DUZ>
A;Golecule type: DNA
A;Go
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement C9 precursor [validated] - human
C;Species: Homo sapiens (man)
C;Date: 27-Nov-1985 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004
C;Accession: A59363, IS2400; A91029; A94019, S68647; A59364; A03208
R;Marzaitti, D.; Eggertsen, G.; Fey, G.H.; Stanley, K.K.
unpublished results, 1988, cited by GenBank
A;Bescription: Relationships between the gene and protein structure in human complement
A;Reference number: A59363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTOBB-references: UNIPROT:PD2748; GB:X02176; NID:929580; PIDN:CAA26117.1; PID:929581; Marazziti, D.; Eggertsen, G.; Fey, G.H.; Stanley, K.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

49.2%; Score 59; DB 2; Length 1268;
Best Local Similarity 25.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 12; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.8%; Score 58.5; DB 2; Length 250; ilarity 32.0%; Pred. No. 1e+02; Conservative 11; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 PVFNQYAMQPANDCC---CRCGSPC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 XIXNOXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 XNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-559 <MAR1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A59363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

```
A Molecule type: mRNA
A; Residues: 2-12, Xr, 14-16, Xr, 18-42, Rr, 44-313, 315-416, Pr, 418-559 < DIS>
A; Cross-references: GB: K02766; NID: g1/9725; PIDN: AAA51889.1; PID: g1/9726
R; Lengweiler, S.; Schaller, J.; Rickli, E.E.
FRBS Lett. 380, 8-12, 1996
A; Title: Identification of disulfide bonds in the ninth component (C9) of human complemer!
A; Reference number: S68647; MUID: 96181657; PMID: 8603752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Wolecule type: protein
A;Residues: 34-47;52-59;69-87, X', 89-93, T', 94-98;106-113;118-131;136-145;180-181, X', 18:
R;Witze. Schlomp, K.; Hobart, M.J; Fernie, B.A.; Orren, A.; Wurzner, R.; Rittner, C.; Kaulmunogenetics 48, 144-147, 1998
A;Title: Heterogeneity in the genetic basis of human complement C9 deficiency.
A;Reference number: A59864; MUID:98298010; PMID:9634479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description: The four terminal components of the complement system are C-mannosylated on mult A; Reference number: A59362; MUID:20020247; PMID:10551839
A; Reference number: A59362; MUID:20020247; PMID:10551839
A; Contention: Annotation
A; Role: identification and location of C-mannosylation sites by mass-spectroscopy and (1)
A; Genetics:
A; Genetics: Spi3-5pi3
C; Genetics: Spi3-5pi3
C; Complex: monomer in plasma; 10 to 16 chain multimer in transmembrane form
C; Function:
A; Description: in association with complement C5b-8 complex polymerizes to form a transme
C; Superfamily: complement pathway; cytolysis; glycoprotein; inflammation; membrane attack c; Superfamily: complement C9; EGF homology; LDL receptor ligand-binding repeat homology;
C; Superfamily: complement C9 # #status predicted <81G>
C; Superfamily: complement C9 # status predicted <69A>
C; Superfamily: complement C9 # status predicted <69A>
C; Superfamily: complement C9 # status predicted <69A>
C; Superfamily: complement C9 # status predicted <69B>
C; Superfamily: complement C9 # 
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 'S', 1-313, 315-559 <STA>
A; Cross-references: GB: X02176; ND: 929580
R; DiScipio, R.G.; Gehring, M.R.; Podack, E.R.; Kan, C.C.; Hugli, T.E.; Fey, G.H.
Proc. Natl. Acad. Sci. U.S.A. 81, 7298-7302, 1984
A; Title: Nucleotide sequence of cDNA and derived amino acid sequence of human complement
A; Reference number: A94019; MUID: 85063778; PMID: 6095282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 27-559 < WIT>
A; Cross-references: GB: V08545; NID:g1834472; PIDN:CAA69849.1; PID:g2258128
A; Experimental source: macronuclear; tissue type blood; cell type lymphocyte
R; Hofsteenges, J.; Blommers, M.; Hess, D.; Furmanek, A.; Miroshnichenko, O.
A; Diol. Chem. 274, 32786-32794, 1999
A; Title: The four terminal components of the complement system are C-mannosyl
A Molecule type: DNA
A; Residues: 62-159 < MAR2>
A; Residues: 62-159 < MAR2>
A; Residues: 62-159 < MAR2>
A; Cross-references: G8-302833; NID:g179727; PIDN:AAA51890.1; PID:g179728
B; Stanley, K.K.; Kocher, H.P.; Luzio, J.P.; Jackson, P.; Tschopp, J.
EMBO J. 4, 375-382, 1985
A; Title: The sequence and topology of human complement component C9.
A; Reference number: A91029; MUID:85257464; PMID:4018030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

48.8%; Score 58.5; DB 1; Length 559;
Best Local Similarity 26.3%; Pred. No. 1.8e+02;
Matches 10; Conservative 12; Mismatches 3; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Status: preliminary; not compared with conceptual translation
```

```
A;Accession: A47171
A;Status: preliminary
A;Molecule type: nucleic acid
A;Rosidues: 1-3562 <sH1>
A;Residues: 1-3662 <sH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: A47171
R;Shinomura, T.; Nishida, Y.; Ito, K.; Kimata, K.
J. Biol. Chem. 268, 14461-14469, 1993
A;Title: cDNA cloning of PG-M, a large chondroitin sulfate proteoglycan expressed during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L.; Ramachandran, J.; Mi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          omega-conotoxin MVIIA [validated] - cone shell (Conus magus)
C;Species: Conus magus (magus cone)
C;Date: 17-Apr-1993 #sequence revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: JH0700; C60133; Ā34115
R;Hillyard, D.R.; Monle, V.D.; Mintz, I.M.; Bean, B.P.; Nadasdi, L.; Ramacha Neuron 9, 69-77, 1992
A;Title: A new conus peptide ligand for mammalian presynaptic Ca2+ channels. A;Reference number: JH0699; MUID:92337922; PMID:1352886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chondroitin sulfate proteoglycan PG-M core protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
R;Reaume, A.G.; Conlon, R.A.; Zirngibl, R.; Yamaguchi, T.P.; Rossant, J. Dev. Biol. 154, 377-387, 1992
A;Title: Expression analysis of a Notch homologue in the mouse embryo. A;Reference number: A48825; MUID:93050801; PMID:1426644
                                                                                                                                                                                                          A:Status: preliminary; not compared with conceptual translation A:Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA A;Molecule type: mRNA A;Molecule type: mBNA A;Molecule type: mBNA B;Molecule type: mBNA B;Molecule tallource: embryo A;Molecule tallource: embryo A;Note: sequence extracted from NCBI backbone (NCBIP:119144) C;Molecule typerfamily: Note, protein; ankyrin repeat homology; EGF homology F;64-95/Domain: EGF homology <EGXI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.3%; Score 58; DB 2; Length 3562; 23.1%; Pred. No. 6.8e+02; tive 14; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;3258-3289/Domain: EGF homology <EGF1>
F;3268-3327/Domain: EGF homology <EGF>
F;334-3454/Domain: C-type lectin homology <LCH>
F;3461-3517/Domain: complement factor H repeat homology <FHD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Reference number: A47171; MUID:93300846; PMID:8314802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 48.3%; Score 58; DB 2; Best Local Similarity 20.8%; Pred. No. 2.6e+02; Matches 5; Conservative 14; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3283 GFNGEQCELDIDECQSNPCRNGATCI 3308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 XIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                384 HGSNCSEEINECLSQPCQNGGTCI 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 XNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;198-229/Domain: EGF homology <EGF2>
F;441-472/Domain: EGF homology <EGX2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Molecule type: mRNA
                                                                                                                                                                                    A; Accession: A48825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  පු
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A Experimental source: embryo
A Note: sequence extracted from NCBI backbone (NCBIP:126159)
A Note: sequence extracted from NCBI backbone (NCBIP:126159)
C; Comment: This protein has many EGF repeats and lin-12/Notch repeats.
C; Comment: This protein is one of the neurogenic proteins controlling the decision betwee (S; Usperfamily: Notch protein; ankyrin repeat homology; EGF homology
F; 77-56/Domain: EGF homology «EGF»
F; 73-104/Domain: EGF homology «EGF»
F; 151-185/Domain: EGF homology «EGF»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Molecule type: mRNA
A,Residues: 1-387 <LAR>
A,Cross-references: UNIPROT:Q01705; EMBL:X68278; NID:g287987; PIDN:CAA48339.1; PID:g2879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nighternate names: Motch house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: 21-Jan-1994 #sequence revision 05-Jan-1996 #text_change 16-Aug-2004
C;Accession: B49175; PH1569; $32109
R;Lardelli, M.; Lendahl, U.
Exp. Cell Res. 204, 364-372, 1993
A;Title: Motch A and Motch B--two mouse Notch homologues coexpressed in a wide variety A;Reference number: A49175; MUID:93178563; PMID:8440332
A;Accession: B49175
A;Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UMIPROT:P15787
C;Superfamily: metallothionein
C;Keywords: blocked amino end
F;1/Modified site: blocked amino end (Met) (probably acetylated) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                       metallothionein 2 - pigeon
G/Species: Columba livia (domestic pigeon)
C/Species: Columba livia (domestic pigeon)
C/Accession: S08191
R/Lin, L.Y.; Lin, W.C.; Huang, P.C.
Biochim. Biophys. Acta 1037, 248-255, 1990
A/FILLE: Pigeon metallothionein consists of two species.
A/Reference number: S08190; MUID:90167121; PMID:2407296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A48825
Notch homolog Motch protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2004
C;Accession: A48825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 58; DB 2; Length 63;
Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48.3%; Score 58; DB 2; Length 387
20.8%; Pred. No. 1.5e+02;
tive 14; Mismatches 5; Indels
                                                                                                       ::::::|::|::|::|
CVPTEPCEDAEDDCGNDFQCSTGRCIKMRLRCNGDNDC 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CXIXN----QXCXQXLDDCCSXXC-NXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 CKCKNCRCQSCRKSCCSCCPASCSNCAKGCV 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HGSNCSEEINECLSQPCQNGGTCI 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 XNQXCXQXLDDCCSXXCNXXNXCV 27
                                                       -SD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Motch A protein - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 32.34
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein A; Residues: 1-63 <LIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
es 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S:
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 60
                                                       8
                                                                                                                            유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
```

us-10-627-685a-1.rpr

Page 18

ö

Gaps

```
C; Accession: T42218
R; Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O. Genomics 51, 27-34, 1998
A; Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs takeerence number: Z14126; MUID:98360089; PMID:96933030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-1531 <NAK>
A;Cross-references: UNIPROT:088279; EMBL:AB011530; NID:g3449289; PIDN:BAA32460.1; PID:g3;
A;Experimental source: strain Sprague-Dawley; brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C. Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein re
                                                                                                                                                                                                                                                                                                                                                                                                                                    jagged protein precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 21-Jul-2003
C;Accession: A56136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        slit-1 protein homolog - rat
N'Alternate names: MEGF4 protein
C'Species: Rattus norvegicus (Norway rat)
C'Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C'Accession: T4218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S23244
hypochetical protein ZK643.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1531;
                                                                           Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47.5%; Score 57; DB 2; Length 122
26.1%; Pred. No. 4.1e+02;
... Mismatches 5; Indels
                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R.Lindsell, C.E.; Shawber, C.J.; Boulter, J.; Weinmaster, G. A; Fitle: 909-917, 1995
A; Fitle: Jagged: a mammalian ligand that activates Notchl.
A; Reference number: A56136; MUID:95211842; PMID:7697721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47.5%; Score 57; DB 2; I ilarity 30.4%; Pred. No. 4.8e+02; Conservative 10; Mismatches 6;
                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNA
                                                                                                          54;
                                                                                                                                         12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative 12; Mismatches
                                                                    47.5%; Score 57;
26.9%; Pred. No.
                                                                                                                                                                                                                                          18 CKCSNCACTSCKKSCCSCCPSGCSKC 43
                                                                                                                                                                                                       1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  +81 AGDHCERDIDECASNPCLNGGHC 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KGRNCEVSLDSCSSNPCGNGGTC 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 XNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;379-410/Domain: BGF homology <EGF1>
F;492-523/Domain: BGF homology <EGF>
F;634-665/Domain: BGF homology <EGF2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 XNQXCXQXLDDCCSXXCNXXNXC
                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Molecule type: mRNA
A, Residues: 1-1220 <LIN>
A, Cross-references: GB:L38483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: T42218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: MEGF4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99
                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
A; Residues: 1-25 cHIL>
A; Cross-references: UNIPROT: P05484
R; Olivera, B.M.; Gray, W.R.; Zeikus, R.; McIntosh, J.M.; Varga, J.; Rivier, J.; de Santc Science 230, 1338-1343, 1985
A; Title: Peptide neurotoxins from fish-hunting cone snails.
A; Reference number: A43620; MUID: 86070213; PMID: 4071055
A; Recession: C6013
A; Roleidues: 1-25 cOLI->
A; Rolivera, B.M.; Cruz, L.J.; de Santos, V.; LeCheminant, G.W.; Griffin, D.; Zeikus, R.; Biochemistry 26, 2086-2090, 1987
A; Title: Neuronal calcium channel antagonists. Discrimination between calcium channel subcohemistry 26, 2086-2090, 1987
A; Ritle: Neuronal calcium channel antagonists. Discrimination between calcium channel submitted to the Brookhaven Protein Data Bank, August 1996
A; Rielsen, K.J.; Thomas, L.; Lewis, R.J.; Alewood, P.F.; Craik, D.J.
A; Contents: annotation; conformation by (1)H-NWR, residues 1-25
B; Nielsen, K.J.; Thomas, L.; Lewis, R.J.; Alewood, P.F.; Craik, D.J.
A; Reference number: A57648; PDB:1MVI
A; Contents: annotation; conformation by (1)H-NWR, residues 1-25
B; Nielsen, K.J.; Thomas, L.; Lewis, R.J.; Alewood, P.F.; Craik, D.J.
A; Roleisence number: A58619; MUID: 97070382; PMID: 8913308
A; Rothor, T.; Kim, J.I.; Kobayashi, K.; Kodera, Y.; Maeda, T.; Sato, K.
Biol., T.; Kim, J.I.; Kobayashi, K.; Kodera, Y.; Maeda, T.; Sato, K.
B; Kohno, T.; Kim, J.I.; Kobayashi, K.; Rodera, Y.; Maeda, T.; Sato, K.
B; Rochents: annotation; conformation by Rollings Bioly, Mullings 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ArItie: Three-dimensional structure in solution of the calcium channel blocker omega-co
A/Reference number: A58627; MUID:95367555; PMID:7640281
A/Contents: annotation; conformation by (1)H-NMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Keywords: acetylcholine release inhibition; amidated carboxyl end; calcium channel inh F;1-16,8-20,15-25/Disulfide bonds: #status predicted F;25/Modified site: amidated carboxyl end (Cys) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Kille, P.; Stephens, P.E.; Kay, J.
Biochim. Biophys. Acta 1089, 407-410, 1991
A;Title: Elucidation of CDNA sequences for metallothioneins from rainbow trout, stone ld
A;Reference number: S16996; MUID:91316146; PMID:1859844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecule type: DNA
Residues: 1-60 <KI3>
Cross references: UNIPROT:P25127; EMBL:X70042; NID:g62782; PIDN:CAA49636.1; PID:g62783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 63
831723
metallothionein - northern pike
C; Species: Esox lucius (northern pike)
C; Daceis: Esox lucius (northern pike)
C; Dacession: S38334; S17175; $\overline{81503}$; S31723
K; Kille: P.; Kay, J.; Sweeney, G.E.
Biochim: Biophys. Acta 1216, 55-64, 1993
A; Title: Analysis of regulatory elements flanking metallothionein genes in Cd-tolerant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: EMBL:X59392; NID:g62780; PIDN:CAA42035.1; PID:g62781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47.5%; Score 57; DB 2; Length 25; 24.0%; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: metallothionein
C;Keywords: chelation; metal binding; metal-thiolate cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CXIXNQXCXQXLDDCCSXXCNXXNX 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |: : : | : : : | | | : : : | CKGKGAKCSRLMYDCCTGSCRSGKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Superfamily: omega-conotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-60' < KIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Introns: 9/1; 31/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S17175
```

Query Match Matches

g ò

ö

19

```
Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: S38335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S:
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-1044,1318-1810 <-JO2>
A; Residues: 1-1044,1318-1810 <-JO2>
A; Cross-references: GB:J04519
R; Spring, J.; Beck, K.; Chiquet-Ehrismann, R.
Cell 59, 325-334, 1989
A; Title: Two contrary functions of tenascin: dissection of the active sites by recombina
A; Reference number: A33379; MUID:90030407; PMID:2478295
A; Accession: A33379
A; Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wolecule type: DNA
;Residues: 1-1810 <JON>
;Cross-references: UNIPROT:Q90824; GB:J04519; NID:g211717; PIDN:AAA48745.1; PID:g211718
                                                                       ਲੁ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecule type: mRNA
FREBIGHOB: 1-204, G',206-221,'A',223-380,'D',382-386,'H',388-444,'HN',447-450,'V',452-5
FROSE-references: GB:M23121; NID:G212746; PIDN:AAA49086.1; PID:G212749
Accession: B33379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text change 09-Jul-2004
C;Accession: A32230; B32230; B33379; C33379; S01292; A30903
R;Jones, F.S.; Hoffman, S.; Cunningham, B.A.; Edelman, G.M.
Proc. Natl. Acad. Sci. U.S.A. 86, 1905-1909, 1989
A;Title: A detailed structural model of cytotactin: protein homologies, alternative RNA
A;Reference number: A32230; MUID:89184536; PMID:2467292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfâmily: tenascin; EGF homology; fibrinogen beta/gamma homology; fibronectin type 
C;Keywords: alternative splicing; calcium binding; cell adhesion; duplication; extracell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Residues: 1-204,'G',206-221,'A',223-380,'D',382-386,'H',388-444,'HN',447-450,'V',452-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 27-181,'R',183-204,'G',206-221,'A',223-380,'D',382-386,'H',388-444,'HN',447.
A,Cross-references: EMBL:X08030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: Ī-204,'G',206-221,'A',223-380,'D',382-386,'H',388-444,'HN',447-450,'V',452-!
A;Accession: C33379
k;Sulston, J.; Du, Z.; Thomas, K.; Wilson, R.; Hillier, L.; Staden, R.; Halloran, N.; awkins, T.; Ainscough, R.; Waterston, R.
submitted to the EMBL Data Library, October 1991
A;Reference number: $23239
A;Accession: $23244
A;Molecule type: DNA
A;Residues: 1-217 <SUL>A;Cross-reference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pearson, C.A.; Pearson, D.; Shibahara, S.; Hofsteenge, J.; Chiquet-Ehrismann, R. BO J. 7, 2977-2982, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:P30652; EMBL:Z11126; NID:g6967; PID:g6973
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
47.1%; Score 56.5; DB 2; Length 217;
Best Local Similarity 21.4%; Pred. No. 1.4e+02;
Matches 9; Conservative 10; Mismatches 4; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Note: part of this sequence was confirmed by protein sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | ::||:|:|
140 GTQECTDLANDCSYNQNRCSVKEYSSLMHRLCPKTCNACNIC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----CSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Title: Tenascin: cDNA cloning and induction by TGF-beta. A,Reference number: S01292; MUID:89030589; PMID:2460335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N,Alternate names: cytotactin; hexabrachion N;Contains: tenascin 190K; tenascin 200K
                                                                                                                                                                                                                                                                                                                                                                                              A;Introns: 26/3; 68/3; 99/3; 143/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 XNOXCXQXLDDC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: GB:M23121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tenascín precursor - chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Accession: A32230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
```

```
metallothionein - stone loach
C;Species: Noemacheilus barbatulus (stone loach)
C;Daces: Noemacheilus barbatulus (stone loach)
C;Dacession: S38335; S17176; S15505
R;Kille, P.; Kay, J.; Sweeney, G.E.
Biochim. Biophys. Acta 1216, 55-64, 1993
A;Title: Analysis of regulatory elements flanking metallothionein genes in Cd-tolerant final A;Reference number: S38334; MUID:94032489; PMID:8218416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Kille, P.; Stephens, P.E.; Kay, J.
iochim. Biophys. Acta 1089, 407-410, 1991
;Title: Blucidation of cDNA sequences for metallothioneins from rainbow trout, stone los Reference number: S16996; MUID:91316146; PMID:1859844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      к;килп, R.; Kuhn, C.; Boersch, D.; Glaetzer, K.H.; Schaefer, U.; Schaefer, M.
Mech. Dev. 35, 143-151, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             testis-specific protein Mst84Dd - fruit fly (Drosophila melanogaster)
C,Species: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 47.1%; Score 56.5; DB 1; Length 1810; 1 Similarity 29.7%; Pred. No. 5.9e+02; 11; Conservative 9; Mismatches 4; Indels 13
                                                                                                                                                                                                                                                                                                  F;1046-1129/Domain: fibronectin type III repeat homology cFN3F> F;1131-1219/Domain: fibronectin type III repeat homology cFN3F> F;1228-1310/Domain: fibronectin type III repeat homology cFN3G> F;1318-1399/Domain: fibronectin type III repeat homology cFN3I> F;1401-1487/Domain: fibronectin type III repeat homology cFN3I> F;1405-1575/Domain: fibronectin type III repeat homology cFN3I> F;1495-1575/Domain: fibronectin type III repeat homology cFN3K> F;1590-1798/Domain: fibrinogen beta/gamma homology cFN3K>
                            723-249/Domain: EGF homology <EGF1>
7316-342/Domain: EGF homology <EGF1>
759-673/Domain: EGF homology <EGF1>
769-673/Domain: EGF homology <EGF1>
769-673/Domain: Eibronectin type III repeat homology <EGF18>
777-859-679/Domain: Eibronectin type III repeat homology <EGF18>
778-857/Domain: Eibronectin type III repeat homology <EGF18>
7865-949/Domain: Eibronectin type III repeat homology <EGF18>
957-1037/Domain: Eibronectin type III repeat homology <EGF18>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A)Introns: 9/1; 31/1
C;Superfamily: metallothionein
C;Keywords: chelation; metal binding; metal-thiolate cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;1734-1747/Domain: calcium binding #status predicted <CAB>
-1810/Product: tenascin 230K #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    353 GNGRCENGLCVCHEGFVGDDCSQKRCPKTCNNRGRCV 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 XNQXCXQXL-----DDC----CSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.7%; Score 56; DB 26.9%; Pred. No. 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-60 <KIL>
A;Cross-references: UNIPROT:P25128; EMBL:X70043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-4,'E',6-60 <KI2>
A;Cross-references: EMBL:X59393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 26.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 11; Conserv
```

ò g

ö

Gaps

```
A;Cross-references: UNIPROT:Q18238; EMBL:US8760; NID:g1330384; PID:g1330389; PIDN:AAB00731
A;Experimental squrce: strain Bristol N2; clone C27A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:022179; EMBL:Z78200; PIDN:CAB01583.1; GSPDB:GN00023; CESP:T04
A;Experimental source: clone T04H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein C27A2.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep.1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein T04H1.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24476
R;Harris, B.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z19896
                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 5
A; Introns: 33/1; 75/1; 120/1; 159/1
F; 34/4/Domain: LDL receptor ligand-binding repeat homology <LDL1>F; 77-115/Domain: LDL receptor ligand-binding repeat homology <LDL2>F; 77-115/Domain: LDL receptor ligand-binding repeat homology <LDL3>F; 121-158/Domain: LDL receptor ligand-binding repeat homology <LDL3>F; 162-197/Domain: LDL receptor ligand-binding repeat homology <LDL4>F; 162-197/Domain: LDL4<F; 162-197/Domain: LDL4-F; 162-197/Domain: LDL4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46.7%; Score 56; DB 2; Length 198 illarity 24.2%; Pred. No. 1.5e+02; Conservative 13; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, May 1996
A;Description: The sequence of C. elegans cosmid C27A2.
A;Reference number: 218382
                                           ed. No. 1.4e+02;
Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 23.1%; Pred. No. 1.4e+02;
Matches 6; Conservative 12; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Status: preliminary; translated from GB/EMBL/DDBJ;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CXIXNQXCXQXLDDC-----CSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 KVEEECCGGAKDDCCGGHEHEHEVC 150
                                                                                                                                                                                 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                       2 XIXNQXCXQXLDDCCSXXCNXXNXC
                                           Pred.
24.0%; Pre-
                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 8; Conserva
                                 Best Local Similarity
Matches 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-188 <NHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-198 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position: 2
A; Introns: 19/3; 91/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: CESP: C27A2.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: CESP:T04H1.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession: T15651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
S53718
                                                                                                                                                                       à
                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
A;Title: A cluster of four genes selectively expressed in the male germ line of Drosophil A;Reference number: A56565; MUD: 92102953; PMID:1684716
A;Recession: 825778
A;Molecule type: DNA
A;Residues: 1-68 «KUH>
A;Cross-references: UNIPROT:001645; EMBL:X67703; NID:G11072; PIDN:CAA47940.1; PID:G11076
C;Genetics: Mat8406
C;Genetics: Mst8406
A;Note: sequence extracted from NCBI backbone (NCBIN:74217, NCBIP:74223)
C;Genetics: A;Note: Sequences: FlyBase:FBgn0004175
A;Cross-references: FlyBase:FBgn0004175
C;Superfamily: fruit fly testis-specific protein
C;Keywords: spermatogenesis; tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Reference number: 219867
A, Accession: T42472
A, Accession: T42472
A, Molecule type: DNA
A, Molecule type: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Riglass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H. submitted to GenBank, February 2000
A; Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min A; Reference number: A82870
A; Reference number: A82870
A; Reference number: A82870
A; Residue: preliminary
A; Relicule type: DNA
A; Residues: 1-188 <GLA>
A; Residues: 1-188 <GLA>
A; Residues: GB: AE002110; GB: AF222894; NID: g6899051; PIDN: AAF30507.1; GSPDB: GN001
A; Experimental gource: gerovar 3; blovar 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oʻ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        724272
hypothetical protein TolB7.8 - Caenorhabditis elegans
hypothetical protein TolB7.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 115-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24272
R;Sims, M.
R;Sims, M.
Submitted to the EMBL Data Library, October 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Length 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.7%; Score 56; DB 2; Length 164
23.1%; Pred. No. 1.38+02;
ive 12; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 23.1%; Pred. No. 73;
Matches 6; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 CGPCGPCCGPCCGPCCGPCGPC 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.7%; Score 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 23.1%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 2
A; Introns: 20/3; 90/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: CESP:T01B7.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Genetic code: SGC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C, Genetics:
A, Gene: UU101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
```

ద õ

; 0

Gaps

1,

Gaps

21

```
9/
                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-78 'G', 80-249, 'P', 251-319, 'CWAPWESSFSTSAKPGCPTCATTCFARRRTSCCSITAARSWRSISS
A; Residues: 1-78 'G', 80-249, 'P', 251-319, 'CWAPWESSFSTSAKPGCPTCATTCFARRRTSCCSITAARSWRSISS
A; Cross-references: 68:L12721; NID:930992; PIDN:AAA37175.1; PID:9309093
A; Note: sequence extracted from NCBI backbone (NCBIN:132685, NCBIP:132713)
A; Note: this sequence appears to have been corrected in reference A45484
C; Reywords: alternative splicing; tandem repeat; transmembrane protein
F; 1-385/Product: preadipocyte factor 1; precursor splice form A #status predicted
F; 1-230, 304-385/Product: preadipocyte factor 1 precursor splice form C #status predicted
F; 1-230, 304-385/Product: preadipocyte factor 1 precursor splice form C #status predicted
F; 1-230, 304-385/Product: preadipocyte factor 1 precursor splice form C2 #status predicted
F; 1-210, 304-385/Product: preadipocyte factor 1 precursor splice form D #status predicted
homeotic protein dlk - mouse
Cispecies: Mus musculus (house mouse)
Cipate: 15-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
Cipate: 15-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
Cipate: 15-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
RiLee, Y.L.; Helman, L.; Hoffman, T.; Laborda, J.
RiLee, Y.L.; Helman, L.; Hoffman, T.; Laborda, J.
A;Title: dlk, pGZ and Pref-1 mRNAs encode similar proteins belonging to the EGF-like sup
A;Reference number: S53716; MuID:95226449; PMID:7711066
A;Accession: S53718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preadipocyte factor 1 precursor, long form - mouse
N;Alternate names: delta-like dik homeotic protein; pref-1
C;Species: Mus musculus (house mouse)
C;Accession: A54785; A45484; A40746; S21585
R;Smas, C.M.; Green, D.; Sul, H.S.
Biochemistry 33, 9257-9265, 1994
A;Title: Structural characterization and alternate splicing of the gene encoding the pre A;Reference number: A54785; MUD:94325292; PMID:7519443
                                                                                                                                                                                                                                                                                                                                                                                 A,Molecule type: mRNA
A,Residues: 1-385 <LEE>
A,Residues: 1-385 <LEE>
A,Cross-references: UNIPROT: Q09163; EMBL: U15980; NID: 9562107; PIDN: AAB60495.1; PID: 95621
C,Superfamily: preadipocyte factor 1; EGF homology
C,Reywords: transmembrane protein
F;54-85/Domain: EGF homology <EGF1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-78, 'G', 80-343, 'TF', 346-385 < LAB>
A; Residues: 1-78, 'G', 80-343, 'TF', 346-385 < LAB>
A; Residues: 1-78, 'G', 80-343, 'TF', 346-385 < LAB>
A; Crose-references: EMBL: 212171, NID: 950716; PIDN: CAA78162.1; PID: 950717
A; Note: sequence extracted from NCBI backbone (NCBIP: 125744)
A; Note: species designations for this sequence report and for B45484 originally were tra
R; Smas, C.M.; Sul, H.S.
A; 725-734, 1993
A; 715-734, 1993
A; 716-1; a protein containing EGF-like repeats, inhibits adipocyte differentiati
A; Reference number: A40746; MUID: 93272313; PMID: 8500166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Status: 1-385 <SMA> A;Residues: 1-385 <SMA> A;Reference numbar: A45484; MUID:93179372; PMID:8095643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length.385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;131-167/Domain: EGF homology <EGF3>
F;214-246/Domain: EGF homology <EGX1>
F;303-332/Domain: transmembrane #status predicted <TM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.7%; Score 56; DB 2; 1
19.2%; Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GFVDKTCSRPVSNCASGPCQNGGTCL 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C, Keywords: transmembrane protein
F;54-85/Domain: EGF homology <EGFl>
F;92-124/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 19.2*
E.thog 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
```

```
F;1-210,306-385/Product: preadipocyte factor 1 precursor splice form D2 #status predictec F;92-124/Domain: EGF homology <EGF> F;214-246/Domain: EGF homology <EGF1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 11491 <WIL>
A;Cross-references: UNIPROT:P90850; EMBL:Z81070; PIDN:CAB03007.1; GSPDB:GN00019; CESP:F26
A;Experimental source: clone F26E4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prematurely terminated mRNA decay factor NAM7 - yeast (Saccharomyces cerevisiae)
NiAlternate names: protein YM9583.05c; protein YMR080c; UPF1 protein
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Accession: S23408; A44388; S54455
N;Atamura, N; Groudinsky, O; Dujardin, G; Slonimski, P.P.
A;Title: NAM7 nuclear gene encodes a novel member of a family of helicases with a Zn-ligs A;Reference number: S23408
A;Reference number: S23408
A;Reference number: S23408
A;Reference number: S23408
A;Reference number: AMITSAT: PROMOT: PROMOTE PROMOTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 1
A;Introns: 23/3; 67/1; 108/1; 134/1; 149/2; 179/2; 232/2; 261/2; 306/2; 334/2; 419/2; 466
                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Molecule type: DNA
A,Residues: 1-971 <LEE>
A;Cross-references: GB:M76659; NID:g173141; PIDN:AAA35197.1; PID:g173142
R;Gentles, S.; Bowman, S.
submitted to the EMBL Data Library, May 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residudes: 1-971 cGBN
A;Cross-references: EMBL:Z49259; NID:g807956; PID:g807962; MIPS:YMR080c
A;Experimental source: strain AB972
                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 46.7%; Score 56; DB 2; Length 491; Similarity 23.1%; Pred. No. 2.8e+02; 6; Conservative 14; Mismatches 6; Indels
                                                                                                                                                                                             Length 385
                                                                                                                                                                                                                                                                                                 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein F26E4.3 - Caenorhabditis elegans
                                                                                                                                                                                             h Similarity 19.2%; Pred. No. 2.3e+02; 5; Conservative 16; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rilightning, J. submitted to the EMBL Data Library, October 1996 A;Reference number: 219419 A;Accession: T21421
                                                                                                                                                                                                                                                                                                                                                                                                                                            201 GFVDKTCSRPVSNCASGPCONGGTCL 226
                                                                                                                                                                                                                                                                                                                                                                                           2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |::: :|:::| |:::|
70 CSVRTHTCCENRDDDCTVPILGDHLC 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: S54451
                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A44388
```

C, Genetics:

```
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: Z19351
A;Accession: T20968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity
Matches 6; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: CESP: F15B9.7
                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         homeotic protein lin-12 precursor - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Aug-2004
C;Accession: 506434; A24769
R;Yochem, J.; Weston, K.; Greenwald, I.
R;Yochem, J.; Weston, K.; Greenwald, I.
A;Title: The Caenorhabditis elegans lin-12 gene encodes a transmembrane protein with ove
A;Reference number: 506434; MUID:88334747; PMID:3419531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;MOJECULE type: DNA
A;Residues: 1-1429 <YOC>
A;Cross-references: UNIPROT:P14585; EMBL:M12069; NID:g156357; PIDN:AAA70191.1; PID:g1563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NiAlternate names: slit protein homolog
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T11953
R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A;Reference number: Z14126; MUID:98360089; PMID:9693030
                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
AjGene: SGD.NAM7; UPF1
AjGross-references: SGD.S0004685; MIPS.YMR080c
AjMap position: 138
Cj.Keywords: GTP binding, mitochondrion; nucleotide binding; nucleus; P-loop
F;430-437/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Molecule type: DNA
A,Residues: 173-712 cGRE>
C,Genetics:
A,Introns: 50/2; 90/1; 109/1; 172/3; 545/1; 589/2; 632/2; 1273/3; 1389/3
C;Superfamily: ankyrin repeat homology; EGF homology
C;Keywords: glycoprotein; transmembrane protein
F;547-84 Domain: EGF homology cEGF1>
F;507-540,Domain: EGF homology cEGF2>
F;507-578/Domain: EGF homology cEGF2>
F;909-931/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1429;
                                                                                                                                                                                                                   Length 971;
                                                                                                                                                                                                             Query Match
46.7%; Score 56; DB 2; Length 971
Best Local Similarity 28.0%; Pred. No. 4.4e+02;
Matches 7; Conservative 12; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;900-931/Domain: transmembrane #status predicted <TMM>
F;1093-1125/Domain: ankyrin repeat homology <AN1>
F;1206-1238/Domain: ankyrin repeat homology <AN2>
F;1240-1272/Domain: ankyrin repeat homology <AN3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Greenwald, I.
Cell 43, 588-590, 1985
A;Reference number: A24769; MUID:86079540; PMID:3000611
A;Accession: A24769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

46.7%; Score 56; DB 2; Le
Best Local Similarity 20.8%; Pred. No. 5.6e+02;
Matches 5; Conservative 14; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1523 <NAK>
                                                                                                                                                                                                                                                                                                                                                            1 CXIXNQXCXQXLDDCCSXXCNXXNX 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    280 SGSYCQEGKDNCVNNKCEAGSKCI 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 XNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 79
T13953
MEGFS protein - rat
                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

```
A;Cross-references: UNIPROT:088280; EMBL:AB011531; NID:g3449291; PIDN:BAA32461.1; PID:g34 C;Genetics: A;Gene: MEGF5 C;Cyperfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein received.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2610 <WIL>
A;Cross-references: UNIPROT:Q19482; EMBL:Z78013; PIDN:CAB01427.1; GSPDB:GN00023; CESP:F1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phospholipase A2 homolog, inactive [validated] - eastern cottonmouth C;Species: Agkistrodon piscivorus piscivorus (eastern cottonmouth)
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 16-Aug-2004
C;Accession: A00767, A60719
R;Maraganore, J.M.; Heinrikson, R.L.
J. Biol. Chem. 261, 4797-4804, 1986
A;Title: The lysine-49 phospholipase A-2 from the venom of Agkistrodon piscivorus piscivc A;Reference number: A00767; MUID:86168190; PMID:3082870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Molecule type: protein
A.Residues: 1-121 < MAR>
A.Cross-references: UNIPROT: p04361
A.Cross-references: UNIPROT: p04361
J. Cell. Biochem. 39, 379-390, 1989
A.Title: The role of Asp-49 and other conserved amino acids in phospholipases A2 and thei
A.Recession: A60719, MUD: 89255682, PMID: 2722967
A.Molecule type: protein
A.Molecule type: protein
A.Residues: 1-8 < VAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Map position: 5
A,Introns: 169/2; 217/3; 239/3; 284/3; 515/2; 550/3; 738/3; 810/1; 838/3; 890/2; 977/1; 1
                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RiBaynes, C.
Submitted to the EMBL Data Library, August 1996
A;Refearen umber: 220187
A;Refearen umber: 220187
A;Accession: T26278
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-2610 «M12>
A;Cross-references: EMBL:278018; PIDN:CAB01449.1; GSPDB:GN00023; CESP:F15B9.7
A;Experimental source: clone W07G4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein F15B9.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20968; T26278
                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                           ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                              'Match 46.7%; Score 56; DB 2; Length 1523;
Local Similarity 29.2%; Pred. No. 5.9e+02;
les 7; Conservative 11; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46.7%; Score 56; DB 2; Length 2610; 28.6%; Pred. No. 8.5e+02; ive 12; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, August 1996
                                                                                                                                                                                                                                                                                                                                                             1067 SGKLCETDNDDCVAHKCRHGAQCV 1090
                                                                                                                                                                                                                                                                                                                     4 XNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :|::::||
1280 DCDTRIDECYRGRCSNNSTCV 1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 XCXQXLDDCCSXXCNXXNXCV 27
```

23

ä

us-10-627-685a-1.rpr

```
alpha-amylase inhibitor precursor (clone pUP-44) - barley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-118 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene: NCSP:B14D6.670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: I51601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Accession: T49515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetics:
                                                                                                                                                                                                                                                                                                                               84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 86
                                                                                                                                                                                                                                                                                                                                                             S15468
                                                                                                                                                                      ò
                                                                                                                                                                                                                          유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       엄
A;Note: the authors confirmed the identity of the purified protein by composition and per R;Holland, D.R. "Clancy, L.L.; Muchmore, S.W.; Rydel, T.J.; Einspahr, H.M.; Finzel, B.C. A;Reference number: A51920; PDB:1.PpA
A;Reference number: A51920; PDB:1.PpA
A;Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 1-121
B;Holland, D.R.; Clancy, L.L.; Muchmore, S.W.; Ryde, T.J.; Einspahr, H.M.; Finzel, B.C.; J. Biol. Chem. 265, 17649-17656, 1990
A;Title: The crystal structure of a lysine 49 phospholipase A-2 from the venom of the constant annotation; X-ray crystallography, 2.0 angstroms
C;Comment: This homolog of phospholipase A2 lacks enzymatic activity because a Lys-48 rec;Superfamily: Phospholipase A2 lacks enzymatic activity because a Lys-48 rec;Comment: This homolog of phospholipase A2 lacks enzymatic activity because a Lys-48 rec;Superfamily: Phospholipase A2
C;Keywords: venom
F;26-115,28-44,413-95,49-121,50-88,57-81,75-86/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T40996
R;Lyne, M; Rajandream, M.A.; Barrell, B.G.; Volckaert, G.
submitted to the EMBL Data Library, March 1999
A;Reference number: 221962
A;Reference number: 221962
A;Accession: T40996
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residuas: 1-571 < LYN>
A;Cross-references: UNIPROT: Q9Y7P1; EMBL: AL049559; PIDN: CAB40181.1; GSPDB: GN00068; SPDB: A;Experimental source: strain 972h-; cosmid c1450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:P49121; EMBL:U21335; NID:g809484; PIDN:AAC59887.1; PID:g8094
A;Accession: S74296
A;Molecule type: protein
A;Residues: 17-36 cDER-
C;Superfamily: phospholipase A2
F;1-16/Domain: signal sequence #status predicted <SIG>F;1-137/Product: myotoxin #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Agkistrodon contortrix contortrix (southern copperhead)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
R;de Araujo, H.S.S.; White, S.P.; Ownby, C.L.
Arch. Biochem. Biophys. 326, 21-30, 1996
A;Title: cDNA cloring and sequence analysis of a lysine-49 phospholipase A(2) myotoxin A;Reference number: S68429; WUID:96154243; PMID:8579368
A;Accession: S68429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conserved hypothetical protein SPCC1450.14c - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | : ::: | ::: | | | CCFVHKCCYKKLTDCHKTDRYSYSWKNKAIICEEKNPCL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CXIXNQXCXQXLDDC-----CSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 CCFVHKCCYKKLTDCNHKTDRYSYSWKNKAIICEEKNPCL 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----CSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 55.5; DB 2;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 55.5; DB 1;
; Pred. No. 1.2e+02;
15; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  myotoxin precursor - southern copperhead
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 20.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 20.0 Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CXIXNQXCXQXLDDC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: SPDB:SPCC1450.14c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-137 <DEA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: 3
A; Introns: 4/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
```

```
N'Alternate names: C3b/C4b inactivator factor I
C;Species: Xenopus laevis (African clawed frog)
C;Accession: I51601, 815468
R;Kunnath-Wuglia, L.M.; Chang, G.H.; Sim, Ř.B.; Day, A.J.; Ezekowitz, R.A.
Mol. Immunol. 30, 1249-1255, 1993
A;Fitle: Characterization of Xenopus laevis complement factor I structure--conservation of A;Reference number: I51601; MUID:94019415; PMID:7692240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q03711; EMBL:X59958; NID:g64595; PIDN:CAA42582.1; PID:g64596 C;Superfamily: human complement factor I; LDL receptor ligand-binding repeat homology; t:C;Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C,Accession: T49515
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25022
                                                                                                                                                                                                                                                                                                                                                             complement C3b/C4b inactivator (EC 3.4.21.-) precursor - African clawed frog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;220-254/Domain: LDL receptor ligand-binding repeat homology <LDL1>F;257-290/Domain: LDL receptor ligand-binding repeat homology <LDL2>F;370-599/Domain: trypsin homology <TRY>
                                                                ñ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 6
C;Superfamily: Neurospora crassa hypothetical protein B14D6.670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match

45.8%; Score 55; DB 2; Length 118;
Best Local Similarity 27.3%; Pred. No. 1.38+02;
Matches 6; Conservative 10; Mismatches 6; Indels
                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - Neurospora crassa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.2%; Score 55.5; DB 2; 30.8%; Pred. No. 3.6e+02;
Score 55.5; DB 2;
Pred. No. 3.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:AL356173; GSPDB:GN00116; NC
A;Experimental source: BAC clone B14D6; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary, translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-613 <KUN>
Query Match
46.2%; Score 55.5; D
Best Local Similarity 36.0%; Pred. No. 3.4e
Matches 9; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 30.8%; Pred. No. 3.6e
Matches 8; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 CDSKN-DCGDLSDELCCKSCNAGFHC 263
                                                                                                                                                                         86 NLFNKECRYNLDDNVACGSSACNVL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56
                                                                                                                                2 XIXNOXCXQXLDD---CCSXXCNXX 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein B14D6.670 [imported]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CXIXNQXCXQXLDDCCSXXCNXXNXC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSSACASVLSDCCRHRCRWNGL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 XNQXCXQXLDDCCSXXCNXXNX 25
```

ï

```
A.Residues: 1-344,346-383 <LAB1>
A.Cross-references: EMBL:U15979; NID:9562105; PIDN:AAA75364.1; PID:9562106
A.Cross-references: EMBL:U15979; NID:9562105; V. V. Sausville. E.A., Hoffman, T.; Notario, V. V. B.A. Chem. 268, 3817-3820; 1993
A.Title: dlk, a putative mammalian homeotic gene differentially expressed in small cell J. A.Reference number: A45484; MUID:93179372; PMID:8095043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Molecule type: mRNA
A,Residues: 1-45,'HV',48-383 <LAB2>
A,Cross-references: EMBL:212172; NID:938478; PIDN:CAA78163.1; PID:938479
A,Note: sequence extracted from NOEI backbone (NCBIP:125735)
B,Jonsen, C.H.; Krogh, T.N.; Hojrup, P.; Clausen, P.P.; Skjodt, K.; Larsson, L.I.; Enghill Eur. J. Biochem. 225, 83-92, 1994
A;Title: Protein structure of fetal antigen 1 (FA1). A novel circulating human epidermal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ViGene: GDB:DLK1; dlk; FAl; PG2; PREF-1
A;Gene: GDB:DLK1; dlk; FAl; PG32
C;Superfamily: preadipocyte factor 1; EGF homology
C;Reywords: alternative splicing; glycoprotein; transmembrane protein
F;1-23/Domain: EGF homology #status artypical «EGPs-
F;21-54/Domain: EGF homology #status experimental «MATA»
F;24-228,7Product: delta-like homeotic protein dlk, short splice form #status prec
F;24-228,7Product: delta-like homeotic protein dlk, short splice form #status prec
F;24-228,7Domain: EGF homology «EGF2»
F;37-85/Domain: EGF homology «EGF2»
F;31-167/Domain: EGF homology «EGF8»
F;32-124/Domain: EGF homology «EGF8»
F;30-124/Domain: EGF homology «EGF8»
F;30-244/Domain: EGF homology «EGF8»
F;30-244/Domain: EGF homology «EGF8»
F;30-244/Domain: EGF homology «EGF8»
F;31-244/Domain: EGF homology «EGF8»
F;31-24/Domain: EGF homology «EGF8»
F;31-25-34/Domain: EGF homology «EGF8»
F;31-25/Dainding site: carbohydrate (Asn) (covalent) #status experimental
F;143/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
F;165,172/Binding site: carbohydrate (Asn) (c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Modecule type: protein
A; Residues: 24-107, 'D', 109-282 <JEN>
R; Hojrup, P.; Jensen, C.H.; Skjodt, K.; Teisner, B.
Protein Sci. 2(Suppl.1), 259S, 1993
A; Title: Primary structure of human fetal antigen 1 (FA1), a putative homeotic glycoprote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                A; Cross-references: EMBL:U15981; NID:g562109; PIDN:AAA75365.1; PID:g562110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.8%; Score 55; DB 2; Length 383;
19.2%; Pred. No. 2.9e+02;
ive 16; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reference number: $48713; MUID:95010145; PMID:7925474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      intrinsic factor-B12 receptor Cubilin precursor - human C; Species: Homo sapiens (man)
                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, October 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199 GFIDKTCSRPVTNCASSPCQNGGTCL 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 XIXNOXCXQXLDDCCSXXCNXXXXX 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A/Status: preliminary
A/Molecule type: protein
A/Residues: 24-107,'VASM',112-283 <HOJ>
C/Genetics:
                                                                                                         1-228,302-383 <LEE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 19.2*;
"-hes 5; Conservative 5; Conservative
                                                                                                                                                                                                                                                                                                                                  A; Reference number: S71068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reference number: A44549
                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S71068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Accession: B45484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: S48713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reratin KAP5.5 - sheep (fragment)
C;Species: Ovis anmon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Date: 16-Aug-1996 #sequence_revision of genes
R;Johnins, B.J.
J. Invest. Dermatol. 103, 310-317, 1994
A;Title: Differential expression of genes encoding a cysteine-rich keratin family in the A;Reference number: 146412; MUID:94358466; PMID:7521375
A;Retaus: preliminary; translated from GB/EMBL/DDBJ
A;Retaus: preliminary; translated from GB/EMBL/DDBJ
A;Retaus: preliminary;
A;Retaus: preliminary;
A;Retaus: Dreliminary;
A;Retaus: Dreliminary;
A;Retaus: Dreliminary;
A;Retaus: Dreliminary;
A;Retaus: Dreliminary;
A;Retaus: Dreliminary;
A;Retaus: MRNA
A;Retaus: Dreliminary;
C;Species: Hordeum vulgare (barley)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: 800332
R;Lazaro, A.; Sanchez-Monge, R.; Salcedo, G.; Paz-Ares, J.; Carbonero, P.; Garcia-Olmedc
Bur. J. Blochem 172, 129-134, 1988
A;Title: A dimeric inhibitor or insect alpha-amylase from barley. Cloning of the cDNA army. Recession: 800332
A;Reterence number: $00332; MUID:88151978; PMID:3257914
A;Recession: S00332
A;Recess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Molecule type: mRNA
A,Residues: 1-383 <LEE1>
A,Residues: 1-383 <LEE1>
A,Residues: U.383 <LEE1>
A,Cross-references: UNIPROT:P80370; EMBL:U15979; NID:g562105; PIDN:AAA75364.1; PID:g5621
A,Note: the authors translated the codon CAG for residue 46 as His and CCT for residue 4
A,Note: the sequence in GenBank entry HSU15979 has a 3 base deletion mutation in the req
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Home sapiens (man)
C;Species: Home sapiens (man)
C;Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text change 09-Jul-2004
C;Accession: S33716; S33717; S1068; B45484; S48713; A44549; S31973; S31974
R;Lee, Y.L.; Helman, L.; Hoffman, T.; Laborda, J.
Biochim. Biophys. Acta 1261, 223-232, 1995
A;Title: dlk, pG2 and Pref-1 mRNAs encode similar proteins belonging to the EGF-like A;Accession: S53716; MUID:95226449; FMID:7711066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 88
SS311-
SS31-
Adelta-like homeotic protein dlk, long splice form precursor - human
N'Alternate names: fetal antigen 1 (FA1)
N'Contains: delta-like homeotic protein dlk, short splice form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; De L.
1.8e+02;
The 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.8%; Score 55; DB 2; I
29.2%; Pred. No. 1.6e+02;
tive 12; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
45.8%; Score 55;
Best Local Similarity 28.6%; Pred. No. ...
Matches 6; Conservative 10; Mismatc)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CVGNRVPEDVLRDCCQEVANISNE 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 XIXNOXCXQXLDDCCSXXCNXXNX 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 SCGGSQSSCCQHTCSQSSCCV 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 XCXQXLDDCCSXXCNXXVXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 29.27
Best Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઢ
```

ï

Gaps

'n

C; Keywords: neurotoxin; venom

```
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolecule type: DNA
A;Nosidues: 1-398 cLNN-
A;Residues: 1-398 cLNN-
A;Cross-references: UNIRROT:074728; EMBL:AL031852; PIDN:CAA21242.1; GSPDB:GN00067; SPDB:£
A;Experimental source: strain 972h-; cosmid c1709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C,Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004
C;Accession: E71414
R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirks
P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; Giels
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
Nature 391, 485-488, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech, erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ansc C.; Chalwatzis, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.; Chalwatzis, N.
A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thali
A;Reference number: A71400; MUID:98121113; PMID:9461215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Cross-references: UNIPROT:023362; GB:297337; NID:g2244829; PID:e327432; PID:g2244865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein SPBC1709.03 - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.Species: Schizosaccharomyces pombe
C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Introns: 209/3
C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPBC1709.03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 24.3%; Pred. No. 5e+02;
Matches 9; Conservative 14; Mismatches 3; Indels 1.
                                                                                                         DB 1; Length 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     289 CYISEEACSKATNDCSGHGRCSKYGQLDSCYVCQCSNSVV 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R.Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, M. submitted to the EMBL Data Library, October 1998
A;Reference number: Z21868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 CILCNAEVRKFSKHCRSCDKCV-DCFDHHCRWLNNCV 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CXIXNQXCXQXLDDC----CS-----XXCNXXNXCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CXIXN-----QXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
45.4%; Score 54.5; DB 2;
Best Local Similarity 25.0%; Pred. No. 3.3e+02;
Matches 10; Conservative 13; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: columbia
                                                                                                                                                                                                                                                                                              1 CXIXNQXCXQXLDDCCSXXC----NXXNXC 26
                                                                                                                                                                                                                                                                                                                                                          Query Match 45.4%; Score 54.5; I Best Local Similarity 25.8%; Pred. No. 73; Matches 8; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Map position: 4COP9-4G3845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: SPDB:SPBC1709.03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-736 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: E71414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: T39631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Accession: T39631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 93
                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Molecule type: mRNÅ
*Residues: 1-3633 <KOZ>
A;Cross-references: UNIPROT:O60494; EMBL:AF034611; NID:g3929528; PIDN:AAC82612.1; PID:g3
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    versutoxin - funnel-web spider (Atrax versutus)
C;Species: Atrax versutus
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
B;Accession: 5. 250, 401-405, 1988
A;Attle: Amino acid sequence of versutoxin, a lethal neurotoxin from the venom of the funt A;Reference number: S00343; MUID:88183358; PMID:335530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A)Cross-references: UNIPROT: P01478
C;Comment: In this species, the venom of the male is lethal rather than that of the fema C;Comment: Four disulfide bonds are present.
C;Superfamily: robustoxin
C;Keywords: neurotoxin; venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  robustoxin - funnel-web spider (Atrax robustus)
C.Species: Atrax robustus
C.Species: Atrax robustus
C.Jate: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 09-Jul-2004
C.JAccession: A01738
R.Sheumack, D.D.; Claassens, R.; Whiteley, N.M.; Howden, M.E.H.
FEBS Lett. 181, 154-156, 1985
A.Jitle: Complete amino acid sequence of a new type of lethal neurotoxin from the venom A.Reference number: A01738; MUID:85127480; PMID:3972101
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T09456
R;Kozyraki, R.; Kristiansen, M.; Silahtaroglu, A.; Hansen, C.; Jacobsen, C.; Tommerup, N
Blood 91, 3593-3600, 1998
A;Title: The human intrinsic factor-vitamin B12 receptor, cubilin: Molecular characteriz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: intrinsic factor-B12 receptor cubilin, EGF homology
C;Superfamily: intrinsic factor-B12 uptake
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-3623/Product: intrinsic factor-B12 receptor #status predicted <MAT>
F;36-467/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.8%; Score 55; DB 2; Length 3623; 28.6%; Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.4%; Score 54.5; DB 1; Length 42; 25.8%; Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 1-42 <BRO>
A;Cross-references: UNIPROT:P13494
C;Comment: All cysteine residues are linked by disulfide bonds.
C;Superfamily: robustoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Indels
                                                                                                                                                                                                                                                                               A,Reference number: 216677; MUID:98241400; PMID:9572993
A,Accession: T09456
A,Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CXIXNQXCXQXLDDCCSXXC----NXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | : : | | | : : | | : : | 1 | : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : | 1 | : : : | 1 | : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : : | 1 | : : | 1 | : : | 1 | : : | 1 | : : | 1 | : : | 1 | : : | 1 | : : | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : |::::::| |::| :: :||
NCTENINECLSNPCLNGGTCV 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 XCXOXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 28.68
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 25.8%
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein A; Residues: 1-42 <SHE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position: 10p12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: A01738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
```

~

Gaps

13;

Indels

Length 398;

7

Gaps

11;

us-10-627-685a-1.rpr

26

Page

```
1 CXIXNQ----XCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Gene: VSPA6
C,Keywords: surface antigen; tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: A38856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein ZKZ87.4 - Caenorhabditis elegans
C.Species: Caenorhabditis
C.Sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 96
442125
trophozoite cysteine-rich surface antigen 170 - Giardia lamblia
N.Alternate names: CRP170; cysteine-rich surface antigen CRP170
C;Species: Giardia lamblia
C;Species: Giardia lamblia
C;Species: Giardia lamblia
C;Accession: A42125; B42125; S00330; S48056
R;Adam, R.D; Yang, Y.M.; Nash, T.E.
Mol. Cell. Biol. 12, 1194-1201, 1992
Mol. Cell. Biol. 12, 1194-1201, 1992
A;Title: The cynteine-rich protein gene family of Giardia lamblia: loss of the CRP170 generation mumber: A42125; MUID:92186850; PMID:1545800
                                                                                                                              C; Accession: A2638
R; Ceccarelli, A.; McRobbie, S.J.; Jermyn, K.A.; Duffy, K.; Early, A.; Williams, J.G. Nucleic Acids Res. 15, 7463-7476, 1987
A; Title: Acids Res. 15, 7463-7476, 1987
A; Title: Structural and functional characterization of a Dictyostelium gene encoding a I A; Reference number: A26838; MUD:88015608; PMID:3658700
A; Accession: A26838
A; Accession: A26838
A; Accession: Bail acquence not shown; not compared with conceptual translation A; Molecule type: DNA
A; Caross references: UNTRROT: P11976
A; Experimental source: strain Ax-2
F;1-18/Domain: signal sequence #status predicted <NGC>
F;19-1046/Product: prestalk protein #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Map position: 5
A,Introns: 44/1; 131/3; 167/1; 259/1; 319/1; 355/1; 484/3; 713/3; 765/1; 840/2; 1036/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1,
restalk protein precursor - slime mold (Dictyostelium discoideum)
;Species: Dictyostelium discoideum
;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
45.4%; Score 54.5; DB 2; Length 1046;
Best Local Similarity 27.0%; Pred. No. 6.3e+02;
Matches 10; Conservative 11; Mismatches 5; Indels 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-98 <ADAL>
A;Cross-references: UNIPROT:P15799; GB:M83937; NID:g159124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             955 CVHTPMNCDDGNFCTLDSCCSTGCTHTPIIIDDNNPC 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CXIXNOXCXQ----XLDDCCSXXC-----NXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
45.4%; Score 54.5; DB 2;
Best Local Similarity 39.1%; Pred. No. 6.9e+02;
Matches 9; Conservative 9; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 XNOXCXOXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: clone 2K287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: CESP: ZK287.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

```
A;Experimental source: trophozoite
A;Note: sequence extracted from NCBI backbone (NCBIN:88421, NCBIP:88427); this ORF is not.
A;Note: the authors report but do not show 19 tandem repeats of the sequence of residues 1A;Note: the authors report but do not show 19 tandem repeats of the sequence of residues A;Notes batter type: DNA
A;Notes. 1269-1766 (ADM2)
A;Residues: 1269-1766 (ADM2)
A;Residues: 1269-1766 (ADM3933; NID:9159122
A;Note: sequence extracted from NCBI backbone (NCBIN:88424, NCBIP:88431); this ORF is not!
A;Note: sequence extracted from NCBI backbone (NCBIN:88424, NCBIP:88431); this ORF is not!
C; Exp. Med. 167, 109-118, 1988
A;Title: Antigenic variation of a cysteine-rich protein in Giardia lamblia.
A;Reference number: S00530; MUID:88089405; PMID:3335828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Molecule type: DNA

A Residues: 1154-1409, 'A', 1411-1420, 'K', 1422-1425, 'R', 1427-1481 <ADA3>

A; Residues: 1154-1409, 'A', 1411-1420, 'K', 1422-1425, 'R', 1427-1481 <ADA3>

B; Residues: 126-1409, 'A', 1804, 'A', 1994

B; Rang, Y.; Adam, R.D.

B; Rang, Y.; Adam, R.D.

B; Rang, Y.; Adam, R.D.

A; Title: Allele-specific expression of a variant-specific surface protein (VSP) of Giardin A; Reference number: S48056; MUID:94301794; PMID:8029018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Molecule type: DNA
A.Residues: 1-56 <YAN>
A.Cross-references: EMBL:L25059
A.Experimental source: trophozoites WBA6
A.Note: the source is designated as Giardia intestinalis
C.Comment: This translation was produced by PIR staff from information provided by the and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1780-1798 < RU2>
A; Residues: 1780-1798 < RU2>
A; Comment: This protein mediates the motor neuron-induced aggregation of acetylcholine re-
C; Comment: This protein mediates the motor neuron-induced aggregation of acetylcholine re-
C; Comment: 90% of rat embryonic transcripts encode the variant labeled below as form 3. F
C; Comment: 90% of rat embryonic transcripts encode the variant labeled below as form 3. F
C; Comment: 90% of rat embryonic transcripts encode the variant labeled below as form 3. F
C; Superfamily: agrin, EGF homology; Razal proteinase inhibitor homology; laminin G repeat C; Superfamily: agrin, EOrm 1 # status predicted < AGI>
F; 1-1959/Product: agrin, form 4 # status predicted < AGI>
F; 1-179, 1799-1959/Product: agrin, form 3 # status predicted < AGI>
F; 1-1779, 1788-1959/Product: agrin, form 5 # status predicted < AGI>
F; 1-1779, 1788-1959/Product: agrin, form 5 # status predicted < AGI>
F; 1-1779, 1788-1959/Product: agrin, form 5 # status predicted < AGI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-1779;1799-1959 < RUP>
A; Residues: 1-1779;1799-1959 < RUP>
A; Cross-references: UNIPROT: P25304; GB: M64780; NID: 9202798; PIDN: AAA40703.1; PID: 9202800
A; Roperimental source: embryonic spinal cord
A; Note: it is uncertain whether Met-1, Met-18, or Met-24 is the initiator
B; Rupp, F: Oezcelik, T: Linial, M: Peterson, K: Francke, U: Scheller, R.
J. Neurosci. 12, 3535-3544, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cispecies: Rattus norvegicus (Norway rat)
Cibate: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
Cibate: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
Cibacession: JH0399, A38856
R;Rupp, F; Payan, D.C.; Magill-Solc, C.; Cowan, D.M.; Scheller, R.H.
Neuron 6, 811-823, Magill-Solc, C.; Cowan, D.M.; Scheller, R.H.
A;Title: Structure and expression of a rat agrin.
A;Reference number: JH0399; MUID:91222570; PMID:1851019
A;Accession: JH0399.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A/Title: Structure and chromosomal localization of the mammalian agrin gene.
A/Reference number: A38856; MUID:92407628; PMID:1326608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
45.4%; Score 54.5; DB 2; Length 1766;
Best Local Similarity 29.0%; Pred. No. 9e+02;
Matches 9; Conservative 12; Mismatches 3; Indels 7;
```

```
C;Accession: I51538
R;Saint-Jacques, E. S. Sequin, C.
DNA Cell Biol. 12, 329-340, 1993
A;Title: Cloning and nucleotide sequence of a complementary DNA encoding Xenopus laevis n A;Reference number: I51538; MUID:93263990; PMID:8494609
A;Accession: I51538
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, October 1995
A; Description: Isolation, charcterization and deduction of primary structure by PCR-ampla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
*Residues: 1-62 - 5A1.>
A;Cross-references: UNIRROT:Q05890; GB:M96729; NID:g214585; PIDN:AAB59949.1; PID:g214586
C;Superfamily: metallothionein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: 21782
A;Reference number: 21788
A;Recession: T11547
A;Returus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-67 <SCU>A;Cross-references: UNIROT:Q26497; EMBL:Z66530; NID:g1045269; PID:g1045270
C;Superfamily: metallothionein
C;Keywords: chelation; metal binding; metal-thiolate cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       metallothionein - purple sea urchin (fragment)
C;Species: Sphaerechinus granularis (purple sea urchin)
C;Date: (5-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                       metallothionein - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.0%; Score 54; DB 2; Length 62; 26.9%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 45.0%; Score 54; DB 2; Length 67; Best Local Similarity 26.9%; Pred. No. 1.1e+02; Matches 7; Conservative 11; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Indels
                                                              1065 CIKQSQVCDGKMQCLDGLDEEHCNEEEKCL 1094
                   1 CXIXNQXC---XQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 CSCSNCKCTSCKKSCCSCCPAECSKC 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CXIXNOXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:|: :|:::|
23 CCITGSCCKEGDGLCCGKCSNAACKC 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: April 18, 2005, 20:38:44 Job time : 29.5 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 26.9%
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parisi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: T11547; Scudiero, R.; Par.
                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ଚ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;1224-1257/00main: EGF homology <EG1>
F;1287-1442/Domain: EGF homology <EG1>
F;1287-1442/Domain: EGF homology <EG2>
F;1444-146/Domain: EGF homology <EG3>
F;1441-146/Domain: EGF homology <EG3>
F;1555-1706/Domain: EGF homology <EG3>
F;1713-1747/Domain: EGF homology <EG4>
F;1807-1959/Domain: EGF homology <EG4-263, 252-284, 316-335, 324-356, 389-408, 397-429, 454-473
F;97-116, 105-137, 171-191, 180-121, 244-263, 252-284, 316-335, 324-356, 389-408, 397-429, 454-473
F;77-1483-1494, 1488-1504, 1506-1515/Disulfide bonds: #status predicted
F;145, 672, 827, 957/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Map position: 1
A,Imb position: 1
A,Imtrons: 29/1; 78/1; 124/1; 216/1; 256/1; 1222/3; 2036/3; 2127/2; 2478/3; 2522/3; 2589
A;Introns: 29/1; 78/1; 124/1; 216/1; 256/1; 1222/3; 2589
E;44-77/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;81-124/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F;130-166/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F;925-964/Domain: LDL receptor ligand-binding repeat homology <LDL4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-2643 <DUZ>
A;Cross-references: UNIPROT:001552; EMBL:U97017; PIDN:AAB52363.1; GSPDB:GN00019; CESP:F4
A;Experimental source: strain Bristol N2; clone F47B3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Species: Caenorhabditis elegans
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004;
Accession: T29149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;969-1005/Domain: LDL receptor ligand-binding repeat homology (LDL5) F;1013-1047/Domain: LDL receptor ligand-binding repeat homology (LDL6) F;1013-1087/Domain: LDL receptor ligand-binding repeat homology (LDL6) F;1053-1132/Domain: LDL receptor ligand-binding repeat homology (LDL8) F;1140-1175/Domain: LDL receptor ligand-binding repeat homology (LDL9) F;1180-1216/Domain: LDL receptor ligand-binding repeat homology (LDL9) F;1228-1265/Domain: LDL receptor ligand-binding repeat homology (LD19)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.4%; Score 54.5; DB 2; Length 2643; 30.0%; Pred. No. 1.2e+03; ive 12; Mismatches 6; Indels 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 45.4%; Score 54.5; DB 1; Length 1959; Local Similarity 20.0%; Pred. No. 9.6e+02; nes 8; Conservative 14; Mismatches 5; Indels 13
F;1-1143,1153-1959/Prodypt: agrin, form 2 #status predicted <AG2>F;22-50/Region: "Mydrophobic
                                                                              F;88-137/Domain: Kazal proteinase inhibitor homology «KPI1»
F;163-212/Domain: Kazal proteinase inhibitor homology «KPI2»
F;130-284/Domain: Kazal proteinase inhibitor homology «KPI3»
F;307-356/Domain: Kazal proteinase inhibitor homology «KPI3»
F;308-429/Domain: Kazal proteinase inhibitor homology «KPI5»
F;446-494/Domain: Kazal proteinase inhibitor homology «KPI5»
F;540-542/Region: motor neuron attachment (L-R-E) motif
F;540-542/Region: motor neuron attachment (L-R-E) motif
F;540-545/Domain: Kazal proteinase inhibitor homology «KPI8»
F;748-786/Domain: laminin-type EGF-like homology «LE2»
F;148-992/Region: serine/Lhreonine-rich
F;108-1086/Region: serine/Lhreonine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |::: :|:|
116 CELQRAQCNQQRIRLLRQGPCGSRDPCANVTCSFGSTCV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CXIXNQXCXQ------XLDDCCSXXCNXXNXCV,27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Du, Z.; Le, T.T.
submitted to the EMBL Data Library, April 1997
A;Description: The sequence of C. elegans cosmid F47B3.
A;Reference number: 220579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein F47B3.8 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: T29149
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 30.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Gene: CESP: F47B3.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

ö

This Page Blank (uspto)

xenopus lae gallus gall caenorhabdi

mus musculu rattus norv nomo sapien Lytechinus

mus musculu

cynops pyrr brachydanio

strongyloce

phytophthor phytophthor homo sapien drosophila caenorhabdi

homo sapien halocynthia rattus norv

ucilia cup hytophthor

0907207 092374 092374 090727 090762 090762 090762 090762 091772 06198 06198 06198 06198 06198 06467 06467 06994 06994 06994 06994 06124 06124 06124 06124 06124 06124

strongyloce mus musculu homo sapien rattus norv

mus musculu xenopus lae

P49013 Q80w06 Q8nbs4 Q88671 Q88516 Q9nyj7 P79941

homo sapier

colinus vir

xenopus lae rattus norv homo sapien

Q7zxt4 P97607 Q9y219

conus geogr conus tulip

phytophthor

phytophthor

mus musculu anopheles g

mus musculu

09qye5 061204

phytophthor phytophthor

mus musculu homo sapien anopheles g

sesamum ind

phytophtho

Q71ks8 Q646u3 Q646u3 Q646u4 Q646w2 Q646w2 Q646w3 Q646w6 Q9aud1 Q8k1e3 Q07pm27

podocoryne rattus norv mus musculu

061483

strongyloce anopheles g brachydanio

homo sapien oikopleura

06pfv7 000548 066804 P10079

mus musculu

anopheles g boophilus m branchiosto

plasmodium

Q7qct2 Q9de37 Q9u4a2 Q7qf82 Q8i6x6

agelenopsis arabidopsis arabidopsis

conus arena

099pa5 P11057 Q9bp77 Q8lag1 Q8vze5 Q9zvz7 Q8ik03

arabidopsis

conne

NTC4_MOUSE NTC3_RAT NTC3_HUMAN P91526 NTC4_HUMAN 061240 070244 MTB_COLVI Q80W06 Q80W06 DLL3_RAT DLL3_MOUSE DLL3_MOUSE DLL3_HUMAN P79941 072XT4 JAG2_RAT JAG2_RAT JAG2_RAT JAG2_RAT JAG2_MOUSE G01204 G01204 CXO7_CONGE CXO7_CONGE CXO7_CONGE CXO7_CONGE Q9AUD1 EFL9 MOUSE EFL9 HUMAN Q7PMZ7 0962W9 DLL1 RAT DLL1 MOUSE QGPFV7 DLL1 HUMAN QG6SO4 FBP1 STRPU 27QCT2 39DE37 Q81K03 CXOD_CONMA us-10-627-685a-1.rup

```
Signal; Toxin.
SIGNAL 1
PROPEP 23
Craik D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Naranjo D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Moran 0.;
                                                                                                                                                                                                                                                                                                                                                                                               dependent
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Venom;
MEDLINE=98104087; PubMed=9438859; DOI=10.1016/S0969-2126(97)00307-9;
Scanlon M.J., Naranjo D., Thomas L., Alewood P.F., Lewis R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Olivera B.M.; "Strategy for rapid immobilization of prey by a fish-hunting marine
                                         05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Four-loop conotoxin preproprotein (Fragment).
Comus purpurascens (Purple cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Canoidea; Conidae; Sorbeoconcha; Hypsogastropoda;
NCBI_TaxID=41690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., SYNTHESIS, AND MASS SPECTROMETRY. MEDLINE=98079023; PubMed=9417043; DOI=10.1074/jbc.273.1.33; Shon K.-J., Stocker M., Terlau H., Stuehmer W., Jacobsen R.B., Walker C.S., Grilley M.M., Watkins M., Hillyard D.R., Gray W.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conus purpurascens (Purple cone).
Eukaryota, Metazoa, Mollusca, Gastropoda, Orthogastropoda,
Apogastropoda, Caenogastropoda, Sorbeoconcha, Hypsogastropoda,
Neogastropoda, Conoidea, Conidae, Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 46-72, AND SYNTHESIS.
MEDLINE-22068471; PubMed-12074021; DOI=10.1038/381148a0;
Terlau H., Shon K.-J., Grilley M.M., Stocker M., Stuehmer W.,
                                                                                                                                                                                                                                                                                                                                                                                                                   0; DB 2; Length 67; 6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kappa-conotoxin PVIIA is a peptide inhibiting the shaker K+
                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                        Duda T.F. Jr., Palumbi S.R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AF480312; AAQ0S864.1; -.
HSSP; P56633; 1AV3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-DEC-1998 (Rel. 37, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Kappa-conotoxin PVIIA precursor (Fin-popping peptide).
                                                                                                                                                                                                                                                                               GO; GO:0005576; C:extracellular; IEA.
GO; GO:0008200; F:ion channel inhibitor activity; IEA
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR004214; Conotoxin.
                                                                                                                                                                                                                                                                                                                                                                        41 67 four-loop conotoxin.
67 AA; 7712 MW; E7E77CC61873E1DB CRC64;
                                      67 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 AA
                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 120; D 63.0%; Pred. No. 6e-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |:|:||:||:||:||CRIPNQKCFQHLDDCCSRKCNRFNKCV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          channel.";
J. Biol. Chem. 273:33-38(1998).
                                                                                                                                                                                                                                                                                                                                           Pfam; PF02950; Conotoxin; 1
                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 63.03
Matches 17; Conservative
                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 381:148-151(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=41690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRUCTURE BY NMR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONPU
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                 Q71KT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CXCCCONPU
ID CXK7 CC
DT 15-DEC 1
DT 28-DEC 1
DE X8DPA-C-
RA MALKET
RA MALKET
RA MALKET
RA MALKET
RA MALKET
RA MALKET
RA MADLINI
RA MADLINI
RA MEDLINI
RA CHARACA
RY MEDLINI
RY SERVET
RY STRUCT
RY STRUCT
RY MEDLINI
RY STRUCT
RY MEDLINI
RY SERVET
RY STRUCT
RY MEDLINI
RY STRUCT
RY MEDLINI
RY STRUCT
RY MEDLINI
RY STRUCT
RY MEDLINI
RY MEDLINI
RY STRUCT
RY MEDLINI
RY STRUCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P56633
    RESULT 1
Q71KT2
                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

```
Hardring D.;

"Inhibition of single Shaker K channels by kappa-conoctoxin-PVIIA.";

Biophys. J. 82:3003-3011(2002).

"Inhibition of single Shaker K channels by kappa-conoctoxins bind and inhibit voltage-sensitive potassium channels. The rat brain voltage-gated potassium channels. The rat brain voltage-gated potassium channels. The rat brain voltage-gated potassium channels. The shaker (Drosophila) is sensitive. The potassium channel protein Shaker (Drosophila) is sensitive. The interaction site between the Shaker channel. In fish, this toxin is within the S5-S6 loop of the Shaker channel. In fish, this toxin catension of major fins, without immobilization or death.

"Injection of this peptide together with the delta-conocoxin pvIA causes the sudden tetanus of prey (STOP) syndrome, which is a single, lethal "fin-pop" in envenomated fish. In mice, induces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUTAGENESIS OF ARG-47; ILE-48; PRO-49; ASN-50; GLN-51; LYS-52; PHE-54; PHE-54; GLN-55; HIS-56; LEU-57; ASP-58; ASP-59; SER-62; ARG-63; LYS-64, ARG-67; PHE-68; ASN-69 AND LYS-67.0.

MEDLINE-20387358; PubMed=10818087; DOI=10.1074/jbc.C900990199; Jacobsen R.B., Koch E.D., Lange-Malecki B., Stocker M., Verhey.J., Van Wagoner R.M., Vyazovkina A., Olivera B.M., Terlau H.; Fingle amino acid substitutions in kappa-conotoxin PVIIA disrupt interaction with the shaker K+ channel.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular simulation of the interaction of kappa-conotoxin-PVIIA with the Shaker potassium channel pore.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SÜBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: Expressed by the venom duct.
MASS SPECIFICITY: MM=1268.4; METHOD=FAB; RANGE=46-72; NOTE=Ref.1.
SIMILARITY: Belongs to the conotoxin O-superfamily. Kappa-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAUTION: Because analogs resulting of mutagenesis of Hyp-49, Asn-50, Leu-57 and Asp-59 gave very low yields upon folding, the results of mutagenesis on these residues should be interpreted with caution.
                                                                                                                                                                                                                                                                        s:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99329121; PubMed=10398696;
Terlau H., Boccaccio A., Olivera B.M., Conti F.;
"The block of Shaker K+ channels by kappa-conotoxin PVIIA is state
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; AS8997; AS8997.

PDB; 1AV3; NMR; @=1-27.

PDB; 1KCP; NMR; @=1-27.

InterPro; IPR04214; Conotoxin.

Pfam; PF02950; Conotoxin; 1.

3D-structure; Direct protein sequencing; Hydroxylation;

Ionic channel inhibitor; Neurotoxin; Potassium channel inhibitor;
                                                                                                                                                                                                                                                  Savarin P., Guenneugues M., Gilquin B., Lamthanh H., Gasparini Zinn-Justin S., Menez A.;
Zinn-Justin S., Menez A.;
"Three-dimensional structure of kappa-conotoxin PVIIA, a novel potassium channel-blocking toxin from cone snails.";
Biochemistry 37:5407-5416(1998).
"Solution structure and proposed binding mechanism of a novel potassium channel toxin kappa-conotoxin PVIIA."; Structure 5:1585-1597(1997).
                                                                                                                                                                 STRUCTURE BY NMR.
MEDLINE=98217295; PubMed=9548922; DOI=10.1021/bi9730341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MODEL OF THE SHAKER-PVIIA INTERACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLOCKADE OF SHAKER CHANNEL BY PVIIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gen. Physiol. 114:125-140(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BLOCKADE OF SHAKER CHANNEL BY PVIIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21678121; PubMed=11820396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eur. Biophys. J. 30:528-536(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22017751; PubMed=12023223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22
45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hyperactivity
```

```
7741 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        calcium channel subtypes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE, AND SYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Omega-conotoxin CVIC.
Conus catus (Cat cone).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22
45
71
71
71
71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=101291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Venom;
                                                                                                                                                                                                                                family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CXOC CON P58919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
   유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93003172; PubMed=1390774; Ramilo C., Zafaralla G.C., Nadasdi L., Hammerland L.G., Yoshikami D., Gray W.R., Kristipati R., Ramachandran J., Miljanich G., Olivera B.M., Cruz L.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Venom duct;
MEDLINE=20037955; PubMed=10573284; DOI=10.1016/S0196-9781(99)00116-3;
Lu B.-S., Yu F., Zhao D., Huang P.-T., Huang C.-F.;
"Conopeptides from Conus striatus and Conus textile by cDNA cloning.";
Peptides 20:1139-1144(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                         R-A,K,0:
1-A: 3-fold decrease of toxicity.
1-A: 3-fold decrease of toxicity.
1-A: 100% reduction of toxicity.
N-A: 100% reduction of toxicity.
Q-A: 13-fold decrease of toxicity.
Q-A: 100% reduction of toxicity.
F-A,M: 100% reduction of toxicity.
F-A,M: 100% reduction of toxicity.
G-A: 3-fold decrease of toxicity.
H-A: 3-fold decrease of toxicity.
D-A: 100% reduction of toxicity.
D-A: 100% reduction of toxicity.
N-A: 100% reduction of toxicity.
D-A: 100% reduction of toxicity.
N-A: 100% reduction of toxicity.
S-A: 15-fold decrease of toxicity.
S-A: 15-fold decrease of toxicity.
R-A: 3-fold decrease of toxicity.
R-A: 3-fold decrease of toxicity.
R-A: 12-fold decrease of toxicity.
                                                                                                                                                                                                                                                                                                                                                      17-fold decrease of toxicity.
                                                                                                                                                                                                                                                                                                                                                                                         117-fold decrease of toxicity
                                                                                                                                                                                                                                                                                                                                       5-fold decrease of toxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Novel alpha- and omega-conotoxins from Conus striatus venom.";
Biochemistry 31:9919-9926(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P2881; Q9UB25; Created)
01-DEC-1992 (Rel. 24, Created)
16-OCT-2004 (Rel. 40, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Omega-conotoxin SVIB precursor (SNX-183).
Conus striatus (Striated cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 120; DB 1; Length 72; 63.0%; Pred, No. 6.4e-05; cive 10; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72
8317 MW; 53BFAF79EE751C16 CRC64;
   Kappa-conotoxin PVIIA
                                                                  4-hydroxyproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 46-71, AND SYNTHESIS.
TISSUE=Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 63.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 AA;
   CONST
PEPTIDE
DISULFID
DISULFID
DISULFID
MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                             MUTAGEN
MUTAGEN
MUTAGEN
                                                                                                                                                             MUTAGEN
MUTAGEN
MUTAGEN
                                                                                                                                                                                                           MUTAGEN
MUTAGEN
MUTAGEN
                                                                                                                                                                                                                                                         MUTAGEN
MUTAGEN
MUTAGEN
MUTAGEN
MUTAGEN
MUTAGEN
MUTAGEN
                                                                                                                                              MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                       HELIX
STRAND
STRAND
                                                                                                                                                                                                                                                                                                                                                                                                        STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONST
                                                                                                                                                                                                                                                                                                                                                                                                                         I GRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETT E 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-20519630; PubMed=10938268; DOI=10.1074/jbc.M002252200; Lewis R.J., Nielsen K.J., Craik D.J., Loughnan M.L., Adams D.A., Shazpe I.A., Luchian T., Adams D.J., Bond T., Thomas L., Jones A., Macheson J.-L., Drinkwater R., Andrews P.R., Alewood P.F.; "Novel omega-conotoxins from Conus catus discriminate among neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cysteine amide (G-72 provides amide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF02950; Conotoxin; 1.
3D-structure; Amidation; Calcium channel inhibitor;
Direct protein sequencing; Ionic channel inhibitor; Neurotoxin;
Presynaptic neurotoxin; Signal; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Mollugca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64.2%; Score 77; DB 1; Length 72; 34.6%; Pred. No. 1.3; ive 12; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      group).
1F753546AAD39908 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Omega-conotoxin SVIB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46 CKLKGQSCRKTSYDCCSGSCGRSGKC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; C44379; C44379.
PDB; 1MVJ; NMR; @=46-72.
InterPro; IPR004214; Conotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF146346; AAD31906.1; -.
```

STITIES

ð

```
calcium-binding (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gnaling pathway; Repeat; Signal; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neurogenic locus notch protein homolog.
Extracellular (Potential).
Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PSSC037; ANK REP REGION; 1.
PROSITE; PSSC088; ANK REPEAT; 4.
PROSITE; PSSC0088; ANK REPEAT; 4.
PROSITE; PSC0010; ASK-HYDROXYL; 23.
PROSITE; PSC0112; EGF 2; 29.
PROSITE; PSSC0126; EGF 2; 29.
PROSITE; PSSC0126; EGF 31 36.
PROSITE; PSSC0126; EGF 31 36.
PROSITE; PSSC0126; EGF 31 36.
PROSITE; PSC01187; EGF 21.
PROSITE; PSC01287; EGF 21.
PS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGF-like 1.

EGF-like 2.

EGF-like 3.

EGF-like 4.

EGF-like 5.

EGF-like 6.

EGF-like 7.

EGF-like 7.

EGF-like 9.

EGF-like 10.

EGF-like 10.

EGF-like 11.

EGF-like 11.

EGF-like 11.

EGF-like 12.

EGF-like 12.

EGF-like 13.

EGF-like 14.

EGF-like 14.

EGF-like 15.

EGF-like 16.

EGF-like 17.

EGF-like 17.

EGF-like 18.

EGF-like 19.

EGF-like 20.

EGF-like 20.

EGF-like 19.

EGF-like 19.

EGF-like 19.

EGF-like 19.

EGF-like 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              calcium-binding (calcium-binding (calcium-binding (calcium-binding (calcium-binding (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               calcium-binding calcium-binding calcium-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      calcium-binding calcium-binding calcium-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       calcium-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytoplasmic (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGF-like 21, CEGF-like 22, EGF-like 23, CEGF-like 24, CEGF-like 25, CEGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGF-like 34.
EGF-like 35.
EGF-like 36.
Lin/Notch 1.
Lin/Notch 2.
Lin/Notch 3.
ANK 1.
ANK 2.
ANK 3.
ANK 5.
                InterPro; IPR006209; BGF like.
InterPro; IPR010660; NOD.
InterPro; IPR008207; Notch.
InterPro; IPR008000; Notch.region.
Pfam; PP00023; Ank; 6.
Pfam; PP00081 BGF; 36.
Pfam; PP00066; Notch; 3.
Pfam; PP00066; Notch; 3.
Pfam; PP00066; Notch; 3.
PRINTS; PR01415; ANKYRIN.
PRINTS; PR01415; ANKYRIN.
PRINTS; PR00415; ANKYRIN.
PRINTS; PR00415; NOTCH.
SWART; SM00248; ANK; 6.
SWART; SM00179; BGF CA; 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1018
1056
1094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1218
1264
1304
1346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20
1729
1751
20
58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1144
1182
1220
1266
1306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-aib.ch/announce/or send an email to license@isb-sib.ch).
J. Biol. Chem. 275:35335-35344(2000).
-1- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind and block voltage-sensitive calcium channels (VSCC) (By similarity). This toxin blocks N-, P-, and Q-type calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                             Family.

HSSP, P05484; 1DW4.

Amidation, Calcium channel inhibitor; Direct protein sequencing; Amidation, Calcium channel inhibitor; Presynaptic neurotoxin; Toxin. DISULFID

B 20 By similarity.

DISULPID 18 26 By similarity.

MOD RES 26 Cysteine amide.

SEQUENCE 26 AA; 2790 MW; SEEFC382335C4A8B CRC64;
                                                                                                                                    -1- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom duct.
-!- SIMILARITY: Belongs to the conotoxin O-superfamily. Omega-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopus laevis (African clawed frog).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Amphibia, Batrachia; Anura, Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1991 (Rel. 18, Created)
01-OCT-1996 (Rel. 34, Last sequence urdate)
25-JMN-2005 (Rel. 46, Last annotation update)
Neurogenic locus notch protein homolog precursor (XOTCH protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60.8%; Score 73; DB 1; Length 26; 30.8%; Pred. No. 1.3; 4; Indels Live 14; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=90385285; PubMed=2402639;
Coffman C., Harris W., Kintner C.;
Xotch, the Xenopus homolog of Drosophila notch,";
Science 249:1438-1441(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 2524 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CXIXNOXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P46531; 1PB5.
InterPro; IPR003110; ANK.
InterPro; IPR000112; Asx.hydroxyl_S.
InterPro; IPR000142; EGF_Z.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001438; EGF_II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M33874; AAB02039.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 30.87
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                      channels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
NOTC_XENLA
ID NOTC_XENLA
AC P21783;
```

(Potential).
(Potential).
(Potential).

(Potential)

(Potential) (Potential)

(Potential)

(Potential). (Potential). (Potential).

(Potential) (Potential) (Potential)

(Potential)

(Potential).

(Potential) (Potential)

```
similarity
                                                                                                                                                                                                                     similarity.
similarity.
similarity.
                                                                                                                similarity.
similarity.
similarity.
similarity.
similarity.
                                                                                                                                                     similarity.
                                                                                                                                                            similarity.
Similarity.
Similarity.
Similarity.
Similarity.
Similarity.
Similarity.
Similarity.
Similarity.
Similarity.
Similarity.
Similarity.
Similarity.
Similarity.
Similarity.
Similarity.
Similarity.
                                                                                                                                                                                                                               similarity,
similarity,
similarity,
similarity,
similarity,
similarity,
similarity,
                                                                                                                                                                                                                                                              similarity.
similarity.
similarity.
similarity.
                                                                                                                                      similaritý.
similarity.
                                                                                                                                   similarity.
                                                                                                                                                  similarity
                                                                                                                                              similarity
    2086
35
45
56
74
87
112
8117
1139
1156
1165
2114
2214
232
                                                                   253
271
280
291
                                                                                          REPEAT,
DISULFID
                                                                                                                                                                                       DISULFID
DISULFID
DISULFID
DISULFID
                                                DISULFID
DISULFID
DISULFID
DISULFID
                                                               DISULFID
DISULFID
DISULFID
                                                                              DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
                                                                                                                                                                    DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                         DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
                                                                                                                                                                                                                                                              DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                            DISULFID
                                                                                                                                                                                                                                                   DISULFID
                                                                           DISULFID
                                                                                                                    SULFID
                                                                                                                        SULFID
                                                                                                                                   SULFID
                                                                                                                                      DISULFID
                                                                                                                                          DISULFID
                                                                                                                                              SULFID
                                                                                                                                                  DISULFID
                                                                                                                                                      DISULFID
                                                                                                                                                         DISULFID
                                                                                                                                                             DISULFID
                                                                                                                                                                DISULFID
                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                           DISULFID
                                                                                                                            DISULFID
                                                                                                                               DISULFID
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P/0-type calcium channel.";
Blochem. Biophys. Res. Commun. 214:305-309(1995).
-!- FUNCTION: Omega-conoctoxins act at presynaptic membranes, they bind and block voltage-sensitive calcium channels (VSCC). This toxin blocks N-type calcium channels as well as types of high-threshold voltage-gated calcium channels resistant to both dihydropyridines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Structure-activity relationships of omega-conotoxins MVIIA, MVIIC and 14 loop splice hybrids at N and P/Q-type calcium channels."; J. Mol. Biol. 289:1405-1421(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LINCTURE BY NMR.
MEDLINE-99303703; PubMed-10373375; DOI-10.1006/jmbi.1999.2817;
Nielsen K.J., Adams D., Thomas L., Bond T., Alewood P.F., Craik D.J.,
                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Solution structure of omega-conotoxin MVIC, a high affinity ligand of P-type calcium channels, using 1H NMR spectroscopy and complete relaxation matrix analysis.";
J. Mol. Biol. 248:106-124(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SYNTHESIS.
MEDIATE=92337922; PubMed=1352986; DOI=10.1016/0896-6273(92)90221-X;
MEDIATE=9237922; PubMed=1352986; DOI=10.1016/0896-6273(92)90221-X;
MIJJyard D.R., Monie V.D., Minte T.M., Bean B.P., Nadasdi L.,
Ramachandran J., Miljanich G.P., Azimi-Zoonooz A., McIntosh J.M.,
Caraz L.J., Imperial J.S., Olivera B.M.,
"A new Conus peptide ligand for mammalian presynaptic Ca2+ channels.
Neuron 9:69-77(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUTAGENESIS OF TYR-15.
MEDLINE-9540821; PubMed=7677735;
Kim J.I., Takahashi M., Martin-Moutot N., Seagar M.J., Ohtake A.,
Sato K.;
"Tyr13 is essential for the binding of omega-conotoxin MVIC to the
                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                   01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
03-OCT-2004 (Rel. 45, Last annotation update)
Comega-conotoxin MVIcc precursor (SNX-230) (Fragment).
Conus magus (Magus cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
NCBI_TAXID=6492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRUCTURE BY NMR.
MEDLINE=55248539; PubMed=7731037;
Farr-Jones S., Miljanich G.P., Nadasdi L., Ramachandran J.,
                                                                                                                                             DB 1; Length 2524;
1e+02;
                                                                                                                                                                           5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and omega-conotoxin GVIA.
SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: Expressed by the venom duct.
                                                                                                                                        similarity.
similarity.
similarity.
similarity.
similarity.
similarity.
similarity.
similarity.
similarity.
                                                                                                                                                                                                                                                                                                  Ź
                                                                                                                                                                                                                                                                                                  59
                                                                                                                                                                                                                   247 GFSGQNCEENIDDCPSNNCRNGGTCV 272
                                                                                                                                                                                                     27
                                                                                                                                                                                                    2 XIXNOXCXQXLDDCCSXXCNXXNXCV
  Query Match
Beet Local Similarity 34.55,
Conservative
Process 9; Conservative
                                                                                                                                                                                                                                                                                                  STANDARD;
997
1006
1017
1035
1044
1055
1073
1082
1121
986
991
1024
1029
1046
1067
1067
                                                                                                                                                                                                                                                                                                  CONMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [2]
STRUCTURE
DISULFID
                                                                                                                                                                                                                                                                                                  CXOC CON
P37300;
                                                                                                                                                                                                                                                                      KESULT 6
CXOC_CONMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ++
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ξ
 à
                                                                                                                                                                                                                             셤
```

```
Phytophthora
                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q646U5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q646U7
Q646U7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
064607
10 0646
AC 0646
DT 25-0
DT 25-0
DE Phyt
OC Euka
OC Phyt
COX NCBI
RP SEQU
RA Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q646U5
                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Why and A. Beriman M., Churcher C., Harris B., Harris D., A. Handlan, Beriman M., Churcher C., Harris B., Brooks K., A. Handlan, Beriman B., Baker S., Barron A., Brooks K., A. Buckee C.O., Burrows C., Cherevach I., Chillingworth C., Corto C., A. Chillingworth T., Christodoulou Z., Clark L., Clark R., Corto C., A. Cronin A., Davies R., Davies P., Dearlen F., Doggett J., R. Hamber D., Hauser H., Hornsby T., Holroyd S., Horrocks P., Hander Z., A. Humphray S., Jagels K., James D., Johnson D., Kernonou A., Knight A., A. Mardison M., McLean J., Mooney P., Moule S., Murphy L., Oliver K., A. Maddison M., McLean J., Mooney P., Moule S., Murphy L., Oliver K., A. Maddison M., Price C., Quall M.A., Rabbinowlisch B., Rajandream M.A., Ra A. Rutter S., Rutherford K.M., Sanders M., Simmonds M., Seeger K., Taylor K., Sharp S., Smith R., Squares R., Squares S., Sulston J.E., Craig A., Ra Tivey A., Unwin L., Whitehead S., Woodward J., Sulston J.E., Craig A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                         PDB; ICNN; NWR; A=3-29.
PDB; 1OMN; NWR; @=3-29.
3D-structure; Amidation; Calcium channel inhibitor; Hydroxylation; Ionic channel inhibitor; Neurotoxin; Presynaptic neurotoxin; Toxin.
-!- SIMILARITY: Belongs to the conotoxin O-superfamily. Omega-type
                                                                                                                                                                                                                                                                                                                                                                                                                                    Omega-conotoxin MVIIc.
Essential for calcium channel binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hydroxyproline (Probable).
Cysteine amide (G-29 provides amide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         group).
Y->A: High decrease in binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypotherical protein.
08-Names-MAL6P1.41, PFF0185c;
Plasmodium falciparum (isolate 3D7).
Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.5%; Score 69; DB 1; Length 29; 30.8%; Pred. No. 3.5; tive 12; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3071 MW; AC7A68948474728A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1820 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CXIXNOXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 CKGKGAPCRKTMYDCCSGSCGRRGKC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                   EMBL; S40826; AAB22674.1; -. PIR; JH0699; JH0699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                  28
22
28
28
28
28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                PEPTIDE
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOD RES
                                                                                                                                                                                                                                                                                                                                                                                     TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O6LFM8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 7
OGLEMB
ID QGLET
DT 05-U
DT 05
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
```

```
I K.,
C., Doggett J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kamoun S.;
"Patterns of Diversifying Selection in the Phytotoxin-like scr74 Gene Family of Phytophthara infestans.";
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY723722; AAU21463.1; -.
EMBL; AY723721, AAU21463.1; -.
EMBL; AY723721, AAU21462.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                          Chervach I., Davis P., Goodhead I., Stevens K., Mungall K.,
Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggel
Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B.G;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR382398; CAG25208.1;
InterPro; IPR000875; Cecropin.
InterPro; IPR000875; Cecropin.
PROSITE; P800286; CECROPIN; UNKNOWN I.
Newbold C., Barrell B.G; "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13."; Nature 419:527-531(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                             57.5%; Score 69; DB 2; Length 1820; 32.1%; Pred. No. 1.5e+02; ive 12; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phytophthora infestans (Potato late blight fungus).
Eukaryota, stramenopiles, Oomycetes, Pythiales, Pythiaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phytoxin-like SCR74.
Phytophthora infestans (Potato late blight fungus).
Eukaryota, stramenopiles, Oomycetes, Pythiales, Pythiaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.7%; Score 68; DB 2; Length 74; 29.0%; Pred. No. 10; 2: Indels
                                                                                                                                                                                                                                                                                                                                                                        1820 AA; 218564 MW; 84F330EE57FA6150 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-0CT-2004 (TrEMBLrel. 28, Created)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 XIXNQXCXQ-----XLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 GVVSQCCKAINAEPVAFNDCCSKSCNTGSPC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:|:|:|::|::|
1301 CDIYNEFCDDECCDDECCDDEYC 1328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CXIXNQXCXQXL--DDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phytoxin-like SCR74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 9; Conserv
                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4787;
```

1;

ï

```
Name=NOTCH1; Synonyms=TAN1;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDENTIFICATION OF LIGANDS.
                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell 66:649-661(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERACTION WITH DIX1
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                          NTC1_HUMAN .
P46531;
                                                                                                                                                                                       RESULT 11
NTC1 HUMAN
                                                                                                                                                                                                                      셤
                                                                                                                                         ठे
                                                                                                  7;
         Kamoun S.;
"Patterns of Diversifying Selection in the Phytotoxin-like scr74 Gene Family of Phytophthora infestans.";
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY723720; AAU21461.1; -.
SEQUENCE 74 AA; 7802 MW; 57A8231D29AB5F8F CRC64;
                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-Brown Norway;
Boehm S., Borzym K., Gelling S., Gimmel V., Heitmann K., Kosiura A.,
Lang N., Lehrack S., Thiel J., Sontag M., Hurt P., Himmelbauer H.,
                                                                                                                                                                                                                                                                                                                        STRAIN-Brown Norway;

Bubmed=15060004, DoI=10.1101/gr.19877004;

Hurt P., Walter L., Sadbrak R., Klages S., Mueller I., Shiina T.,

Inoko H., Lehrach H., Guenther E., Reinhardt R., Himmelbauer H.;

The genomic sequence and comparative analysis of the rat major histocompatibility complex.";

Genome Res. 14:611-639(2004).
                                                                                                  9
Torto.Alalibo.T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
                                                                            56.7%; Score 68; DB 2; Length 74; 29.0%; Pred. No. 10; ative 14; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                     2 XIXNQXCXQ-----XLDDCCSXXCNXXNXC 26
                                                                                                                               41 DVVSQCCKAINAEPVAFNDCCSKSCNTGSPC 71
                                                                                                                                                                                         PRT; 1961 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR00210; ANK.
InterPro; IPR00152; Ask hydroxyl_S.
InterPro; IPR00152; Ask hydroxyl_S.
InterPro; IPR001881; EGF_G.
InterPro; IPR001881; EGF_II.
InterPro; IPR006209; EGF_II.
InterPro; IPR006209; EGF_II.
InterPro; IPR006800; NOCCh_region.
InterPro; IPR008805; Rieske.
Pfam; PF00003; Ank; 6.
Pfam; PF00008; EGF_ 24.
Pfam; PF00008; EGF_ 24.
Pfam; PF00006; Notch; 2.
                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00248; ANK; 5.
SMART; SM00181; EGF; 28.
SMART; SM00179; EGF_CA; 21.
SMART; SM00004; NL; 3.
PROSITE; PS50088; ANK_REPEAT; 5.
                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS, PRO1415; ANKYRIN.
PRINTS; PR00010; EGFBLOOD
PRINTS; PR01452; NOTCH.
                                                                                      Local Similarity 29.08
                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                               [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                         Notch homolog 4,.
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                      Name=Notch4;
                                                                             Query Match
                                                                                                                                                                                                  QEMGB9;
                                                                                                                                                                                         Q6MG89
                                                                                                                                                                     Matches
SAFTERS
                                                                                                                      ð
                                                                                                                                      a
```

```
PROSITE; PS01010; ARX_INPROXIT; NO.

PROSITE; PS01010; ARX_INPROXIT; NO.

PROSITE; PS01186; ERF_2; 12.

OURSY MARCHEL, PS01186; ERF_2; 12.

OURSY MARCHEL, PS01186; ERF_2; 12.

PROSITE; PS01186; ERF_2; 13.

PROSITE; P
```

```
Surfacellular (Potential).

Retracellular (Potential).

Egrafike 1.

Egr-like 2.

Egr-like 3.

Egr-like 4.

Egr-like 6, calcium-binding (Potential).

Egr-like 7, calcium-binding (Potential).

Egr-like 10, calcium-binding (Potential).

Egr-like 11, calcium-binding (Potential).

Egr-like 12, calcium-binding (Potential).

Egr-like 13, calcium-binding (Potential).

Egr-like 14, calcium-binding (Potential).

Egr-like 15, calcium-binding (Potential).

Egr-like 15, calcium-binding (Potential).

Egr-like 15, calcium-binding (Potential).

Egr-like 15, calcium-binding (Potential).

Egr-like 20, calcium-binding (Potential).

Egr-like 21, calcium-binding (Potential).

Egr-like 22, calcium-binding (Potential).

Egr-like 23, calcium-binding (Potential).

Egr-like 24, calcium-binding (Potential).

Egr-like 25, calcium-binding (Potential).

Egr-like 26, calcium-binding (Potential).

Egr-like 27, calcium-binding (Potential).

Egr-like 28, calcium-binding (Potential).

Egr-like 31, calcium-binding (Potential).

Egr-like 32, calcium-binding (Potential).

Egr-like 33, calcium-binding (Potential).

Egr-like 34, calcium-binding (Potential).

Egr-like 35, calcium-binding (Potential).

Egr-like 36, calcium-binding (Potential).

Egr-like 37, calcium-binding (Potential).

Egr-like 38, calcium-binding (Potential).

Egr-like 39, calcium-binding (Potential).

Egr-like 30, calcium-binding (Potential).

Egr-like 31, calcium-binding (Potential).

Egr-like 32, calcium-binding (Potential).

Egr-like 33, calcium-binding (Potential).

Egr-like 34, calcium-binding (Potential).

Egr-like 36, calcium-binding (Potential).

Egr-like 37, calcium-binding (Potential).

Egr-like 38, calcium-binding (Potential).

Egr-like 39, calcium-binding (Potential).

Egr-like 30, calcium-binding (Potential).

Egr-like 31, calcium-binding (Potential).

Egr-like 32, calcium-binding (Potential).

Egr-like 33, calcium-binding (Potential).

Egr-like 34, calcium-binding (Potential).

Egr-like 36, calcium-binding (Potential).
                             Neurogenic locus notch homolog protein 1.
Notch extracellular truncation (By
                                                                               Notch intracellular domain (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       By similarity.
                                            Notch extraction of the second of the second
                                                                                                               1446
1482
1524
1928
1961
1961
1995
2028
2061
                                                                                                               DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                      NOMAIN
                       CHAIN
                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
DOMAIN
SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                       bonds (By similarity). Interacts with DTX1 and DTX2.

SUBCELLULAR LOCATION: Type I membrane protein. Following proteolytical processing NICD is translocated to the nucleus (By similarity).

TISSUE SPECIFICITY: In fetal tissues most abundant in spleen, brain stem and lung. Also present in most adult tissues where it is found mainly in lymphoid tissues.

PTM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C. terminal fragment NITM) and a N-terminal fragment NIEC). Following (TACE) to yield a membrane associated intermediate fragment called notch extracellular truncation (NEXT). This fragment is then notch-derived peptide containing the intracellular domain (NICD) in PIN: Phosphorylated (By similarity).

In DISBASE: NOTCH1 truncation is associated with T-cell acute | Numbhoblastic leukemia. ShW respeats.

SIMILARITY: Contains 5 ANK repeats.

SIMILARITY: Contains 3 Lin/Notch repeats.

SIMILARITY: Contains 3 Lin/Notch repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00021; MSA_MLEACAID; 20.
PROSITE; PS00022; BGF 1; 34.
PROSITE; PS01086; BGF 2; 26.
PROSITE; PS01187; BGF 3; 36.
PROSITE; PS01187; PGF 2A; 18.
3D-sttucture; Activator; ANK repeat; Developmental protein;
Differentiation; EGF-like domain; Glyccprotein;
Notch signaling pathway; Phosphorylation; Receptor; Repeat; Signal;
SIGNAL 1 18 Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50088, ANK REPEAT; 4.
PROSITE; PS50297; ANK REP REGION; 1.
PROSITE; PS00010; ASX HYDROXYL; 20.
```

Gaps

; 0

```
Query Match 55.8%; Score 67; DB 2; Length 487; Best Local Similarity 28.0%; Pred. No. 72; Matches 7; Conservative 13; Mismatches 5; Indels
                           52498 MW; C69E5B14E36B3D22 CRC64;
                                                                                                                                                                                                                   164 GFEGOHCEONIDECADOPCHNGGNC 188
                                                                                                                                                                                     2 XIXNOXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50026; EGF_2; 10.
PROSITE; PS50026; EGF_3; 13.
PROSITE; PS50187; EGF_CA; 6.
PROSITE; PS50187; EGF_CA; 6.
EGF-11ke domain; Signal.
SIGNAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 XNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00010; ASX HYDROXYL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mech. Dev. 93:233-237(2000).
EMBL; AB027453; BAA95001.1; -.
HSSP; Q12780; 1HAE.
                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopodinae; Xenopus.
                              487 AA;
  EGF-like domain.
SEQUENCE 487 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRB DROME
                                                                                                                                                                                                                                                                                                                                                                       Q9IBG4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
CRB_DROME
ID CRB_DI
                                                                                                                                                                                                                                                                                                                   RESULT 13
Q9IBG4
                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Canniver S. 1,

Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.

Bublitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.

Bublitted (JUN-2002) AAM49878.1;

Bublitted (JUN-2004) is the submitted (JUN-2004) is the subm
                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise B., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.,
                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                            / Match 56.7%; Score 68; DB 1; Length 2556; Local Similarity 30.8%; Pred. No. 2.6e+02; les 8; Conservative 12; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                          487 AA
By similarity. By similarity.
                                                                                                                                                                                                                248 GFTGQNCEENIDDCPGNNCKNGGACV 273
                                                                                                                                                                                     2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS01187; EGF_CA; 4.
PROSITE; PS50025; LAM G DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00054; Laminin G 1; 1. PRINTS; PR00010; EGFBLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRO0010; EGFBLOOD
SM00179; EGF CA; 3
                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00008; EGF; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Berkeley;
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=crb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                       QBMSX5
QBMSX5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART;
                                                                                                                                                                                                                                                                                                                RESULT 12

OGNESSS

AC QGNESSS

AC QGNESSS

AC QGNESSS

AC QGNESS

DT 01-0C

                                                                                                                              Matches
                                                                                                                                                                                                                                   g
                                                                                                                                                                                     ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE PROM N.A. MEDLINE=20245325; PubMed=10781962; DOI=10.1016/S0925-4773(00)00280-X; MEDLINE=20245325; PubMed=10781962; Xi Xinoshita T.; Kuriyama S., Miyatani S., Kinoshita T.; "Xerl; a novel secretory protein expressed in eye and brain of Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 55.8%; Score 67; DB 2; Length 778; Best Local Similarity 33.3%; Pred. No. 1.1e+02; Matches 8; Conservative 12; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO; 0005198; F: Calcium ion binding; IEA.
GO; GO; 0005198; F: F: Calcium ion binding; IEA.
GO; GO; 0005198; F: F: Calcium ion binding; IEA.
GO; GO; 0007155; P: Calcium ion binding; IEA.
GO; GO; 0007155; P: Calcium ion binding; IEA.
InterPro; IPR00152; Asx bydroxyl S.
InterPro; IPR00142; EGF 2.
InterPro; IPR001481; EGF 7.
InterPro; IPR001481; EGF 7.
InterPro; IPR001438; EGF 11ke.
InterPro; IPR001439; EGF 11ke.
InterPro; IPR001791; Laminin G.
InterPro; IPR001791; Laminin G.
InterPro; IPR001791; GGF; I.
InterPro; IPR001791; EGF 11k.
INTERP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 27 Potential.
778 AA; 85516 MW; 462D2C84AE435CF6 CRC64;
                                                                                                               01-007-2000 (TrEMBLrel. 15, Created)
01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Secretory protein containing EGF domain precursor.
Xenopus laevis (African clawed frog).
778 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2139 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   285 DGELCQQDIDECQSQPCQNGGRCV 308
```

```
Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Repeat; Signal;
SIGNAL
CHAIN 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91
2085
2112
267
306
348
388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nam. S.-C., Choi K.-W.;

"Interaction of Par-6 and Crumbs complexes is essential for

"Interaction of Par-6 and Crumbs complexes is essential for

photoreceptor morphogenesis in Drosophila.";

Development 130:4363-4372(2003).

-I FUNCTION: Plays a central role in cell polarity establishment.

Participates in the assembly, positioning and maintenance of
adherens junctions via its interaction with the SAC complex.

Controls the coalescence of the spots of zonula adherens (ZA) into
a adhesive ring around the cells. It may act as a signal. Involved
in morphogenesis of the photoreceptor rhabdomere, for positioning
attd growth of rhabdomere and AJ during the crucial period of
photoreceptor extension along the proximodistal axis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-87218537; PubMed-3107986;
Knust E., Dietrich U., Tepass U., Bremer K.A., Weigel D., Vaessin H.,
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=Cregon-R; TISSUE=Embryo;
MEDLINE=90263104; PubMed=2244615; DOI=10.1016/0092-8674(90)90189-L;
Tepass U., Theres C., Knust E., Tepass U., Theres C., Knust E., Crumbs encodes an EGF-like protein expressed on apical membranes of prosephila epithelial cells and required for organization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERACTION WITH PAID.

MEDLINE=99200334; PubMed=10102271; DOI=10.1016/S0092-8674(00)80593-0;
Bhat M.A., Izaddoost S., Lu Y., Cho K.-O., Choi K.-W., Bellen H.J.;
"Discs Lost, a notoes multi-PDZ domain protein, establishes and maintains epithelial polarity.";
Cell 96:833-845(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: Component of the SAC complex, a complex composed of crb, Patj and sdt. May interact with the par-6 complex, which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bhat M.A., Izaddoost S., Lu Y., Cho K.-O., Choi K.-W., Bellen H.J.;
Cell 115:765-766(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=11076972; DOI=10.1083/jcb.151.4.891;
Tanentzapf G., Smith C., McGlade J., Tepass U.;
"Apical, lateral, and basal polarization cues contribute to the development of the follicular epithelium during Drosophila
                                                                                                                                                                                             Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     iDENTIFICATION IN A SAC COMPLEX WITH PART AND SDT.
MEDLINE=21603015; PubMed=11740560; DOI=10.1038/414638a;
Bachmann A., Schneider M., Theilenberg E., Grawe F., Knust E.;
"Drosophila Stardust is a partner of Crumbs in the control of epithelial cell polarity.";
Nature 414:638-643(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Campos-Ortega J.A.;
"EGF homologous sequences encoded in the genome of Drosophila melanogaster, and their relation to neurogenic genes.";
EMBO J. 6:761-766 (1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION, AND INTERACTION WITH PAIJ.
01-MAR-1989 (Rel. 10, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERACTION WITH THE PAR-6 COMPLEX.
                                                                                                 Crumbs protein precursor (95F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oogenesis.";
J. Cell Biol. 151:891-904(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1663-1955 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell 61:787-799(1990).
                                                                                                                                                                                                                                                                                                  NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=12900452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    retina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ERRATUM
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGF-like 4. calcium-binding (Potential).
EGF-like 5.
EGF-like 6.
EGF-like 6.
EGF-like 7.
EGF-like 8.
EGF-like 10.
EGF-like 10.
EGF-like 11.
EGF-like 11.
EGF-like 12.
EGF-like 13.
EGF-like 13.
EGF-like 13.
EGF-like 13.
EGF-like 14.
EGF-like 14.
EGF-like 15.
EGF-like 15.
EGF-like 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Potential).
(Potential).
(Potential).
composed of par-6, baz and aPKC, via its interaction with Patj.
Interacts with other proteins with Patj and sdt via its short
cytoplasmic teal.
-1- SUBCELLULAR LOCATION: Type I membrane protein. Specifically
localized to the apical membrane.
-1- PTM: Phosphorylated in the cytoplasmic domain (Potential).
-1- SIMILARITY: Contains 29 EGF-like domains.
-1- SIMILARITY: Contains 3 laminin G-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Crumbs protein.
Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytoplasmic (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Potential
                                                                                                                                                       EMBL; X05144; CAA28793.1; -. CAA28793.1; -.
```

```
RR PERCENCE FROM N.A.

Adama M.D. Celniker S.E. Holf R.A., Bvans C.A. Gocapus J.D.,

Adama M.D. Celniker S.E., Holf R.A., Bvans C.A. Gocapus J.D.,

RA Amanatides P.G. Scherer S.E., 19 W. Hoskins R.A., Galle R.F.

RA Amanatides P.G. Scherer S.E., Richards S. Ashburner M., Henderson S.N.,

RA Amanatides P.G., Rogers Y.H., Blazej R.G., Champe M., Feiffer B.D.,

RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Feiffer B.D.,

RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Feiffer B.D.,

RA Abril J.F., Agbayani A., Andrews-Pfannkoch C., Baldwin D.,

Ballew R.M., Baus A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Ballew R.M., Baus A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Borkova D. Botchen M.R., Bouck J., Broketein P., Bentler P.,

Rochery J.M., Cawley S., Dahlke C. Davenport L.B., Center A., Chandra I.,

RA Borkova D. B., Bullar H., Cawley B.C., Davises P.,

RA Borkova D., Botcher A., Deng Z., Mays A.D., Dew I. Dietz S.M.,

Rochery J.M., Cawley S., Dahlke C. Davenport L.B., Davises P.,

RA Boblos B., Delcher A., Deng Z., Mays A.D., Dew I. Dietz S.M.,

RA Boblos B., Delcher A., Gorne G.C., Ferraz C., Ferrac C., Ferrac C., Serrica S., Pleischmann W.,

RA Houston K.J., Brangalista C.C., Ferraz C., Ferrac C., Serrica S., Plaischmann W.,

RA Houston K.J., Houston K.J., Mary M.A., May M.H., Ibegwam C.,

Alali M., Kalush F., Karpen G.H., Ke Z., Kanpison J.A., Ketchum K.A.,

Alali M., Kalush F., Karpen G.H., Ke Z., Kanpison J.A., Matteri B.L., Kodira C.D., Kraft C., Kratt E.S., Kulp D., Lai Z.,

Liu X., Mattei B.L., McIntosh T.C., McLeod M.P., Mary D.M., Nalson D.L.,

Rabon D.R., Moy M., Murphy B., Murphy L., Murny D.M., Nalson D.L.,

Rabon D.R., Nalson W.R., Nixon K.N., Wassern D., Puri V., Rese M., Shin E.,

Syleras R., Spadilan A.C., Stapleton M., Strong R., Sun E.,

Syleras R., Spadilan A.C., Stapleton M., Strong R., Sun E.,

Syleras R., Spadilan A.C., Shan M., Shon W., Sunber M., Shin R., Sheng X., Wasserman D.A., Weinschoef S., Shon W., Silen K., Shon W., Wang Z.Y., Wasserman D.A., Weinschoef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE=22426065; PubMed=12537568;

MEDLINE=22426065; PubMed=12537568;

Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,

Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,

George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,

Pacled J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,

Svirskas R., Tabor P.E., Wan K., Stapheton M., Sutton G.G., Venter C.,

Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;

"Finishing a whole-genome shotgun: Release 3 of the Drosophila

melanogaster euchromatic genome sequence.",

Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E., "The transposable elements of the Drosophila melanogaster euchromatin: a genomics perspective.";
Genome Biol. 3.RESEARCH0084-RESEARCH0084 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; brosophila.,
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=22426070; Pubmed=12537573;
                                                                                                                SEQUENCE FROM N.A.
  ö
                                                                                                                                                                                                                                                                                                                          (Potential)
                          (Potential)
                                                                                                                                                                                                                                      (Potential)
                                                                                                                                                                                                                                                         (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                              EGF-11ke 26.
EGF-11ke 27.
EGF-11ke 29.
EGF-1
                                                                                                                                                                             Laminin G-like 3.
EGF-like 22.
EGF-like 23, calcium-binding
EGF-like 24, calcium-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08 1; LC...
2.8e+02;
5; Indels
                     calcium-binding calcium-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                      Laminin G-like 2.
EGF-like 21.
Laminin G-like 3.
                                                                                           Laminin G-like 1.
EGF-like 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 2146 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
EGF-like 16.
EGF-like 17,
EGF-like 18,
EGF-like 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1826 GFEGQHCEQNIDECADQPCHNGGNC 1850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 XIXNOXCXOXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sec
01-MAR-2004 (TrEMBLrel. 26, Last anr
CG6383-Pa.
Name=crb, ORFNames=CG6383;
Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 28.0%,
To Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
902
940
978
1021
1205
1243
1480
1517
1758
1758
1795
1833
                                                                                                                                                                                                                                                                          1915
1915
1989
2029
2010
201
302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      610
634
634
673
673
702
7111
98.40

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98.00

98
                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULPID
DISULPID
DISULPID
                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9VC97
Q9VC97;
                                                                                                                                                                                                       DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                              DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
09VC97
1D 09VC9
AC 09VC9
DT 01-MA
DT 01-MA
DT 01-MA
DT 01-MA
DF 01-MA
DF 01-MA
DF 01-MA
DF 01-MA
```

8 g

```
Name=notchla; Synonyms=notch;
                                                                                                                                                                                              FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   head regions.
                                                                                                                                                                                              SEQUENCE
                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell po. . .; IMP. polarit. . .; IMP. polarit. . .; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                          Trypasse; Fapploutouses, crb.

BY GO: GO: 0016324; C: apical plasma membrane; NAS.

BY GO: GO: 0016327; C: apical plasma membrane; NAS.

BY GO: GO: 0016327; C: apical plasma membrane; IDA.

BY GO: GO: 0016327; C: apical complex; TAS.

BY GO: GO: 00163203; C: subapical complex; TAS.

BY GO: GO: 0016329; P: sectablishment and/or maintenance of polarit. . ; III

BY GO: GO: 0016332; P: setablishment and/or maintenance of polarit. . ; III

BY GO: GO: 001634; P: setablishment and/or maintenance of polarit. . ; III

BY GO: GO: 001634; P: setablishment of epithelial cell polarit. . ; III

BY GO: GO: 001634; P: membrane organization and biogenesis; TAS.

BY GO: GO: 001644; P: membrane organization and biogenesis; TAS.

BY GO: GO: 001644; P: membrane organization; TAS.

BY GO: GO: 001644; P: protein localization; TAS.

BY GO: GO: 001431; P: protein localization; TAS.

BY GO: GO: 001431; P: protein localization; TAS.

BY GO: GO: 001431; EGF Z.

BY InterPro: IPRO01821; EGF Z.

BY InterPro: IPRO01831; EGF Z.

BY InterPro: IPRO01831; EGF Z.

BY InterPro: IPRO01943; EGF Z.

BY InterPro: IPRO01943; EGF Z.

BY Flam; PF000054; Lamïnin G.

BY Flam; PF000054; Lamïnin G.

BY Flam; PF00019; EGFELÖDE.

BY SWART; SWOO282; Lamïnin G.

BY SWART; SWOO282; Lamïnin G.

BY SWART; SWOO282; Laminin G.

BY SWART; SWOO282; Laminin G.

BY SWART; SWOO282; Laminin G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
  Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                        "Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.8%; Score 67; DB 2; Length 2146; 28.0%; Pred. No. 2.8e+02; ive 13; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                  Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003747; AAF56276.1; -.
HSSP; P00740; 1EDM.
                                                                                                                                                                                                                   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2146 AA; 233570 MW; 8E23B9E32B761115 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NTC1 BRARE
ID PAGE A STANDARD; PRT; 2437 AA.
AC 946530,
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 02-JAN-2005 (Rel. 46, Last annotation update)
DE Neurogenic locus notch homolog protein 1 precursor.
                                                                                            systematic review.";
Genome Biol. 3:RESEARCH0083-RESEARCH0383(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : | : | : | : | : | : | : | : | 1823 GFEGQHCEQNIDECADQPCHNGGNC 1847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWART, SW00283, Lang, 3, 11.

PROSITE; PS00010; ASX HYDROXYL; 16.

PROSITE; PS00010; BGF_1; 25.

PROSITE; PS0026; EGF_3; 17.

PROSITE; PS0026; EGF_3; 27.

PROSITE; PS01187; EGF_CA; 13.

PROSITE; PS0025; LAM_G_DOMAIN; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 XIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                  FlyBase; FBgn0000368; crb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 28.08
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
RAPER REPORT OF THE PROPERTY O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

```
Description of the control (Exchanging) for the control of the con
```

```
Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QTTQ52 PRELIMINARY, PRT; 2516 AA.
Q7TQ52;
01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
O1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Transmembrane receptor Notchl B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.8%; Score 67; DB 1; 30.0%; Pred. No. 3.1e+02; ive 13; Mismatches 4
                                similarity
similarity
similarity
similarity
similarity
similarity
similarity
similarity
similarity
                                                                                                                                                                                                                                                                                                                                                                                                                        similarity
similarity
similarity
similarity
similarity
similarity
similarity
similarity
similarity
similarity
similarity
similarity
similarity
similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CXIXN----QXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |: :| :| :| :::::| CVCVNGWTGDDCSENIDDCASAACSHGATC
          Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata;
Mammalia, Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
   Query Match
Best Local Similarity
Matches 9, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1] SEQUENCE FROM N.A.
DISULFID
DIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERIOR DISTRICTOR DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 17
077052
1D 077055
AC 07705
DT 01-0C
DT 01-0C
DT 01-MB
DE Trans
DE Trans
CS Muss m
OC Mamma
OC
   g
                                                   Porential.

Extracellular (Potential).

Potential.

Cytoplasmic (Potential).

EGF-like 1.

EGF-like 4.

EGF-like 4.

EGF-like 5.

EGF-like 6.

EGF-like 8.

EGF-like 10.

EGF-like 11.

EGF-like 11.

EGF-like 12.

EGF-like 13.

EGF-like 13.

EGF-like 14.

EGF-like 15.

EGF-like 16.

EGF-like 17.

EGF-like 19.

EGF-like 19.

EGF-like 19.

EGF-like 10.

EGF-like 10.

EGF-like 10.

EGF-like 10.

EGF-like 20.

EGF-like 21.

EGF-like 21.

EGF-like 22.

EGF-like 23.

EGF-like 24.

EGF-like 25.

EGF-like 25.

EGF-like 25.

EGF-like 27.

EGF-like 27.

EGF-like 27.

EGF-like 28.

EGF-like 29.

EGF-like 20.

EGF-like 20.

EGF-like 20.

EGF-like 20.

EGF-like 21.

EGF-like 22.

EGF-like 23.

EGF-like 24.

EGF-like 25.

EGF-like 25.

EGF-like 26.

EGF-like 27.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Potential). (Potential). (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Potential)
Transcription regulation; Transmembrane. Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGF-like 25, Carcium-Dinding (Fouring EgF-like 26, EGF-like 26, EGF-like 29, EGF-like 29, EGF-like 29, EGF-like 30, Calcium-binding (Potent EGF-like 31, Calcium-binding (Potent EGF-like 32, EGF-like 33, EGF-like 34, EGF-like 34, EGF-like 35, Lin/Notch 1, Lin/Notch 1, Lin/Notch 2, ANK 1, ANK 2, ANK 3, ANK 4, ANK 5, EGF-like 36, EGF-like 36, EGF-like 37, EGF-like 37, EGF-like 38, EGF-like 39, EGF-like 39, EGF-like 36, E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       981
10057
10095
11143
11265
11365
11365
11446
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11487
11
Receptor; Figure 1 CHAIN CHAIN DOWAIN DOWAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERPRETARION DISCUELLO D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
DOMAIN
DOMAIN
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
```

ä

us-10-627-685a-1.rup

```
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NTC1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 19
                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

STRAIN=C.B-17; TISSUE=Thymus;
X MEDLINE=27551392; PubMed=1280718; DOI=10.1093/carcin/bgg071;
X MEDLINE=22753192; PubMed=1280718; DOI=10.1093/carcin/bgg071;
A Tutji H., Ishii-Ohba H., Ukai H., Katsube T., Ogiu T.,
T "Radiation-induced deletions in the 5' end region of Notchl lead to the formation of truncated proteins and are involved in the favelopment of mouse thymic lymphoma.";
T development of mouse thymic lymphoma.";
T development of mouse thymic lymphoma.";
Carcinogenesis 24:1257-1268(2003).

R BNBL; AB106603; BAC77039.1;
R HSSP;"POT207; 10778.

R GO: GO:001621; C:integral to membrane; IEA.

R GO: GO:0016221; C:acceptor activity; IEA.

R GO: GO:0004872; F:receptor activity; IEA.

R GO: GO:0030154; P:cell differentiation; IEA.
                                                                                                    t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                       MEDLINE-22753192; PubMed=12807718; DOI=10.1003/carcin/bgg071; Tsuji H., Ishii-Ohba H., Ukai H., Katsube T., Ogiu T.; Radiation-induced deletions in the 5' end region of Notchi lead the formation of truncated proteins and are involved in the development of mouse thymic lymphoma."; Carcinogenesis 24:1257-1268(2003).

EMBL; AB100603; BAC77038.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.8%; Score 67; DB 2; Length 2516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANK repeat; EGF-like domain; Receptor; Transmembrane.
SEQUENCE 2516 AA; 269177 MW; 17FD72740EBD6E35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30.8%; Pred. No. 3.2e+02;
ive 12; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                       GO; GO:0016021; Citiegral to membrane; IEA.
GO; GO:0005509; F:calcium ion binding: IEA.
GO; GO:0004842; F:receptor activity; IEA.
GO; GO:000154; F:receptor activity; IEA.
GO; GO:0010154; F:receptor activity; IEA.
InterPro; IPR0001152; Asx hydroxyl_S.
InterPro; IPR000152; Asx hydroxyl_S.
InterPro; IPR000152; Asx hydroxyl_S.
InterPro; IPR000152; Asx hydroxyl_S.
InterPro; IPR000801; EGF_G.
InterPro; IPR000801; EGF_G.
InterPro; IPR0008001; Notch_region.
Pfam; PF000081; EGF, 31.
Pfam; PF00066; Notch, 3.
Ffam; PF00066; Notch, 3.
RAMRT; SM00248; ANK; 6.
SWART; SM00179; EGF CA; 4.
R PROSITE; PS00010; ASX_HYDROXYL; 22.
R PROSITE; PS00010; ASX_HYDROXYL; 22.
R PROSITE; PS001186; EGF_2; 27.
R PROSITE; PS00186; EGF_2; 27.
R PROSITE; PS01186; EGF_2; 27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 2526 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233 GFAGQNCEENVDDCPGNNCKNGGACV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 XIXNQXCXQXLDDCCSXXCNXXXXX 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07TQ51 PRELIMINARY; PRT; 3
07TQ51;
01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane receptor Notchl D.
STRAIN=C.B-17; TISSUE=Thymus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 30.8% Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 18
07705:
AC 07705:
AC 07705:
AC 07705:
DT 01-0C
DT 01-0C
DT 01-0C
DT 01-0C
DX NUB mell
OC BURARY
OC BURARY
OC BURARY
OC RURARY
OC STRAILS
RA MEDLII
RA MEDLII
RA MEDLII
RA MEDLII
RA TRADII
RA TRADII
RA CARCIII
RE 
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

```
NTCI MOUSE STANDARD, PRT, 2531 AA.

001705; Q06007; Q61905; Q99JC2; Q9QW58; Q9R0X7;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1996 (Rel. 33, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Neurogenic locus notch homolog protein 1 precursor (Notch 1) (Motch A) (MI14) (p300).

Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Embryo;
MEDLINE=93194170;
PubMed=8449489;
MEDLINE=93194170;
PubMed=8470;
Copeland Amo F., Gendron-Maguire M., Swiatek P.J., Jenkins N.A.,
Copeland N.G., Gridley T.,
"Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of Drosophila Notch.";
Genomics 15:259-264(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1551-1647 FROM N.A. (ISOFORM 1), AND DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 731-1899 FROM N.A. (ISOFORM 2), AND DEVELOPMENTAL STAGE. STRAIN=CD-1; TISSUE=Embryo;
MEDLINE=93050801; PubMed=1426644;
Reaume A.G., Conlon R.A., Zirngibl R., Yamaguchi T.P., Rossant J.;
"Expression analysis of a Notch homologue in the mouse embryo.";
Dev. Biol. 154:377-387(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    readico del Amo F., Smith D.E., Swiatek P.J., Gendron-Maguire M., Steenspan R.J., MoMahon A.P., Gridley T.;
"Expression patiern of Motch, a mouse homolog of Drosophila Notch, suggests an important role in early postimplantation mouse development.";

Development 115:737-744(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                  R InterPro; IPR001842; EGF 2.

R InterPro; IPR001841; EGF 2.

R InterPro; IPR001841; EGF 2.

R InterPro; IPR001891; EGF 2.

R InterPro; IPR000809; EGF 1ike.

R InterPro; IPR000809; EGF; 31.

Pfam; PF00008; EGF; 31.

R Pfam; PF00006; NotCh; 3.

R SMART; SM00179; EGF CA; 4.

R SMART; SM00179; EGF CA; 2.

R SMART; SM00179; EGF CA; 2.

R SMART; SM00179; EGF CA; 2.

R PROSITE; PS50081, ANK REPAT; 4.

R PROSITE; PS50081, ANK REPAT; 4.

R PROSITE; PS50010; ASX HYDROX'L; 22.

R PROSITE; PS50010; ASX HYDROX'L; 22.

R PROSITE; PS50010; ASX HYDROX'L; 22.

R PROSITE; PS50010; EGF 2; 27.

R PROSITE; PS500186; EGF 2; 27.

R PROSITE; PS501187; EGF 24, 21.

W ANK repeat; EGF-1ike Gonain; Receptor; Transmembrane.

O SEQUENCE 2526 AA; 270583 MW; 017563FCE9703264 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.8%; Score 67; DB 2; Length 2526; 30.8%; Pred. No. 3.2e+02; ive 12; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 GFAGQNCEENVDDCPGNNCKNGGACV 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 XIXNOXCXQXLDDCCSXXCNXXNXCV 27
IPR000742; EGF 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Embryo;
MEDLINE=93048835; PubMed=1425352;
Franco del Amo F., Smith D.E., Swi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 30.8% les 8; Conservative
```

ö

us-10-627-685a-1.rup

wide

```
MEDLINE=98029496; PubMed=9384671; Messerle M., Follo M., Nehls M., Eggert H., Boehm T.; Messerle M., Follo M., Nehls M., Eggert H., Boehm T.; Bynamic changes in gene expression during in vitro differentiation of mouse embryonic stem cells. Therefore Cytokines Cell. Mol. Ther. 1:139-143(1995).
                                                                                                                                                              SEQUENCE OF 1659-1673 FROM N.A.
MEDLINE=99364499; PubMed=10437788; DOI=10.1016/S0014-5793(99)00901-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [11]
INTERACTION WITH DTX1 AND DTX2.
MEDLINE=21123790; PubMed=11226752; DOI=10.1016/S0736-5748(00)00071-X;
Kishi N., Tang Z., Maeda Y., Hirai A., Mo R., Ito M., Suzuki S.,
Nakao K., Kinoshita T., Kadesch T., Hui C.-C., Artavanis-Tsakonas S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse notch: expression in hair follicles correlates with cell fate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUTAGENESIS OF 1651-ARG--ARG-1654.
MEDLINE=98318619; PubMed=9653148; DOI=10.1073/pnas.95.14.8108;
Logeat F., Bessia C., Brou C., LeBail O., Jarriault S., Seidah N.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Okano H., Matsuno K.;
"Murine homologs of deltex define a novel gene family involved in vertebrate Notch signaling and neurogenesis.";
Int. J. Dev. Neuroseci. 19:21-35(2001).
-!- FUNCTION: Functions as a receptor for membrane-bound ligands Jaggedl, Jagged2 and Deltal to regulate cell-fate determination. Upon ligand activation through the released notch intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POST-TRANSLATIONAL PROCESSING.
MEDLINE=21374376; PubMed=11459941; DOI=10.1073/pnas.161269998;
Mizutani T., Taniguchi Y., Aoki T.; Hashimoto N., Honjo T.;
"Conservation of the biochemical mechanisms of signal transduction
SEQUENCE OF 1161-1547 FROM N.A. STRAIN-CSTBL/6 X CBA; TISSUB-Embryo; MEDLINE-93178561; PubMed-8440332; DOI=10.1006/excr.1993.1044; Lardelli M., Lendahl U.; Motch A and Motch B-two mouse Notch homologues coexpressed in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1865-2075 FROM N.A., AND DEVELOPMENTAL STAGE IN HAIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Notch1 receptor is cleaved constitutively by a furin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PARTIAL SEQUENCE, AND POST-TRANSLATIONAL PROCESSING.
MEDILINE=11523956; PubMed=11518718; DOI=10.1074/jbc.M107234200;
Saxena M.T., Schroeter E.H., Mumm J.S., Kopan R.;
"Murine notch homologs (N1-4) undergo presenilin-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1655-1659, CLEAVAGE BY FURIN-LIKE CONVERTASE, AND
                                                                                                                                                                                                      Lee J.S., Ishimoto A., Yanagawa S.I.;
"Murine leukemia provirus-mediated activation of the Notchl
to induction of HES-1 in a mouse T lymphoma cell line, DL-3.
FEBS Lett. 455:276-280(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      among mammalian Notch family members.";
Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 95:8108-8112(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=8486742; DOI=10.1083/jcb.121.3.631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biol. Chem. 276:40268-40273(2001).
                                                                                                                         Cell Res. 204:364-372(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell Biol. 121:631-641(1993).
                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1950-2201 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kopan R., Weintraub H.;
                                                                                                        of tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      determination."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteolysis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          convertase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [srael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
```

domain (NICD) it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus. Affects the implementation of differentiation, proliferation and apoptotic programs (By similarity). May play an essential role in postimplantation development, probably in some aspect of cell specification and/or differentiation. May be involved in mesoderm development, somite formation and neurogenesis. Involved in the

maturation of both CD4+ and CD8+ cells in the thymus. Important for follicular differentiation and possibly cell fate selection

between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). This SWISS-PROT entry is copyright. It is produced through a collaboration y, MGI:97363; Notchl.
G0:0005887; C:integral to plasma membrane; IC.
G0:0005154; F:protein binding; IPI.
G0:0007154; F:protein title frentiation; IMP.
G0:0007386; P:compartment specification; IMP.
G0:0007386; P:compartment specification; IMP.
G0:0007319; P:Notern signaling pathway; IC.
G0:0045944; P:positive regulation of transcription from P. . .; IDA.
G0:0048103; P:somatic stem cell renewal; IDA. terminal fragment N(EC) which are probably linked by disulfide bonds. Interacts with DTX1 and DTX2.
SUBCELLULAR LOCATION: Type I membrane protein. Following proteolytical processing NICD is translocated to the nucleus. VSP_001403, VSP_001404; within the follicle. SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EC) which are probably linked by disulfi Event=Alternative splicing; Named isoforms=2; -i- SIMILARITY: Belongs to the NOTCH family.
-i- SIMILARITY: Contains 5 ANK repeats.
-i- SIMILARITY: Contains 36 EGF-like domains.
-i- SIMILARITY: Contains 3 Lin/Notch repeats. IsoId=001705-2; Sequence=VSP 001402, IsoId=Q01705-1; Sequence=Displayed; EMBL; Z11886; CAA77941.1; -. AJ238029; CAB40733.1; -X82562; CAA57909.1; -. L02613; AAK14898.1; -. X68278; CAA48339.1; -. -!- PTM: Phosphorylated. from the membrane PIR, A46019; A46019. PIR, B49175; B49175. HSSP; P46531; 1PB5. Name=1 EMBL; 8888888 ġ

```
ö
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21094508; PubMed=11182080; DOI=10.1016/S0896-6273(01)00179-9;
Tanigaki K., Nogaki F., Takahashi J., Tashiro K., Kurooka H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Notch and Notch3 instructively restrict bFGE-responsive multipotent neural progenitor cells to an astroglial fate."; Neuron 29:45-55(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21331789; PubMed=11438922; DOI=10.1002/cne.1059.abs; Irvin D.K., Zurcher S.D., Nguyen T., Weinmaster G., Kornblum H.I.; "Expression patterns of Notch1, Notch2, and Notch3 suggest multiple functional roles for the Notch-DSL signaling system during brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Comp. Neurol. 436:167-181(2001).
                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Neurogenic locus notch homolog protein 1 precursor (Notch 1)
                                                                                                                                                                                                                                                                                                            55.8%; Score 67; DB 1; Length 2531; 30.8%; Pred. No. 3.2e+02; Live 12; Mismatches .6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Schwann cell,
MEDLINE=92111383; PubMed=1764995;
Weinmaster G., Roberts V.J., Lemke G.;
"A homolog of Drosophila Notch expressed during mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Weinmaster G.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 2531 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE SPECIFICITY.
MEDLINE-93202015; PubMed=1295745;
Medimaster G., Roberts V., Lemke G.;
"Notch2: a second mammalian Notch gene.";
Development 116:931-941(1992)
                                                                                                                                                                                                                                                                                                                                                                                                              248 GFAGQNCEENVDDCPGNNCKNGGACV 273
                                                                                                                                                                                                                                                                                                                                                                                      2 XIXNOXCXQXLDDCCSXXCNXXNXCV 27
                  Asx hydroxyl_S.
EGF_2.
EGF_Ca.
EGF_II.
                                                                                                                                               InterPro; IPR000800; Notch_region.
                                                                                                                                                                   Pfam; PF00023; Ank; 7.
Pfam; PF00023; Ank; 35.
Pfam; PF00008; EGF; 35.
Pfam; PF00066; Notch; 1.
Plam; PF00066; Notch; 3.
PIRSF; PIRSF002279; Notch; 1.
PRINTS; PR01415; ANKYRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       development.", Development 113:199-205(1991),
                                                                                                                                    InterPro; IPR008297; Notch.
                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REVISIONS TO 1652-1653,
                                                                             PR001438;
                                                                                                InterPro; IPR006209;
                                                                                                                  InterPro, IPR010660;
                                                         InterPro, IPR001881;
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                development.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=Notch1;
                                                                             InterPro; ]
                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NTC1 RAT
007008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION
ò
                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACREA REPORTED TO THE SERVICE OF THE
```

```
contribution in the control of the control of the control of contr
```

```
. .; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=BALB/c; TISSUE=Thymus;
MEDLINE=22119993; PubMed=12123574; DOI=10.1016/S0960-9822(02)00888-6;
FOLTZ D.R., Santiago M.C., Berechid B.E., Nye J.S.;
"Glycogen synthase kinase-3beta modulates notch signaling and
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CSTRAIN-BALB/C; ITSSUE-Thymus;
CSTRAIN-BALB/C; ITSSUE-Thymus;
CSTRAIN-BALB/C; ITSSUE-Thymus;
CSCRAIN-BALB/C; ITSSUE-Thymus;
CSCRAIN-BALB/C; ITSSUE-Thymus;
CSCRAIN-BALB/C; ITSSUE-Thymus;
CSCRAIN-BALB/C; ITSSUE-Thymus;
CSCRAIN-BALB/GB09; AAAL8905.1; -..
CSCRAIN-BALB/GB09; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1] SEQUENCE FROM N.A.
SERQUENCE FROM N.A.
MEDLINE=95044925; PubMed=7956822;
Nye J.S., Kopan R., Axel R.;
"An activated Notch Suppresses neurogenesis and myogenesis but gliogenesis in mammalian cells.";
Development 120:2421-2430(1994).
                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                      Length 2531;
                                                                                                                                                                                                                                  Score 67, DB 1; Length 253; Pred. No. 3.2e+02; 12; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                    By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 2531 AA
                                                                                                                                                                                                                                                                                                                                 248 GFAGONCEENVDDCPGNNCKNGGACV 273
                                                                                                                                                                                                                                                                                                            2 XIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002110; ANK.
InterPro; IPR000152; Asx hydroxyl_S.
InterPro; IPR00742; EGF_2.
InterPro; IPR001881; EGF_Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      stability.";
Curr. Biol. 12:1006-1011(2002)
                                                                                                                                                                                                                                      55.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8K428 PRELIMINARY;
Q8K428;
01-0CT-2002 (TEMBLrel. 22,
01-0CT-2002 (TEMBLrel. 22,
01-MAR-2004 (TEMBLrel. 26,
                                                                                                                                                                                                                                    Query Match
Best Local Similarity 30.8
Matches 8; Conservative
                                                                      117
127
127
138
155
164
175
175
175
175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Notch 1 protein.
Name=Notch1;
                                                                      DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 21
                                                                                                                                                                                                                                                                                                                                                                                                                      Q8K428
                                                                        ttttttt
                                                                                                                                                                                                                                                                                                              ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                           (Potential).
(Potential).
(Potential).
(Potential).
(Potential).
(Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Potential). (Potential). (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Potential). (Potential). (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Potential) (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                       BGF-like 4.
BGF-like 5, calcium-binding (Potential).
EGF-like 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            calcium-binding (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Potential)
                                                                                                                                                                                                                  Potential.
Neurogenic locus notch homolog protein
Notch extracellular truncation (By
similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Poly-Ala.
Poly-Glu.
Poly-Pro.
Poly-Ser.
Cleavage (by furin-like protease)
                                                                                                                                                                                                                                                                                         Notch intracellular domain (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   calcium-binding (calcium-binding (calcium-binding calcium-binding calcium-binding (calcium-binding calcium-binding calcium-bin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     calcium-binding calcium-binding calcium-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              calcium-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                calcium-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7, calcium-binding
8, calcium-binding
9, calcium-binding
                                                                                                                                                                                                                                                                                                                             Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                           Cytoplasmic (Potential).
EGF-like 1.
EGF-like 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity.
similarity.
similarity.
similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGF-like 31, c
EGF-like 31, c
EGF-like 32, c
EGF-like 33.
EGF-like 34.
EGF-like 35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGF-like 18, 6
EGF-like 20, 6
EGF-like 21, 6
EGF-like 22, 6
EGF-like 23, 6
EGF-like 24, 6
EGF-like 25, 6
EGF-like 25, 6
EGF-like 25, 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lin/Notch 1.
Lin/Notch 2.
Lin/Notch 3.
ANK 1.
ANK 2.
ANK 3.
ANK 4.
                                                                                                                                                                                                                                                                                                              similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGF-like 1
EGF-like 1
EGF-like 1
                                                                                                                                                                                                                                                                                                                                                Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ****
                                                                                                                                                                                                                                                                                                                                                                                  58
139
1739
2293
3333
341
4410
4410
601
639
676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7114.
751
789
827
867
965
943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1019
1057
1095
11143
11143
11143
1265
1305
1305
1384
1426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37
46
74
87
98
                                                                                                                                                                                                                                                                                         1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              945
1021
1021
1097
1145
11183
1221
1221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1523
1917
1950
1984
2017
2050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24
31
48
68
68
                                                                                                                                                                                                                                                                                                                                            TRANSMEM
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIAMOC
                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
```

Gaps

```
MEDLINE=20054100; PubMed=10585570; DOI=10.1016/S0925-4773(99)00231-2; Smithers L.E., Haddon C., Jiang Y.-J., Lewis J.; "Sequence and embryonic expression of deltaC in the zebrafish.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=dlc; Synonyms=delC;
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                         'Match 55.8%; Score 67; DB 2; Length 2531;
Local Similarity 30.8%; Pred. No. 3.2e+02;
Les 8; Conservative 12; Mismatches 6; Indels
                                                                        PROSITE; PSS0019, ANK REPEAT; 4.

PROSITE; PSS029; ANK_REP_REGION; 1.

PROSITE; PS00010; ASX HYDROXYL; 22.

PROSITE; PS01186; EGF_2; 27.

PROSITE; PS01186; EGF_2; 27.

PROSITE; PS01187; EGF_CA; 21.

ANK repeat; EGF-11ke Gomain; Receptor; Transmembrane.

SEQUENCE 2531 AA; 270832 WW; 97C91F69BABF02BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        664 AA; 72547 MW; 0AD6C34C8579116B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-007-2000 (TrEMBLrel. 15, Created)
01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-MRR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h
Similarity 30.8%; Pred. No. 1.2e+02;
8; Conservative 11; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 GFAGQNCEENVDDCPGNNCKNGGACV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 XIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00010; EGFBLCOD.
SNART; SN00051; DSL; 1.
SNART; SN00179; EGF CA; 4.
PROSITE; PS001019; ASX HYDROXYL; 2.
PROSITE; PS01186; EGF 1; 8.
PROSITE; PS01186; EGF 2; 8.
PROSITE; PS01187; EGF 2; 8.
PROSITE; PS01187; EGF 3; 6.
PROSITE; PS01187; EGF 3; 6.
                           SMART; SM00179; EGF_CA; 25.
SMART; SM00004; NL; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O9IAT6
ID Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PH THE PARTY SERVICE OF SERVICE O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRAIN=C.B-17; TISSUE=Thymus;

X STRAIN=C.B-17; TISSUE=Thymus;

X WEDDLINE=2775132; PubMed=12807718; DOI=10.1093/carcin/bgg071;

X WEDLINE=2775132; PubMed=12807718; DOI=10.1093/carcin/bgg071;

X Tauji H., Ishii-Ohba H., Ukai H., Katshub T., Ogiu T.;

RT faction-induced deletions in the 5' end region of Notch1 lead to the formation of truncated proteins and are involved in the formation of truncated proteins and are involved in the Gevelopment of mouse thymic lymphoma.";

R development of mouse thymic lymphoma.";

R development of mouse thymic lymphoma.";

R Gavelopment of mouse thymic lymphoma.";

R RBBL; AB100603; BAC77040.1;.-

DR RSSP; POT207; 1078.

GO; GO:001621; C:integral to membrane; IEA.

BR GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:0005509; F:calcium ion binding; IEA.

BR GO; GO:0005124; F:caceptor activity; IEA.

BR GO; GO:0005124; F:caceptor activity; IEA.

BR GO; GO:0005124; F:caceptor activity; IEA.

BR CO: GO:000125; ABC D.

BR THCEPPO; IPRO0182; ABC D.

BR REAM: PRO0008; EGF Jike.

BR FEAM: PPO0008; EGF Jike.

BR FEAM: PPO0008; EGF Jike.

BR FEAM: PPO0006; NOtCh. region.

BR FEAM: PPO0066; NotCh. 3.

SWART; SMO2148; ANK; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                    Query Match 55.8%; Score 67; DB.2; Length 2531; Best Local Similarity 30.8%; Pred. No. 3.2e+02; Matches 8; Conservative 12; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Transmembrane receptor Notchl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 2531 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248 GFAGQNCEENVDDCPGNNCKNGGACV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 XIXNOXCXQXLDDCCSXXCNXXNXCV 27
InterPro; IPR001438; EGF II.
InterPro; IPR006209; EGF Iike.
InterPro; IPR008297; Notch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
```

RESULT 22
077050
D77050
D77050
D7 01-07050
D8 Mus m month of the month of th

Query Match

DR DR DR KW KW KW KW SO

ô

```
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haiteh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Robak S.A., McEwan P.J., McKernan R.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriquez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalsku U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.,
Shan M.D., Smailus D.E., Schnerch A., Schein J.E.,
Rodriquez A., Garcia M.A., Romer M.A.,
Jones S.J., Marra M.A.,
Shan M.D., Smailus D.E., Schnerch A., Schein J.E.,
Rodriquez A., Garcia M.A.,
Rodriquez A., Garcia W.A.,
Rodriquez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriquez A., Marra M.A.,
Rodriquez A., Schnerch A., Schein J.E.,
Rodriquez A., Marra M.A.,
Rodriquez A., Schein J.E.,
Rodriquez A., Gardiwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriquez A., Marra M.A.,
Rodriquez A., Gardiwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriquez A., Marra M.A.,
Rodriquez A., Schnerch A., Schein J.E.,
Rodriquez A., Gardiwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriquez A., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa; Arthropoda; Harapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.0%; Score 66; DB 2; Length 1317; 25.8%; Pred. No. 2.2e+02; tive 14; Mismatches 5; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 28 EGF-like domains.
EMBL; BC071562; AAH71562.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1317 AA; 140756 MW; 1A2674F4AF001646 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0005509; F:calcium ion binding; IEA.
InterPro; IPR00152; Asx hydroxyl_S.
InterPro; IPR00142; BGF_Ca.
InterPro; IPR001438; BGF_II.
InterPro; IPR001438; BGF_II.
InterPro; IPR005209; BGF_II.
InterPro; IPR006209; BGF_I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                406 CVCVNGWSGDDCSENIDDCAFASCTPGSTCI 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CXIXN----QXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1551 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00181; EGF; 31.
SMART; SM00179; EGF_CA; 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00010; EGFBLOOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 25.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00010; ASX
PROSITE; PS00022; EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=SP1070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9NGV4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9NGV4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SP1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9NGV4
           유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. Macd=7596411; DOI=10.1038/37578780; MEDLINE-95319507; PubMed=7596411; DOI=10.1038/37578780; Henrique D., Admu J., Myat A., Chitnis A., Lewis J., Ish-Horowicz D.; Expression of a Delta homologue in prospective neurons in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=95319503; PubMed=7596407; DOI=10.1038/375761a0;
Chitnis A., Henrique D., Lewis J., Ish-Horowicz D., Kintner C.;
Frinary neurogenesis in Xenopus embryos regulated by a homologue of the Drosophila neurogenic gene Delta.";
Nature 375:761-766(1995).
REMBL; L42229; ASG38017.1; -.
HSSP; P00740; IEDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                        Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Testis;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.0%; Score 66; DB 2; Length 721; 32.0%; Pred. No. 1.3e+02; ive 11; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             721 AA; 79922 MW; 9EBDC85C439DD194 CRC64;
                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0016020; C:membrane; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0007154; P:cell communication; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36 GFSGRNCDDNLDDCTSFPCQNGGTC 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 XIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00010; ASX HYDROXXL; 3. PROSITE; PS00022; BGF 1; 8. PROSITE; PS01186; BGF 2; 8. PROSITE; PS50126; BGF 3; 6. PROSITE; PS01187; EGF_CA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01414; DSL; 1.
Pfam; PF00008; EGF; 6.
PRINTS; PR00010; EGFBLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTCH2 protein (Fragment).
Name=NOTCH2;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00051; DSL; 1.
SMART; SM00179; EGF_CA; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 375:787-790(1995).
                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                            Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS01187;
EGF-like domain.
SEQUENCE 721 AA
                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q6IQ50;
                                                                                                               091902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              061050
                                                       RESULT 24
Q91902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 25
061050
DD 061051
DD 061051
DD 05-JUI
DD 061051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
```

Gapa

ઠ В

```
279 CVCVNGWSGLDCSENIDDCDTAACSPGSTCV 309
                                                                                                                                                                                                                                                                                   1 CXIXN----QXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    variety of tissues.";
Exp. Cell Res. 204:364-372(1993).
                                                                                                                                                                                                                                                    Best Local Similarity 29.09
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                        Name=Notch2;
                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UNCTION.
                                                                                                                                                                                                                                                                                                                                   RESULT 28
NTC2 MOUSE
        g
                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL.1997 (TrEWBLrel. 04, Created)
01-JUL.1997 (TrEWBLrel. 04, Last sequence update)
01-JUL-1997 (TrEWBLrel. 26, Last annotation update)
01-MAR-2004 (TrEWBLrel. 26, Last annotation update)
Notch 2 (Fragment)
Fugu rubripes (Japanese pufferfish) (Takifugu rubripes)
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Buteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                            Query Match 55.0%; Score 66; DB 2; Length 1551; Best Local Similarity 33.3%; Pred. No. 2.6e+02; Matches 8; Conservative 11; Mismatches 5; Indels
        TISSUE-Endoplasmic reticulum;
Serano T.L., Pendleton J.D., Rubin G.M.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AR236081 AAR63500.1;
FILYBASES, FBGH0031879; SP1070.
GO; GO:0005198; F:calcium ion binding; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
                                                                                                                                                                                                                                                                                                         1551 AA; 167816 MW; A97EA229E9384F31 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nakamura T., Trowsdale J.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases
EMBL, ABO048929; BAAZ0535.1; -.
HSSP, P07207; 1078.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0016020; C:membrane; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0030154; P:cell differentiation; IEA.
GO; GO:0050793; P:regulation of development; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 24.47 AA.
                                                                                            InterPro; IPR002111; ANK.
InterPro; IPR00152; Asx hydroxyl S.
InterPro; IPR008965; Conh like_lec_gl.
InterPro; IPR00142; EGF Z.
InterPro; IPR001881; EGF Ca.
InterPro; IPR001438; EGF_II.
InterPro; IPR001439; EGF_II.
                                                                                                                                                                                                                                                                                                                                                                              278 TGKNCQHTIDDCASNPCQHGATCV 301
                                                                                                                                                                                                                                                                                                                                                                  4 XNOXCXOXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                             PROSITE; PS00022; EGF 1; 15; PROSITE; PS01186; EGF 2; 12; PROSITE; PS50026; EGF 3; 15; PROSITE; PS50026; EGF 3; 15; PROSITE; PS50825; HYR; 1; EGF-11ke domain.

SEQUENCE 1551 AA; 167816 M
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                    013149
                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

```
SEQUENCE OF 316-1518 FROM N.A.
STRAIN=GS7BL/6 X CBA; TISSUB=Embryo;
MEDLINE-9317863; PubMed=8440332; DOI=10.1006/excr.1993.1044;
Lardelli M., Lendahl U.;
"Morch A and Motch B-two mouse Notch homologues coexpressed in a wide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NTC2 MOUSE STANDARD; PRT; 2470 AA.
035516; Q06008; Q60941;
28-FEB-2003 (Rel. 41, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Neurogenic locus notch homolog protein 2 precursor (Notch 2) (Motch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-CS7BL/6; TISSUE-Thymus;
Hamada Y., Higuchi M., Tsujimoto Y.;
"Complete amino acid sequence and mutliform transcripts encoded by single copy of mouse Notch2 gene.", Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1765-2153 FROM N.A.
MEDLINE-97075110; Pubmed-8917536; DOI=10.1073/pnas.93.23.13014;
Milner L.A., Bigas A., Kopan R., Brashem-Stein C., Bernstein I.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4
R InterPro; IPR008297; Notch.
R InterPro; IPR008000; Notch.
R Pfam; PF000023; Ank; 6.
Ffam; PF0000023; Ank; 6.
R Pfam; PF0000053; Ank; 6.
R Pfam; PF000066; Notch; 3.
R Pfam; PR000066; Notch; 3.
R Pfam; PR000066; Notch; 3.
R PRINTS; PR001415; ANKYRIN.
R PRINTS; PR001415; ANKYRIN.
R PRNTS; PR00179; EGFLOOD.
R SWART; SW00179; EGF_CA; 22.
SWART; SW00004; NL; 3.
R PROSITE; PS50098; ANK REPRAT; 4.
R PROSITE; PS50097; ANK REPRAT; 4.
R PROSITE; PS00010; ASX_HYDROXYL; 22.
R PROSITE; PS00119; EGF_1; 35.
R PROSITE; PS01186; EGF_2; 29.
R PROSITE; PS01187; EGF_1; 35.
R PROSITE; PS01187; EGF_04; 20.
W ANK repeat; EGF_11ke domain.
T NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.0%; Score 66; DB 2; Length 2447; 29.0%; Pred. No. 3.9e+02; Live 15; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Martin D.I.;
"Inhibition of granulocytic differentiation by mNotchl.";
Proc. Natl. Acad. Sci. U.S.A. 93:13014-13019(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-99396706; PubMed=10393120;
Hamada Y., Kadokawa Y., Okabe M., Ikawa M., Coleman J.R.,
```

;

commercial

and for

Usage by

```
modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00248; ANK; 6.
SMART; SM00179; EGF_CA; 23.
SMART; SM00004; NL; 3.
                                                                                                       PIR; A49175; A49175.
HSSP; Q9UCV4; 1NZI.
MGD; MGI:97364; Notch2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2470
1677
1698
2470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
102
143
180
219
256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26
1666
1697
26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are prestrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                          MEDLINE=21374376; PubMed=1145941; DOI=10.1073/pnas.16126998; Mizutani T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.; Conservation of the blochemical mechanisms of signal transduction among mammalian Notch family members, and signal transduction are among mammalian Notch family members, processed in transduction among mammalian Notch family members, so membrane-bound ligands Jagged2 and Deltal to require cell-fate determination. Upon ligand activate of the orbancer of split locus. Company Affects the implementation of differentiation, proliferation and apoptotic programs (By similarity). May play an essential role in specification and/or differentiation, some aspect of cell specification and/or differentiation fragment N(EW) and a C-terminal fragment N(EC) which are probably linked by disulfide
                                                                                          MEDLINE-95333893; PubMed-7609614; DOI=10.1016/0169-328X(94)00257-F; Higuchi M., Kiyama H., Hayakawa T., Hamada Y., Tsujimoto Y.; "Differential expression of Notch1 and Notch2 in developing and adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=035516-2; Sequence=VSP_001405; Note=NO experimental confirmation available; NISSUE SPECIFICITY: Expressed in the brain, liver, kidney, neuroepithelia, somites, optic vesicles and branchial arches, but not heart.
Tsujimoto Y.; ^{\prime} "Mutation in ankyrin repeats of the mouse Notch2 gene induces early embryonic lethality.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Type I membrane protein. Following proteolytical processing NICD is translocated to the nucleus. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                    POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS OF MET-1699. MEDINE=2153956; Pubmed=11518018; DOI=10.10/4/jbc.M107234200; Saxena M.T., Schreetr E.H., Mumm J.S., Kopan R.; Muzine notch homologs (NI-4) undergo presentlin-dependent
                                                                                                                                                                                                                                                                                                  POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS OF MET-1699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Belongs to the NOTCH family. SIMILARITY: Contains 6 ANK repeats. SIMILARITY: Contains 15 EGF-like domains. SIMILARITY: Contains 2 Lin/Notch repeats.
                                                                             DEVELOPMENTAL STAGE, AND ALTERNATIVE SPLICING
                                                                                                                                        mouse brain.";
Brain Res. Mol. Brain Res. 29:263-272(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=035516-1; Sequence=Displayed;
                                                                                                                                                                                                                                                      J. Biol. Chem. 276:40268-40273(2001).
                                             Development 126:3415-3424 (1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phosphorylated.
                                                                                                                                                                                                                                                     proteolysis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               +++
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>-</u>
```

```
CONTROLL SULLEGE, LSC.

R GO; GO:0005887; C:Integral to plasma membrane; IC.

R GO; GO:0005887; C:Integral to plasma membrane; IC.

R GO; GO:0005515; F:protein binding; IPI.

R GO; GO:0005515; F:protein binding; IPI.

R GO; GO:0001705; P:cell cycle arrest; ISS.

R GO; GO:0001709; P:cell growth; ISS.

R GO; GO:001709; P:cell growth; ISS.

R GO; GO:0001709; P:cell growth; ISS.

R GO; GO:0001709; P:development; ISS.

R GO; GO:0000275; P:hemopolesis; ISS.

R GO; GO:0000201; P:hemopolesis; ISS.

R GO; GO:0000201; P:morphogenesis of apoptosis; ISS.

R GO; GO:0007219; P:morphogenesis; ISS.

R GO; GO:0007219; P:neurogenesis; ISS.

R GO; GO:0007219; P:neurogenesis; ISS.

R GO; GO:0007219; P:nourogenesis; ISS.
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Potential.
Murogenic locus notch homolog protein 2.
Notch extracellular truncation.
Notch intracellular domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGF-like 5, calcium-binding (Potential). EGF-like 6 (incomplete).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00022; EGF 1; 33.
PROSITE; PS00022; EGF 2; 27.
PROSITE; PS01186; EGF 2; 27.
PROSITE; PS01187; EGF 3; 35.
Activator; Alternative splicing; ANK repeat; Developmental protein; Differentiantion; EGF 1, 40.
Notch signaling pathway; Phosphorylation; Receptor; Repeat; Signal; Transcription regulation; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR00110; ANK.
InterPro; IPR00110; ANK.
InterPro; IPR00110; ANK.
InterPro; IPR001121; Agk. hydroxyl_S.
InterPro; IPR001138; EGF_I.
InterPro; IPR001438; EGF_II.
InterPro; IPR001891; EGF_II.
InterPro; IPR001660; NOD.
InterPro; IPR008297; Notch.
InterPro; IPR008297; Notch.
InterPro; IPR00800; Notch.
Ffam; PF00008; EGF; 34.
Pfam; PF00008; EGF; 34.
Pfam; PF00006; NOTCh; 2.
Pfam; PF00006; NOtch; 2.
Pfam; PF00006; NOtch; 2.
Pfam; PF00019; EGF; NOTCH; 3.
PRINTS; PR00110; EGFBLOOD.
PRINTS; PR01452; NOTCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50297; ANK REP REGION; 1. PROSITE; PS50088; ANK REPEAT; 4. PROSITE; PS00010; ASX_HYDROXYL; 22.
                                                                                                                                                                                                                                                                                                                                                                    GO:0009986; C:cell surface; ISS.
                                                                                                              EMBL, D32210; BAA22094.1; -. EMBL; X68279; CAA48340.1; -. EMBL; U31881; AAC52924.1; -.
```

us-10-627-685a-1.rup

```
ï
                                                                                                (Potential) (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Correa R.G., Camargo A.A., Moreira E.S., Simpson A.J.G., "Human Notch2, a novel member of cell-fate determining NOTCH family."; Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                  (Potential).
(Potential).
                                                                                                                                                                                                                                                                                                  (Potential)
                                                                                                                                                                                                                                                                                                                    (Potential)
                                                                                                                                                                                                          (Potential)
                                                                                                                                                                                                                                                      (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                            Potential
                                                                                                                                                              Potential
                                                                                                                                                                                     Potential
                                                                                                                                                                                                                                 (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93365135; PubMed=1303260; Stifani S., Blaumueller C.M., Redhead N.J., Hill R.E., Artavanis-Tsakonas S.; "Human homologs of a Drosophila enhancer of split gene product define a novel family of nuclear proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97386453; PubMed=9244302; DOI=10.1016/S0092-8674(00)80336-0; Blaumueller C.M., Qi H., Zagouras P., Artavanis-Tsakonas S.; "Intracellular cleavage of Notch leads to a heterodimeric receptor on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=T-cell;
Lemasson I., Devaux C., Mesnard J.M.;
"Partial sequence of EGF-like repeat domain of human Notch2 mRNA.";
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q04721, Q99734; Q9H240;
28-FFB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last amotation update)
25-JAN-2005 (Rel. 46, Last amotation update)
Neurogenic locus notch homolog protein 2 precursor (Notch 2) (hN2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryora; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutenria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                4
                    EGF-like 9, calcium-binding (PO EGF-like 9), calcium-binding (PO EGF-like 10.

EGF-like 11.

EGF-like 12, calcium-binding (PO EGF-like 12, calcium-binding (PO EGF-like 13, calcium-binding (PO EGF-like 14, calcium-binding (POF-like 16, calcium-binding (POF-like 16, calcium-binding (POF-like 17, calcium-binding (POF-like 19, calcium-binding (POF-like 19, calcium-binding (POF-like 19, calcium-binding (POF-like 20, calcium-binding (POF-like 21, calcium-bin
                                                                                                                                                                                                                                                                                                                                                                                  Length 2470;
    calcium-binding (calcium-binding (calcium-binding (
                                                                                                                                                                                                                                                                                                                                                                  Score 66; DB 1; L....
Pred. No. 3.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete human notch 2 (hN2) cDNA sequence.",
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   322 CVCVNGWSGDDCSENIDDCAYASCTPGSTCI 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CXIXN----QXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 2471 AA
                                                                                                                                                                                                                                                                                                                                                                                                                       14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1810-2447 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 967-1229 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POST-TRANSLATIONAL PROCESSING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Blaumueller C.M., Mann R.S.,
                                                                                                                                                                                                                                                                                                                                                                                                25.8%;
                                                                                                                                                                                                                                                                                                                                                                                55.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                   8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
  2294
3334
4111
4511
4511
558
6611
671
678
716
7753
7791
829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the plasma membrane."
Cell 90:281-291(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=NOTCH2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NTC2_HUMAN
                                                                                                                                                                                                                                                                                    DOMAIN
DOMAIN
DOMAIN
                    DOMAIN
                                                                                         DOMAIN
                                                                                                                                 DOMAIN
                                                                DOMAIN
                                                                                                            DOMAIN
                                                                                                                                                        DOMAIN
                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 29
NTC2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
PT
FT
FT
FT
FT
FT
FT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
```

```
GO; GO:0005887; C:integral to plasma membrane; IDA.
GO; GO:0005887; C:integral to plasma membrane; IDA.
GO; GO:0005634; C:integral to plasma membrane; IDA.
GO; GO:0005634; C:integral to plasma membrane; IDA.
GO; GO:0005106; F:ligand-regulated transcription factor activity; TAS.
GO; GO:00046982; F:protein herecadimerization activity; NAS.
GO; GO:0006816; P:anti-apoptosis; NAS.
GO; GO:0006816; P:anti-apoptosis; TAS.
GO; GO:000709; P:cell grade determination; TAS.
GO; GO:0001709; P:cell grade determination; TAS.
GO; GO:0001709; P:cell grade factoriation; TAS.
GO; GO:00005017; P:induction of apoptosis; TAS.
GO; GO:000517; P:induction of apoptosis; TAS.
GO; GO:0005285; P:negative regulation of cell proliferation; IDA.
GO; GO:0007399; P:neurogenesis; NAS.
GO; GO:0007399; P:neurogenesis; NAS.
GO; GO:0007399; P:neturogenesis; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              bonds (By similarity).

C --- SUBCELLULAR LOCATION: Type I membrane protein. Following proteolytical processing NICD is translocated to the nucleus. Proteolytical processing NICD is translocated to the nucleus. Skeletal muscle and liver.

--- TISSUE SPECIFICITY: Expressed in the brain, heart, kidney, lung, skeletal muscle and liver.

--- THM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in the an active, ligand-accessible form. Cleavage results in a C-terminal fragment N(TW) and a N-terminal fragment N(TW) and a N-terminal fragment N(TW) and a N-terminal fragment (INC). Following control to the fragment N(TW) and a N-terminal fragment called containing the intermediate fragment called containing the intermediate fragment is then notch extracellular truncation (NEXT). This fragment is then cleaved by presentlin dependent gamma-secretase to release a notch-derived peptide containing the intracellular domain (NICD) from the membrane (By similarity).

--- FPM: Phosphorylated (By similarity).

--- SIMILARITY: Contains 5 ANK repeats.

--- SIMILARITY: Contains 5 Lin/Notch repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                   Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L., Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.; Human ligands of the Notch receptor."; Am. J. Pethol. 154:785-794(1999).
-!- FUNCTION: Functions as a receptor for membrane-bound ligands Jaggedl, Jaggedl and Deltal to regulate cell-fate determination. Upon ligand activation through the released notch intracellular
                                                                                                                                                                                                                                                               Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with RBP-J kappe and activates genes of the enhancer of split locus. Affects the implementation of differentiation, proliferation and apoptotic programs (By similarity).
SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EC) which are probably linked by disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
[6]
IDENTIFICATION OF LIGANDS.
MEDLINE=99180765; PUDMed=10079256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO:0009986; C:cell surface; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AF308601, AAA36377.2; -. EBMBL, AF315356; AAG37073.1; -. EMBL; U77493; AAB19224.1; -. HSSP; P00740; 1EDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GG; GG:0005887; C:ntegral GG; GG:0005887; C:ntegral GG; GG:0005545; C:ntegral GG; GG:0005545; F:lgand-r. GG; GG:0005515; F:protein JG; GG:00046892; F:protein JG; GG:00046872; F:receptor GG; GG:000709; P:cell cycle; GG:0007109; P:cell cycle; GG:0007109; P:cell cycle; GG:0007109; P:cell cycle; GG:0007219; P:negative GG: GG:0007219; P:neurogene GG; GG:0007219; P:neurogene GG; GG:0007219; P:neurogene GG; GG:0007219; P:neurogene GG; GG:0007219; P:prostive GG; GG:0019827; P:stem cell InterPro; IPR002110; ANK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HGNC: 7882; NOTCH2.
```

ä

Gaps

```
development: ";

J. Comp. Neurol. 436:167-181(2001)

Jagged2 and Deltal to regulate cell-fate determination. Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus. Affects the implementation of differentiation and apoptotic programs. May play an essential role in postimplantation development, probably in some aspect of cell specification and/or differentiation (By similarity).

J. SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EC) which are probably linked by disulfide bonds (By similarity).

J. SUBCELLULAR LOCATION: Type I membrane protein. Following proteclytical processing NICD is translocated to the nucleus.

J. SUBCELLULAR LOCATION: Expressed in postnatal central neurous system (CNS) germinal zones and, in early postnatal life, within numerous cells throughout the CNS. It is more highly localized to be better and choroid and conticular germinal zones. Also found in the heart, liver and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEVELOPMENTAL STAGE: Expressed in the brain during E14 and E17. PTM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a Cterminal fragment N(TM) and a N-terminal fragment N(EC). Following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY.

MEDLINE=21331789; PubMed=11438922; DOI=10.1002/cne.1059.abb;
Irvin D.K., Zurcher S.D., Nguyen T., Weinmaster G., Kornblum H.I.;
"Expression patterns of Notch1, Notch2, and Notch3 suggest multiple functional roles for the Notch-DSL signaling system during brain development.";
                                                                                                                                                                                                                                                          4 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Neurogenic locus notch homolog protein 2 precursor (Notch 2)
                                                                                                                                                                                                            ; Score 66; DB 1; Length 2471; 
; Pred. No. 4e+02; 
14; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                      324 CVCVNGWSGDDCSENIDDCAFASCTPGSTCI 354
                                                                                                                                                                                                                                                                                             1 CXIXN----QXCXQXLDDCCSXXCNXXXX 27
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 2471 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Weinmaster G., Roberts V.J., Lemke G., "Notch2: a second mammalian Notch gene."; Development 116:931-941(1992).
                               Lin/Notch 1
Lin/Notch 2
ANK 1.
ANK 2.
ANK 3.
ANK 4.
ANK 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93202015; PubMed=1295745;
                                                                                                                                                                                                                  55.0%;
25.8%;
                                                                                                                                                                                                                                     Similarity 25.8 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                1412
1456
1535
1871
1905
1939
1972
2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
            1374
1503
1503
1827
1876
1909
1943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=Notch2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kidney.
                                                                                                                                                                                                                                                                                                                                                                                               RESULT 30
NTC2_RAT
ID _NTC2_RAT
                                                                                                                                                                                                                Query Match
Best Local S:
Matches 8
            DOMAIN
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>:</u>
                                                                                                                                                                                                                                                                                                                                   셤
              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Potential). (Potential). (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Potential).
(Potential).
(Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neurogenic locus notch homolog protein 2. Motch extracellular truncation (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Potential).
(Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Potential). (Potential). (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5, calcium-binding (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGF-like domain; Glycoprotein; Notch signaling pathway;
Phosphorylation; Receptor; Repeat; Signal; Transcription regulation;
                                                                                                                                                                                     | Prami, Fronton | Profession |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          calcium-binding (calcium-binding (calcium-binding)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            calcium-binding
calcium-binding
calcium-binding
calcium-binding
calcium-binding
calcium-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     calcium-binding
calcium-binding
calcium-binding
calcium-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          calcium-binding (calcium-binding (calcium-binding)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        calcium-binding calcium-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    calcium-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         calcium-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytoplasmic (Potential).
EGF-like 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGF-like
EGF-like
EGF-like
EGF-like
EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGF-like
EGF-like
EGF-like
EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGF-like
EGF-like
EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGF-like
EGF-like
EGF-like
EGF-like
EGF-like
EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Potential
Asx_hydroxyl_s.
EGF 2
                                                                    InterPro; IPR001438; EGF_II.
InterPro; IPR005209; EGF_IIke.
InterPro; IPR005209; EGF_IIke.
InterPro; IPR008297; Notch.
InterPro; IPR000800; Notch_region.
Pfam; PP00023; Ank; 6.
Pfam; PP00008; EGF; 35.
                                           EGF Ca.
EGF II.
EGF like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25
2471
2471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               985
023
061
099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2471
                                                    InterPro; IPR001881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26
1666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
```

```
(Potential).
(Potential).
(Potential).
                                                                                                                                                                                                                                                                  (Potential). (Potential). (Potential).
                                                                                                                                                                                                                                                                                                           (Potential).
(Potential).
(Potential).
(Potential).
(Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                      (Potential).
(Potential).
(Potential).
(Potential).
(Potential).
                                                                                                                                                                                                         (Potential). (Potential). (Potential).
                                                                                                                                                                                                                                                                                                                                                                                               (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                           (Potential)
                                                                                                                                                                             calcium-binding (Potential)
                        extracellular truncation (By
                                                                      Extracellular (Potential).

Cytoplasmic (Potential).

EGF-like 1.

EGF-like 2.

EGF-like 3.

EGF-like 4.

EGF-like 6.

EGF-like 6.

EGF-like 9.

EGF-like 10.

EGF-like 10.

EGF-like 11.

EGF-like 12.

EGF-like 12.

EGF-like 13.

EGF-like 13.

EGF-like 14.

EGF-like 14.

EGF-like 15.

EGF-like 15.

EGF-like 16.

EGF-like 16.

EGF-like 17.

EGF-like 17.

EGF-like 18.

EGF-like 19.

EGF-like 19.

EGF-like 19.

EGF-like 19.

EGF-like 20.

EGF-like 21.

EGF-like 21.

EGF-like 22.

EGF-like 22.

EGF-like 23.

EGF-like 24.

EGF-like 24.

EGF-like 29.

EGF-like 31.

EGF-like 31.

EGF-like 32.

EGF-like 33.

EGF-like 34.

EGF-like 34.

EGF-like 35.

EGF-like 36.

EGF-like 37.

EGF-like 37.

EGF-like 38.

EGF-like 39.

EGF-like 30.

EGF-like 30
                                    similarity).
Notch intracellular domain (By
                                                                similarity)
                                                                         1677
2498
6431
1402
1102
1102
11023
11023
11147
11185
11185
1169
11169
11169
11169
11169
11169
11169
11169
11169
11169
11169
11169
11169
11169
11169
11169
11169
11169
11169
11169
11169
11169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                              DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                         DOMAIN
                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                             DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                PRESENT MANAGEMENT OF ILCREMBERSIDE SID. 1.

REMINER, MASSIGAL ARKISSB 11; ...

RADIS AND ARKISSB 12; 
                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                            called
Potential.
Neurogenic locus notch homolog protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25
2471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane.
SIGNAL 1
```

```
repeats
              RESULT 32
NOTC DROME
                                                              ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                              Gaps
                                                                                                                                                                                                                                                             Cynops pyrrhogaster (Japanese common newt).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Amphibia, Batrachia, Caudata, Salamandroidea, Salamandridae; Cynops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                               4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWART; SW00179; EGF_CA; 23.

SWART; SW00179; EGF_CA; 23.

SWART; SW001004; NL; 3.

PROSITE; PS500297; ANK_REPEAT; 4.

PROSITE; PS00010; ASX_HVRGOXL; 23.

PROSITE; PS00025; EGF_1; 32.

PROSITE; PS00025; EGF_2; 27.

PROSITE; PS00026; EGF_3; 36.

PROSITE; PS10186; EGF_2; 27.

PROSITE; PS10187; EGF_CA; 23.

ANK_repeat; EGF_1ike domain; Receptor.

SEQUENCE 2528 AA; 273961 MW; 4F167D51F420D369 CRC64;
                                     Score 66; DB 1; Length 2471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2528;
                                                            5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                GO, GO: 0016020; C: membrane; IEA.
GO, GO: 0005509; F: calcium ion binding; IEA.
GO; GO: 0004872; F: receptor activity; IEA.
GO; GO: 00050154; P: receptor activity; IEA.
GO; GO: 0050793; P: regulation of development; IEA.
InterPro; IPR00110; ANK.
InterPro; IPR000152; BGF_2.
InterPro; IPR001481; EGF_Ca.
InterPro; IPR001481; EGF_Ca.
InterPro; IPR001439; EGF_Ii.
InterPro; IPR001439; EGF_Iike.
InterPro; IPR0018090; NotCh.
InterPro; IPR000800; NotCh.
                                                                                                                                                                                                              55.0%; Score 66; DB 2; 26.7%; Pred. No. 4e+02; ive 15; Mismatches
                                                  4e+02;
                                                                                                  324 CVCVNGWSGDDCSENIDDCAFASCTPGSTCI 354
                                                                                                                                                                          PRT; 2528 AA.
                                                                                     CXIXN----QXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  320 CVCVNGWTGEDCSENIDDCANAACHSGATC 349
                                                 ; Pred. No. 4e+(
 By similarity
By similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CXIXN----OXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF07645; EGF CA; 3.
Pfam; PF00066; NotCh; 3.
PIRSF; PIRSF002279; Notch; 1.
                                  Query Match 55.0%;
Best Local Similarity 25.8%;
Matches 8; Conservative 1
                                                                                                                                                                                                 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR01415; ANKYRIN.
PRINTS; PR00010; EGFBLOOD.
PRINTS; PR01452; NOTCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00023; Ank; 6.
Pfam; PF00008; EGF; 32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                 NCBI_TaxID=8330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                         QBAXP0
QBAXP0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                  RESULT 31
                                                                                                                                                            달년
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                     8
                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
```

```
MEDLINE_2016foll; PubMed=10731137; DOI=10.1126/science.287.5461.2220; Benos P.V. Gatt M.K., Ashburner M., Murphy L., Harris D., Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E., Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S., Papadjannakis G., Spanos L., Cox S., Madueno E., de Pablos B., Modolell J., Peter A., Schoettler P., Werner M., Mourkioti F., Beinert N., Dowe G., Schaefer U., Jaeckle H., Bucheton A., Monilian P., Saulister D.M., Campbell L.A., Darlamitsou A., Henderson N.S., Monilian P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-85099329; PubMed-2981631; DOI=10.1016/0092-8674(85)90308-3; Wharton K.A., Yedvobnick B., Finnerty V.G., Artavanis-Tsakonas S.; "opa: a novel family of transcribed repeats shared by the Notch locus and other developmentally regulated loci in D. melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=87257846; PubMed=3037327;
Kelley M.R., Kidd S., Berg R.L., Young M.W.;
"Restriction of P-element insertions at the Notch locus of Drosophila melanogaster.";
Mol. Cell. Biol. 7:1545-1548(1987).
                                                        GENOME REANNOTATION.

MEDLINE=22426069; PubMed=12537572;

Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B.,

Smith C.D., Tupy J.L., Whitfield B.J., Bayraktaroglu L., Berman B.F.

Bettencourt B.R., Celniker S.B., de Grey A.D.N.J., Drysdale R.A.,

Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Struhl G., Greenwald I., Presentin is required for activity and nuclear access of Notch in
                                                                                                                                                                                                                                                                                                                                                                     Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99221488; PubMed=10206647; DOI=10.1038/19096; Ye Y., Lukinova N., Fortini M.E.; "Neurogenic phenotypes and altered Notch processing in Drosophila Presenilin mutants.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERACTION WITH DX, AND MUTANT SU42C.
MEDLINE=94215489; PubMed=8162848;
Diederich R.J., Matsuno K., Hing H., Artavanis-Tsakonas S.;
Cycosolic interaction between deltex and Notch ankyrin repeats implicates deltex in the Notch signaling pathway.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glover D.M.; "From sequence to chromosome: the tip of the X chromosome of D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Deltex acts as a positive regulator of Notch signaling through interactions with the Notch ankyrin repeats."; Development 121:2633-2644(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERACTION WITH DX.
MEDLINE=95401878; PubMed=7671825;
Matsuno K., Diederich R.J., Go M.J., Blaumueller C.M.,
Artavanis-Tsakonas S.;
                                                                                                                                                                                                                                                                                                                                                                                                            systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99221487; PubMed=10206646; DOI=10.1038/19091;
       Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 287:2220-2222(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-8 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 398:522-525(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell 40:55-62(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLEAVAGE BY PSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLEAVAGE BY PSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila."
RELEASE SEED OF SEED O
```

```
Thereditas 136:89-96 (2002).

Hereditas 136:8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Via its ANK repeats.
SUBCELLULAR LOCATION: Type I membrane protein. Upon activation and the CELELLULAR LOCATION: Type I membrane and enters into the nucleus in conjunction with Su(H).
PTW: Upon binding its ligands such as Delta or Serrate, it is cleaved (S2 cleavage) in its extracellular domain, close to the transmembrane domain. S2 cleavage is probably mediated by Kuz. It is then cleaved (S3 cleavage) downstream of its transmembrane domain, releasing it from the cell membrane. S3 cleavage requires
                                                                                                                                                                                                                                                               MEDLINE-21575956; PubMed=11719214; DOI=10.1016/S0960-9822(01)00562-0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          General outlines of the molecular genetics of the Notch signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                   "Novel Nocch alleles reveal a Deltex-dependent pathway repressing neural fate.";
Curr. Biol. 11:1729-1738(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
0
                                                                                                                                                                                                                                                                                                 Ramain P., Khechumian K., Seugnet L., Arbogast N., Ackermann
Heitzler P.,
                                                                                    MEDLINE=21657146; PubMed=11799064; DOI=10.1101/gad.942302; Lieber T., Kidd S., Young M.W.; "kuzbanian-mediated cleavage of Drosophila Notch."; Genes Dev. 16:209-221(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.0%; Score 66; DB 1; Ler
29.2%; Pred. No. 4.3e+02;
""'ematches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9VMS5 PRELIMINARY; PRT; 3396 AA.
Q9VMS5;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Belongs to the NOTCH family. SIMILARITY: Contains 6 ANK repeats. SIMILARITY: Contains 36 EGF-like domains. SIMILARITY: Contains 3 Lin/Notch repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 XNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22256570; PubMed=12369105;
   Nature 398:525-529(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 29.2
Matches 7; Conservative
                                                        CLEAVAGE BY KUZ.
                                                                                                                                                                                                                                      MUTANT MCD5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Portin P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29VM55
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            업
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PT
```

```
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P. Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stappleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                   Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 66; DB 2; Length 3396;
Pred. No. 5.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3396 AA; 369389 MW; E618E9ACEA13E0E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 2 F5/8 type C domains.
EMBL; AE003615; AAF52472.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO:0005509; F:calcium ion binding; IEA.
GO:0004872; F:receptor activity; IEA.
GO:0005198; F:structural molecule activity; IEA.
                                                                                                                                                                                                                                                                                       Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGF_2.
EGF_Ca.
EGF_like.
EGF_like.
FASE_C.
FASE_C.
Gal_bind_like.
Grow_Eac_recept.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30; GO:0007155; P:cell adhesion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000152; Asx_hydroxyl_S.
InterPro; IPR008985; ConA_like_lec_gl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LDL receptor A
Sushi SCR CCP.
TNFR C6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS00010; ASX HYDROXYL; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       type_C; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF02210; Laminin G 2; 1.
Pfam; PF00057; Ldl_recept_a; 1.
Pfam; PF00084; Sushi; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :lyBase; FBgn0031879; SP1070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGF_1; 15.
EGF_2; 13.
EGF_3; 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00431; CUB; 3.
Pfam; PF004008; EGF; 12.
Pfam; PF007645; EGF CA; 1.
Pfam; PF00754; F5 F8 type_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGFBLOOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR001438; EINTERPRO; IPR006209; EINTERPRO; IPR000491; GINTERPRO; IPR009919; GINTERPRO; IPR003010; HINTERPRO; IPR003112; LINTERPRO; IPR000430; EINTERPRO; IPR000430; EINTERPRO; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nterPro; IPR001368;
nterPro; IPR003129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nterPro; IPR000742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                interPro; IPR000859;
                                                                                                                                                                                                                                                                   systematic review.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nterPro, IPR001881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00032;
SMART: SM00042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SM00179;
                                                                                                                                                                                                      Lewis S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART;
SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART;
                   SO NE REPORTE DE LA RESERVAÇÃO DE LA RESERVAÇÃO DE LA REPORTE DE LA RESERVAÇÃO DE LA RESERV
                                                                                                                                                                                                                                                                             REALINE-COROUNCE FROW N.A.

REALINE-COROUNCE FROW N.A.

REALINE-COROUNCE FROW N.A.

RADIOLINE-COROUNCE FROW N.A.

RADIOLINE-COROUNCE S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RADIOLINE-COROUNCE S.E., Holt R.A., Evans C.A., Galle R.F.,

RADIOLINE-COROUNCE S.E., Holt R.A., Evans G.A., Galle R.F.,

RADIOLINE-COROUNCE S.E., Richards S., Ashburner M., Henderson S.N.,

RADIOLOG G.G., Worten J.R., Yandell M.D., Zhang Q., Chen L.X.,

RADIOLOG G.G., Worten J.R., Yandell M.D., Zhang Q., Chen L.X.,

RADIOLOG G.G., Morten J.R., Yandell M.D., Zhang M., Ffeiffer B.D.,

RADIOLOG G.G., Morten B.G., Helt G., Nelson C.R., Gabor G.L.,

RADIOLOG G.G., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,

RADIOLOG G.G., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,

RADIOLOG G.G., Baxter E.G., Ferraz C.G., Erritar P., Brothiar I.,

RADIOLOG G.G., Butler H., Dayle G.C., Delbakov S.,

RADIOLOG G.G., Butler H., Dayle G.C., Delbakov S.,

RADIOLOG G.G., Butler H., Dayle G.C., Perraz C.,

RADIOLOG G.G., Butler H., Dayle G.C., Dayle G.C., Delbakov S.,

RADIOLOG G.G., Butler H., Dayle G.C., Perraz C.,

RADIOLOG G.G., Butler H., Dayle G.C., Perraz C.,

RADIOLOG G.G., Butler H., Dayle G.C., Perraz C.,

RADIOLOG G.G., Butler H., Dayle G.G., Dayle G.,

RADIOLOG G.G., Butler H., Dayle G.G., Dayle G.,

RADIOLOG G.G., Butler H., Dayle G.G., Dayle G.,

RADIOLOG G.G., Butler H., Gu Z., Guan P., Harris M.,

RADIOLOG G.G., Butler H., Gu Z., Kennison J., Recken M.G.,

RADIOLOG G., Milshina N.V., Moland T.G., Well M.H., Ibegwam C.,

RADIOLOG G., Milshina N.V., Molany R., Marpy D.M., Nelson D.L.,

RODIOL S.M., Moy M., Murphy B., Murpy L., Mursy D.M., Nelson D.L.,

RODIOL S.M., Moy M., Murphy B., Murpy L., Mursy D.M., Nelson D.L.,

RODIOL S.M., Moy M., Murphy B., Wilson K., Strong G., Zhou R., Strong G., Zhen G., Stach H.O.,

RODIOL S.M., Pittenan G.S., Pan S., Pollard J., Pull S., Shon H.,

RODIOL S.M., Woodager, Worley K.C., Wu Strong S., Yao Q.A., Ye J.,

RODIOL S.M., Moy R., Woodager, Worley K.C., Wu Strokes R., Tector C., Truner R., Venter E., Wall B.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.; "The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE=22426065; PubMed=12537568;

Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,

Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,

George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,

Pacleb J.M., Park S., Pfeisfer B.D., Richards S., Sodergren E.J.,

Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.

Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,

"Finishing a whole-genome shotgun: Release 3 of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopteryapta, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
CG9138-PA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gaster euchromatic genome sequence.";
Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Biol. 3: RESEARCH0084-RESEARCH0084 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=22426070; PubMed=12537573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=22426069; PubMed=12537572;
                                                                          Name=SP1070; ORFNames=CG9138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    melanogaster euchromatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genomics perspective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Senome
```

Best Local Similarity

```
Hestin J., Lardelli M.;

Westin J., Lardelli M.;

Westin J., Lardelli M.;

Westin J., Lardelli M.;

RT "Three novel Notch genes in zebrafish: implications for vertebrate covel novel notch genes in zebrafish: implications for vertebrate Large to covel notch genes evolution and function.";

Dev. Genes Evol. 207:51-63 (1997).

BR HSSP; p00740; LEDM.

R HSSP; p00740; LEDM.

R GO; GO:0016202; C:membrane; IEA.

R GO; GO:0004802; F:receptor activity; IEA.

R GO; GO:0004802; F:receptor activity; IEA.

R GO; GO:0005509; F:receptor activity; IEA.

R GO; GO:000162; Asc. hydroxyl_S.

R GO; GO:000162; Asc. hydroxyl_S.

R InterPro; IPR001043; EGF_I.

R Fam; PF00066; NotCh, z.

R Fam; PR00106; EGF. 1.

R PRINTS; RR00104; EGF. CA; 1.

R PRINTS; RR00104; EGF. CA; 1.

R PRINTS; RR00104; NL; Z.

R PRINTS; RR00104; NL; Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pancer Z.;
"Dynamic expression of multiple scavenger receptor cysteine-rich genes in coelomocytes of the purple sea urchin.";
Proc. Natl. Acad. Sci. U.S.A. 97:13156-13161 (2000).

EMBL; AF228824; AF76316.1;
HSSP; P00740; IEDM.
GO; GO:0016509; C:membrane; IEA.
GO; GO:0016509; F:calcium ion binding; IEA.
GO; GO:000510; F:receptor activity; IEA.
GO; GO:000544; F:scavenger receptor activity; IEA.
Interpro; IPR000152; Asx_hydroxyl_S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Scavenger receptor cysteine-rich protein variant 1.
Strongylocentrotus purpuratus (Purple sea urchin).
Bukaryota, Metazoa, Echinodermata; Eleutherozoa; Echinozoa;
Scrinoidea; Eucchinoidea; Echinacea; Echinoida; Strongylocentrotidae;
NCBI_TAXID=7668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=20542095; PubMed=11069281; DOI=10.1073/pnas.230096397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54.2%; Score 65; DB 2; Length 752; 33.3%; Pred. No. 1.7e+02; ive 10; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                752 AA; 82103 MW; 30939E16E0327F8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1075 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 XNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE, PS00010, ASX HYDROXYL, 9. PROSITE, PS00022; EGF_1; 17. PROSITE, PS01186; EGF_2; 15. PROSITE; PS50026; EGF_3; 17. PROSITE; PS01187; EGF_3; 17. EGF-like domain; Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 8; Conserva
                                 NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09NC90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OSONCOO
DT OOJ
D
                             a
                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cynops pyrrhogaster (Japanese common newt).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Caudata, Salamandroidea, Salamandridae, Cynops.
NCBI_TaxID=8330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Notch receptor protein (Fragment).
Name=notch2; (Synonyms=Notch6;
Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                      ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A SEQUENCE FROM N.A.

A Nakamura K., Kikuchi Y., Susaki K., Chiba C., Saito T.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AB095017; BAC41350.2;
R HSSP; P007440; IEDM.

GO; GO:0005509; F:Calcium ion binding; IEA.

GO; GO:0005509; F:Calcium ion binding; IEA.

GO; GO:00154; P:Calcium ion binding; IEA.

GO; GO:00154; P:Calcium ion binding; IEA.

GO; GO:001550; F:Calcium ion binding; IEA.

R GO; GO:00154; P:Calcium ion binding; IEA.

GO; GO:00154; P:Calcium ion binding; IEA.

R InterPro; IPR001152; Asx_hydroxyl_S.

InterPro; IPR001152; Asx_hydroxyl_S.

InterPro; IPR001152; Asx_hydroxyl_S.

InterPro; IPR001181; EGF_Ca.

InterPro; IPR001438; EGF_II.

R InterPro; IPR001438; EGF_II.

R InterPro; IPR00181; EGF_II.

R PFAMT; SM00019; EGF; 6.

R PRNSTT; SM00019; EGF; 8.

R SMART; SM000181; EGF CA; 6.

R RROSITE; PS00010; ASX_HYDROXYL; 3.

R PROSITE; PS01186; EGF_2; 7.

R PROSITE; PS01186; EGF_2; 7.

R PROSITE; PS01187; EGF_CA; 2.

R RRGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.2%; Score 65; DB 2; Length 726; 32.0%; Pred. No. 1.6e+02; 1ve 11; Mismatches 6; Indels
                  5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          726 AA; 79866 MW; 352A402.19AE67F41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Ligand Delta-1.
                                                                                                                                                                                                                                                                                                                                726 AA
   8; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Conservative 11; Mismatches
                                                                                                              2119 TGKNCQHTIDDCASNPCQHGATCV 2142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             437 GFSGRHCDDNLDDCASYPCANGGTC 461
                                                                      4 XNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 XIXNOXCXOXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS01187
EGF-like domain.
SEQUENCE 726 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Delta-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                      Q8AW87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                042374
Matches
                                                                                                                                                                                                                                               RESULT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 35
042374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                Q8AW87
                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                     DE PARTO OCCOSOR DE LA COSO OCCOSOR DE LA COSOR DE LA COSO OCCOSOR DE LA COSOR DE LA COSOR DE LA COSO OCCOSOR DE LA COSOR DE LA
                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

Gaps .

Gaps

ö

```
Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Li H., Leung T.C., Hoffman S., Balsamo J., Lilien J.;
"Coordinate regulation of cadherin and integrin function by the chondroitin sulfate proteoglycan neurocan.";
J. Cell Biol. 149:1275-1288(2000).
EMBL; AFF16855, AAD24546.2;
HSSP; P08661; 1BV4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=20309833; PubMed=10851024; DOI=10.1083/jcb.149.6.1275;
                                                           Length 1214;
                                                                                                    Indels
                   1214 AA; 133807 MW; A9C09C420CC157C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1290 AA; 138876 MW; 182BD86D0E40BE78 CRC64;
                                                                                                                                                                                                                                                                                                                          01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                         Query Match 54.2%; Score 65; DB 2; Le
Best Local Similarity 26.9%; Pred. No. 2.6e+02;
Matches 7; Conservative 14; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005540; F:hyaluronic acid binding; IEA.
GO; GO:0005529; F:sugar binding; IEA.
GO; GO:0007155; P:call adhesion; IEA.
                                                                                                                                                                                                                                                                                        PRT; 1290 AA
                                                                                                                                                                 2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000152; Asx hydroxyl_S.
InterPro; IPR000142; EGF_Z.
InterPro; IPR00148; EGF_Ga.
InterPro; IPR001438; EGF II.
InterPro; IPR005209; EGF like.
InterPro; IPR001599; Ig-like.
InterPro; IPR001304; Lectin_C.
InterPro; IPR001304; Lictin_C.
InterPro; IPR000538; Link.
InterPro; IPR000538; Link.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Link.
Sushi_SCR_CCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00009; EGF; 2.
Pfam; PF00009; Lectin C; 1.
Pfam; PF000084; Sushi; 1.
Pfam; PF00193; Xlink; 2.
PRINTS; PR00101; EGFBLOOD.
PRINTS; PR01265; LINKMODULE.
PRODOM; PD000918; Link; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUSHI; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00179; EGF_CA; 1
SMART; SM00409; IG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00032; CCP; 1.
SMART; SM00034; CLECT; 1.
SMART; SM00179; EGF_CA; 1
                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                            Neurocan core protein.
Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00445; LINK;
PROSITE; PS00010; ASX_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSS0923;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9031;
EGF-like domain.
SEQUENCE 1214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; E
EGF-like
SEQUENCE
                                                                                                                                                                                                                                                                                    Q9W6E1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus
                                                                                                                                                                                                                                                RESULT 38
                                                                                                                                            ò
                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 54.2%; Score 65; DB 2; Length 1075; Best Local Similarity 33.3%; Pred. No. 2.3e+02; Matches 8; Conservative 10; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21541013; PubMed=11685570;
Kiyota T., Jono H., Kuriyama S., Hasegawa K., Miyatani S.,
Kinoshita T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116178 MW; 61395AD6FD30BA3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1214 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : :|: ::||| |::| :: :||
862 TGSSCDTEIDDCSSSPCGDNGVCV 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27
                                                                                                                                                                                                                                                                       SMART; SM0020; SR; 7,
PROSITE; PS00010; ASX_HYDROXYL; 2.
PROSITE; PS00022; EGF 1; 2.
PROSITE; PS01186; EGF 2; 3.
PROSITE; PS01187; EGF 2; 3.
PROSITE; PS01187; EGF 3; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00010; ASX HYDROXYL; 10. PROSITE; PS00022; BGF 1; 16. PROSITE; PS01186; BGF 2; 12. PROSITE; PS50026; BGF 3; 15. PROSITE; PS01187; BGF CA; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 XNOXCXOXLDDCCSXXCNXXNXCV
                                                   InterPro; Irrolland; Ser_like.
InterPro; IPR006209; EGF_like.
InterPro; IPR00190; SrcT_receptc
InterPro; IPR00190; SrcT_receptc
InterPro; IPR000136; SushI_SCR_CC
Pfam; PF00530; SRCR; 7.
Pfam; PF00084; SushI, 1.
PRINTS; PR00109; SCFBLCOD.
PRINTS; PR00258; SPERACTRCPTR.
SMART; SM00321; CCP, 1.
SMART; SM00322; CCP, 1.
                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50287; SRCR_2; 7.
PROSITE; PS50923; SUSHI; 1.
EGF-like domain; Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
  InterPro; IPR000742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                          InterPro; IPR001438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-Serrate-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=X-Serrate-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               090YD2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 37
Q90YD2
DR NO 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
```

```
ö
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                      ö
                 Length 1290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of the nematode C.elegans: A platform for investigating biology."; Science 282:2012-2018(1998).
                                                              6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smye R.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smye R.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WormPep; F40ELO.4; CE32412.

GO; GO:0005199; F:calcium ion binding; IEA.

GO; GO:0005199; F:erructural molecule activity; IEA.

GO; GO:0005195; P:erructural molecule activity; IEA.

GO; GO:0007155; P:call adhesion; IEA.

InterPro; IPR000152; Asx hydroxyl S.

InterPro; IPR000507; Cys Knot C.

InterPro; IPR000507; Cys Knot C.

InterPro; IPR00143; EGF Ca.

InterPro; IPR001438; EGF II.

InterPro; IPR001438; EGF II.

InterPro; IPR001439; EGF II.
                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein F40E10.4.
Query Match 54.2%; Score 65; DB 2; I Best Local Similarity 26.9%; Pred. No. 2.8e+02; Matches 7; Conservative 13; Mismatches 6,
                                                                                                                                                                                                                                                                                                         . PRT; 1410 AA
                                                                                                                                     1005 GFTGENCEIDIDDCLSSPCQNGGTCI 1030
                                                                                                           2 XIXNQXCXQXLDDCCSXXCNXXVX 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, ALO22770; CABG3434.2; EMBL, ALO22270; CABG3434.2; EMBL, Z69792; CABG3434.2; JOINED. EMBL, Z69792; CAA93668.3; -0 PIR, D89711; D8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00008; EGF; 7.
Pfam; PF02210; Laminin G 2; 1.
Pfam; PF01463; LRRCT; 1.
Pfam; PF01462; LRRCT; 1.
Pfam; PF00560; LRR 1; 17.
PRINTS; PR00010; EGPBLOOD.
PRINTS; PR00019; LEURICHRPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001611; LRR.
InterPro; IPR000483; LRR Cterm.
InterPro; IPR000372; LRR Nterm.
InterPro; IPR003591; LRR Vterm.
InterPro; IPR003129; TSP-N;
                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI TaxID=6239;
                                                                                                                                                                                                                                                                                                 Q20204
Q20204;
                                                                                                                                                                                                                                        RESULT 39
Q20204
ID Q2020
                                                                                                           ò
                                                                                                                                                            g
```

```
SEQUENCE OF 1436-1600 FROM N.A.
MEDLINE-99252212; PubMed=10233982;
Lee J.-S., Haruna T., Ishimoto A., Honjo T., Yanagawa S.-I.;
"Intracisternal type A particle-mediated activation of the Notch4/int3
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUB-Lung, and Testis;
MEDINE-56281668; PubMed-8681805;
Uyttendaele H., Marazzi G., Wu G., Yan Q., Sassoon D., Kitajewski J.;
"Notchfiltz", a mammary protco-oncogene, is an endothelial cell-
Specific mammalian Notch gene.";
Development 122:2251-2256(1956).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Rowen L., Mahairas G., Qin S., Ahearn M.E., Dankers C., Lasky S.,

Loretz C., Schmidt S., Tipton S., Traicoff R., Zackrone K., Hood L.;

"Sequence of the mouse major histocompatibility locus class III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The mouse mammary tumor associated gene INT3 is a unique member of the NOTCH gene family (NOTCH4).";
Oncogene 14:1883-1890(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92194507; PubMed=1312643; Sobbins J., Blondel B.J., Gallahan D., Callahan R.; Mouse mammar gene int.3: a member of the notch gene family transforms mammary epithelial cells."; J. Virol. 66:2594-2599(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metaca; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
VCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NTC4_MOUSE STANDARD; PRT; 1964 AA.
P31655; O35442; O88314; O88316; Q62389; Q62390; Q9R1W9; Q9R1X0; O1-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 35, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Neurogenic locus notch homolog protein 4 precursor (Notch 4)
GContains: Transforming protein Int-3]
                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                 A PROSITE; P801225, GF 1; 7.

R PROSITE; P80022; EGF 1; 7.

DR PROSITE; P800026; EGF 2; 5.

DR PROSITE; P800026; EGF 2; 2.

DR PROSITE; P801087; EGF CA, 2.

DR PROSITE; P850025; LAM G DOMAIN; 1.

RGF-like domain; Hypothetical protein.

TOTHEROR 1410 AA; 158221 MW; D33716A9C98EBA9D CRC64;

TOTHEROR 1410 AA; 158221 MW; D33716A9C98EBA9D CRC64;

TOTHEROR 1410 AA; 158221 MW; D33716A9C98EBA9D CRC64;

TOTHEROR 1410 AA; 158221 MW; D33716A9C98EBA9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND REVISIONS.
MEDLINE-97294599; PubMed-9150355; DOI=10.1038/8j.onc.1201035;
Gallahan D., Callahan R.;
                                                                                                                                                                                                                                                                                                                     54.2%; Score 65; DB 2; Length 1410; 26.9%; Pred. No. 3e+02; Live 13; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   region.";
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                               338 GFEGDYCEKNIDDCVNSKCENGGKCV 963
                                                                                                                                                                                                                                                                                                                                                                                            2 XIXNQXÇXQXLDDÇCSXXCNXXNXCV 27
SWART; SWULL,

A SMART; SW00179; LLMG; L.

DR SWART; SW00082; LRRCT; 4.

DR SWART; SW000013; LRRT; 4.

DR SWART; SW000013; LRRT; 7.

DR PROSITE; PS00010; ASX HYDROXYL;

PROSITE; PS01225; CTCK 2; 1.

"TTE; PS00022; ESF 1, 7.

"TTE; PS01022; CTCK 2; 1.

"TTE; PS01022; CTCK 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Notch4; Synonyms=Int-3, Int3; Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 26.94
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 40
NTC4_MOUSE
                     ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                             рp
```

FUNCTION

```
Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001110; ANK.
InterPro; IPR001152; ABx hydroxyl_S.
InterPro; IPR0010182; EGF_2.
InterPro; IPR001891; EGF_II.
InterPro; IPR006209; EGF_III.
InterPro; IPR006209; EGF_III.
InterPro; IPR006209; Grow_fac_recept.
InterPro; IPR006209; Notch.
InterPro; IPR008297; Notch.
InterPro; IPR008209; Notch.
                                         EMBL, 043091, ARC52031, 1.

EMBL, AF030001, AAB82004.1; -

EMBL, AB016772, BAA32281.1; ALT_INIT.

EMBL, AB016773, BAA32283.1; ALT_INIT.

EMBL, AB016774, BAA32285.1; -

EMBL, AB016774, BAA32285.1; -

EMBL, AB016774, BAA32285.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50088; ANK REPEAT; 5.
PROSITE; PS50297; ANK REP REGION; 1
PROSITE; PS00010; ASX HYDROXYL; 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIRSF; PIRSF002279; Notch; 1.
PRINTS; PR01415; ANKYRIN.
PRINTS; PR00010; EGFBLOOD.
PRINTS; PR01452; NOTCH.
  M80456; AAB38377.1; -. U43691; AAC52630.1; -. U43691; AAC52631.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00248; ANK; 6.
SMART; SM00179; EGF_CA; 11.
SMART; SM00004; NL; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00023; Ank; 6.
Pfam; PF00008; EGF; 27.
Pfam; PF06816; NOD; 1.
Pfam; PF00066; Notch; 2.
                                                                                                                                                                                       PIR, A38072; TVMVT3.
PIR, T09059; T09059.
HSSP; P08709; 1BF9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
CHAIN
CHAIN
CHAIN
CHAIN
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                    8888888888888888888
    -I- DEVELOPMENTAL STAGE: Highly expressed in endothelial cells during embryonic development from 9.0 dpc.
-I- PTW: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C-terminal fragment N(TM) and a N-terminal fragment N(EC). Following ligand binding, it is cleaved by TNN-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notch extracellular truncation (NEXT). This fragment is then cleaved by presentlin dependent gamma-secretase to release a notch-derived peptide containing the intracellular domain (NICD) from the membrane.
-I- PTM: Phosphorylated.
-I- DTM: Phosphorylated.
-I- DISEASE: Loss of the extracellular domain causes constitutive activation of the Notch protein, which leads to hyperproliferation of agrandular epithelial tissues and development of mammary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDILIRE-21374376; PubMed=1145941; DOI=10.1073/pnas.161269998;

MEDILIRE-21374376; PubMed=1145941; DOI=10.1073/pnas.161269998;

T. Conservation of the biochemical mechanisms of signal transduction among mammalian Notch family members.";

Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).

I. Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).

Jagged. Sci. U.S.A. 98:9026-9031(2001).

C. I- FUNCTION: FUNCTION: FOR membrane-bound ligands as a receptor for membrane-bound ligands and Doilal to regulate coll-fate determination. Upon 11gand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator of split locus.

C. Affects the implementation of differentiation, proliferation and approprie programs (By similarity). May regulate branching morphogenesis in the developing vascular system.

C. I. SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EC) which are probably linked by disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Type I membrane protein. Following proteolytical processing NICD is translocated to the nucleus. TISSUE SPECIFICITY: Highly expressed in lung, moderately in heart kidney, and at lower levels in the ovary and skeletal muscle. A very low expression is seen in the brain, intestine, liver and
                                                                                                                                                                                                                                                         SEQUENCE OF 1463-1964, POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS
                                                                                                                                        Uyttendaele H., Ho J., Rossant J., Kitajewski J.;
"Vascular patterning defects associated with expression of activated
Notch4 in embryonic endothelium.";
gene in a mouse mammary tumor: generation of truncated Notch4/int3
mRNAs by retroviral splicing events.";
J. Virol. 73:5166-5171(1999).
                                                                                                                                                                                                                                                                                                  MEDLINE=21523956; PubMed=11518718; DOI=10.1074/jbc.M107234200;
                                                                                                                  MEDLINE=21244657; PubMed=11344305; DOI=10.1073/pnas.091584598;
                                                                                                                                                                                                                                                                                                                             Saxena M.T., Schroeter B.H., Mumm J.S., Kopan R.; "Murine notch homologs (NI-4) undergo presenilin-dependent
                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 98:5643-5648(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -:- SIMILARITY: Belongs to the NOTCH family.
-:- SIMILARITY: Contains 5 MNK repeats.
-:- SIMILARITY: Contains 29 EGF-like domains.
-:- SIMILARITY: Contains 3 Lin/Notch repeats.
                                                                                                                                                                                                                                                                                                                                                                                                    J. Biol. Chem. 276:40268-40273(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  POST-TRANSLATIONAL PROCESSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         carcinomas.
                                                                                                                                                                                                                                                                                                                                                                              proteolysis.";
                                                                                                                                                                                                                                                                                    VAL-1463
```

<u>:</u>

+ +

```
SSI !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neurogenic locus notch homolog protein 4. Transforming protein Int-3. Outch extracellular truncation. Notch intracellular domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytoplasmic (Potential).
EGF-like 1.
EGF-like 2.
EGF-like 3.
EGF-like 4.
EGF-like 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00022; EGF 1, 28.
PROSITE; PS01186; EGF 2; 21.
PROSITE; PS01186; EGF 2; 21.
PROSITE; PS01187; EGF 3; 27.
Activator; ANK repeat; Developmental protein; Differentiation; Direct protein sequencing; EGF-like domain; Glycoprotein; Notch agnaling pathway; Phosphorylation; Proto-oncogene; Receptor; Repeat; Signal; Transcription regulation; Transmembrane.
MGD; MGI:107471; Notch4.

GO; GO:0009986; C:cell surface; ISS.
GO; GO:0005887; C:integral to plasma membrane; ISS.
GO; GO:0005887; C:integral to plasma membrane; ISS.
GO; GO:0005535; C:allocum ion binding; ISS.
GO; GO:0005515; F:protein binding; ISS.
GO; GO:0004872; F:protein binding; ISS.
GO; GO:0001763; P:protein binding; ISS.
GO; GO:0001763; P:protein meterodimerization activity; ISS.
GO; GO:0001763; P:protein meterodimerization activity; ISS.
GO; GO:0001763; P:protein meterodimerization activity; ISS.
GO; GO:0001763; P:protein development; IMP.
GO; GO:0001709; P:embryonic development; IMP.
GO; GO:0007219; P:megative regulation of endothelial cell diff...;
GO; GO:0007219; P:Notch signaling pathway; TAS.
GO; GO:0001569; P:postiterning of blood vessels; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Extracellular (Potential).
Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1443
1464
1964
112
112
189
229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
```

us-10-627-685a-1.rup

```
;
             EGF-like 7, calcium-binding (Potential).
EGF-like 8, calcium-binding (Potential).
EGF-like 9, calcium-binding (Potential).
EGF-like 10.
EGF-like 11, calcium-binding (Potential).
EGF-like 12, calcium-binding (Potential).
EGF-like 13, calcium-binding (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Type I membrane protein. Following proteolytical processing NICD is translocated to the nucleus.
-!- TRSUE SPECIFICITY: Proliferating neuroepithelium.
-!- DEVELOPMENTAL STAGE: CNS development.
-!- PTM: Syntheeized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C-
                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=ICR X Swiss Webster, MEDLINE-5950156; PubMed-7918097; DOI=10.1016/0925-4773(94)90081-7; Lardelli M., Dalstrand J., Lendahl U.; "The novel Norch homologue mouse Norch 3 lacks specific epidermal growth factor repeats and is expressed in proliferating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EC) which are probably linked by disulfide
                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS OF MET-1664.
MEDLINE=21523956; PubMed=11518718; DOI=10.1074/jbc.M107234200;
Saxena M.T., Schroeter E.H., Mumm J.S., Kopan R.;
"Murine notch homologs (NI-4) undergo presentlin-dependent
                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Neurogenic locus notch homolog protein 3 precursor (Notch 3)
                                                                                                                             Score 65; DB 1; Length 1964;
Pred. No. 4e+02;
                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                PRT; 2318 AA.
                                                                                                                                                       12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol. Chem. 276:40268-40273(2001).
                                                                                                                                                                                               348 GCEENLDDCAAATCAPGSTCI 368
                                                                                                                                                                                7 XCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POST-TRANSLATIONAL PROCESSING
                                                                                                                             54.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mech. Dev. 46:123-136(1994).
                                                                                                                       Query Match
Best Local Similarity 33.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                STANDARD;
              3309
3350
3388
3427
508
508
                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neuroepithelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteolysis.
                                                                                                                                                                                                                                                                               MOUSE
                                                                                                                                                                                                                                                                               NTC3 MOI
DOMAIN
DOMAIN
DOMAIN
                                                                                 DOMAIN
                                         DOMAIN
                                                       DOMAIN
                                                                                                                                                                                                                                                                MOUSE
                                                                                                                                                                                                                                                                               PT
PT
PT
PT
PT
                                                                                                                                                                                ò
                                                                                                                                                                                                        g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMML outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-aib.ch/announce/or send an email to license@lsb-sib.ch).
terminal fragment N(TM) and a N-terminal fragment N(EC). Following ligand binding, it is cleaved by TNF-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notch extracellular truncation (NEXT). This fragment is then cleaved by presentlin dependent gamma-secretase to release a notch-derived peptide containing the intracellular domain (NICD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neurogenic locus notch homolog protein 3. Notch extracellular truncation. Outch intracellular domain. Extracellular. Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BGF-like 1.
BGF-like 2.
BGF-like 3.
BGF-like 4, calcium-binding (Potential).
BGF-like 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein; Notch signaling pathway;
Receptor; Repeat; Signal; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PSS0297; ANK REP REGION; 1.
PROSITE; PSS0088; ANK_REPEAT; 4.
PROSITE; PSS00010, ASX 'LYDROXYL; 18.
PROSITE; PS00022; EGF 1; 33.
PROSITE; PS01186; EGF 2; 27.
PROSITE; PS01187; EGF 2; 34.
ACLIVATOR; ANK repeat; Developmental protein; Differentiation; PSGF-11ke domain; Glycoprotein; Notch signaling pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                               R GO; GO: 0005887; G: integral to plasma membrane; IC. R GO; GO: 0005887; F: protein binding; IPI. GO; GO: 0007215; F: protein binding; IPI. GO; GO: 0007215; F: protein binding; IPI. GO; GO: 0007215; F: protein binding; IPI. R InterPro; IPR001515; Asx. hydroxyl S. InterPro; IPR001825; Asx. hydroxyl S. InterPro; IPR001821; EGF_Ca. R InterPro; IPR001831; EGF_Ca. R InterPro; IPR001831; EGF_TI. R InterPro; IPR001831; EGF_TI. R InterPro; IPR00180395; Notch. R InterPro; IPR00180397; Notch. R InterPro; IPR0018090; Notch. R INTRS; PR001915; ANKRIN. R INTRS; PR001915; ANKRIN. R INTRS; PR001915; NOTCH. R INTRS; PR001915; NOTCH. R INTRS; PR019192; NOTCH. R INTRS; PR019192; NOTCH.
                                                                                                       from the membrane.
-!- PTM: Phosphorylated.
-! SIMILARITY: Belongs to the NOTCH family.
-!- SIMILARITY: Contains 5 ANK repeats.
-!- SIMILARITY: Contains 34 EGF-like domains.
-!- SIMILARITY: Contains 3 Lin/Notch repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytoplasmic.
PEST.
                                                                                                                                                                                                                                                                                                                                                                              EMBL; X74760; CAA52776.1; -.
PIR; S45306; S45306.
HSSP; P00740; 1EDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00248; ANK; 6.
SMART; SM00179; EGF CA; 19.
SMART; SM00004; NL; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:99460; Notch3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2318
2318
1643
1664
2318
2261
78
119
157
196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1644
1665
2242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
CHAIN
DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
```

ï

```
uppression.

Subburg: Heterodimer of a C-terminal fragment N(TW) and a N-terminal fragment N(EC) which are probably linked by disulfide bonds (By similarity).

-I-SUBCULTLUAR LOCATION: Type I membrane protein. Pollowing proteolytical processing NICD is translocated to the nucleus.

-I-TISSUE SPECIFICITY: Expressed in postnatal life, within numerous cells throughout the CNS. It is more highly localized to ventricular germinal zones and, in early postnatal life, within numerous cells throughout the CNS. It is more highly localized to ventricular germinal zones.

-I-PM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C-terminal fragment N(TM) and a N-terminal fragment N(EC). Following ligand binding, it is cleaved by TNR-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called (TACE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21094508; Pubmed=11182080; DOI=10.1016/S0896-6273(01)00179-9;
Tanigaki K.; Nogaki F., Takahashi J., Tashiro K., Kurooka H.,
Honjo T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Honjo T.;
"Norchl and Notch3 instructively restrict bFGF-responsive multipotent
Neural progenitor cells to an astroglial fate.";
Neuron 29:45-55(2001).
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCB_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          notch extracellular truncation (NEXT). This fragment is then cleaved by presenilin dependent gamma-secretase to release a
                                                                    4
                                                                                                                                                                                                                      NTC3_RAT STANDARD; PRT; 2319 AA.
Q9R172;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Neurogenic locus notch homolog protein 3 precursor (Notch 3)
                                   Length 2318
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. Haritunians T., Boulter J., Weinmaster G., Schanen N.C.; Haritunians T., Boulter J., Notch 3."; "Rattus norvegicus mRNA for Notch 3."; submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                 Pred. No. 4.7e+02;
                                   DB 1;
                                                                                                                        By similarity.
                                                                   13; Mismatches
                                                                                                   1 CXIXN----QXCXQXLDDCCSXXCNXXNXC 26
                                   Score 65;
                                 54.2%;
                                                                    9; Conservative
                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
                                 Query Match
Best Local Similarity
   479
                                                                                                                                                                                                                                                                                                                            Name=Notch3;
   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION
                                                                                                                                                                                      RESULT 42
NTC3_RAT
                                                                    Matches
                                                                                                                                                                                                                           ઠે
                                                                                                                                  엄
                                                                                                                  (Potential). (Potential). (Potential).
                                                                                                                                                                                                                                                         (Potential).
(Potential).
                                                                                                                                                                                                                                                                                                                                                                                            calcium-binding (Potential)
calcium-binding (Potential)
                                                                                                      (Potential)
                                                                                                                                                                      (Potential)
   calcium-binding (Potential)
                                   calcium-binding (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lin/Notch 1.
Lin/Notch 1.
Lin/Notch 2.
ANK 1.
ANK 2.
ANK 3.
ANK 3.
ANK 4.
ANK 4.
ANK 5.
ANK 6.
ANK 9.
By similarity.
                                                               calcium-binding (calcium-binding calcium-binding calcium-bindi
                                                                                                                                                                                                                                                         calcium-binding
calcium-binding
calcium-binding
                                                                                                                                                                                                                      EGF-like 19.
EGF-like 20.
EGF-like 21.
EGF-like 23.
EGF-like 23.
EGF-like 24.
EGF-like 25.
EGF-like 26.
EGF-like 26.
EGF-like 26.
EGF-like 27.
EGF-like 27.
EGF-like 29.
EGF-like 29.
EGF-like 6, c
EGF-like 7.
EGF-like 9.
EGF-like 10,
EGF-like 11,
EGF-like 12,
EGF-like 13,
EGF-like 14,
EGF-like 14,
EGF-like 16,
EGF-like 16,
EGF-like 16,
EGF-like 16,
EGF-like 16,
                                                                                                                                                                                                                                                                                                                                                                                                                             EGF-like 31.
EGF-like 32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGF-like 33.
EGF-like 34.
1035
1083
1121
1159
                                                                                                                                                                                                                                                                                                                                                                                                                                 1245
1288
1326
1374
1428
1467
1503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1085
1123
1161
1206
1247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1336
1388
1429
1468
1839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1906
1939
1972
1572
                                                                                                                                                                                                                                                                                                                                                                                                                                                               290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULPID
DISULPID
DISULPID
DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
REPEAT
SITE
                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                            OMAIN
                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
```

```
(Potential). (Potential). (Potential).
                                                                                                                             (Potential). (Potential). (Potential).
                                                                                                                                                                                                                                                                    calcium-binding (Potential)
calcium-binding (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                EGF-like 15, calcium-binding (Potent: EGF-like 16, calcium-binding (Potent: EGF-like 19, EGF-like 19, EGF-like 19, EGF-like 20, EGF-like 20, EGF-like 21, calcium-binding (Potent: EGF-like 22, calcium-binding (Potent: EGF-like 24, EGF-like 24, EGF-like 25, EGF-like 26, EGF-like 26, EGF-like 27, EGF-like 27, EGF-like 27, EGF-like 27, EGF-like 31, EGF-like 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; L
4.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CXIXN----QXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 65;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.2%;
                    650
657
657
732
772
810
8810
962
1036
1036
1122
1122
1128
11327
1327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Si
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
DISULFID
DISULFID
                  DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
REPEAT
REPEAT
REPEAT
SITE
                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
DOMAIN
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGF-like 1.
EGF-like 2.
EGF-like 2.
EGF-like 4.
EGF-like 4.
EGF-like 6. calcium-binding (Potential).
EGF-like 6.
EGF-like 7.
EGF-like 9.
EGF-like 9.
EGF-like 10.
EGF-like 10.
EGF-like 10.
EGF-like 10.
EGF-like 10.
EGF-like 11.
EGF-like 11.
EGF-like 12.
EGF-like 13.
EGF-like 14.
EGF-like 14.
EGF-like 13.
EGF-like 13.
EGF-like 14.
EGF-like 14.
EGF-like 14.
notch-derived peptide containing the intracellular domain (NICD) from the membrane (By similarity).
PTM: Phosphorylated (By similarity).
SIMILARITY: Belongs to the NOTCH family.
SIMILARITY: Contains 5 ANK repeats.
SIMILARITY: Contains 34 EGF-like domains.
SIMILARITY: Contains 3 Lin/Notch repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neurogenic locus notch homolog protein 3.
Notch extracellular truncation (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Potential).
(Potential).
(Potential).
(Potential).
(Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Activator; ANK repeat Developmental protein; Differentiation;
EGF-like domain; Glycoprotein; Notch signaling pathway;
Phosphorylation; Receptor; Repeat; Signal; Transcription regulation;
I 40 Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Notch intracellular domain (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Extracellular (Potential).
Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytoplasmic (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity)
                                                                                                                                                                                                                                                                                                                Interpro; IPR002110; ANK.
Interpro; IPR002110; ANK.
Interpro; IPR000152; Asx hydroxyl S.
Interpro; IPR000142; EGF Z.
Interpro; IPR00143; EGF Z.
Interpro; EGF Z.
Interpro; IPR00143; EGF Z.
Interpro; EGF Z.
Interpro
                                                                                                                                                                                                                                                                                                                                      Asx hydroxyl S.
ConA like lec_gl.
EGF Ca.
EGF II.
EGF II.
                                                                                                                                                                                                                                                                                     EMBL; AF164486; AAD46653.2; -.
HSSP; P00740; 1EDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41
1631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
TRANSMEM
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
```

```
Carleance From N.A.

Submedia 15057824; DOI=10.1038/nature02399;

Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,

A lemerain J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,

A merts A., Altherr M., Ashworth L., Balorek E., Black S., Branscomb E.,

A cenepeel S., Carrano A.V., Caoile C., Chan Y.M., Christensen M.,

A claind C.A., Copeland A., Dalin E., Dehal P., Danys M., Detter J.C.,

Becobar J., Flowers D., Fotopulos D., Garcia C., Georgescu A.M.,

Becobar J., Flowers D., Fotopulos D., Garcia C., Georgescu A.M.,

Andyu L., Ho I., Huang W., Israni S., Jett J., Radher K., Kimball H.,

Robayashi A., Larionov V., Leem S.-H., Lopez F., Lou Y., Lowry S.,

Malfatti S., Martinez D., McCready P.M., Medina C., Morgan J.,

Nalson K., Nolan M., Ovcharenko I., Pitluck S., Pollard M.,

Rodriguez A., Rogers S., Salamov A., She X., Smith D.,

Slezak T., Solovyev V., Thayer N., Tice H., Tsai M., Ustaszewska A.,

Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I.,

Pennacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,

Rubin E.M., Lucas S.M.,

Rubin E.M., Lucas S.M.,

Rubin E.M., Lucas S.M.,

Nature 428:529-535(2004).
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97032728; PubMed-8878478; DOI=10.1038/383707a0; MEDLINE-97032728; PubMed-8878478; DOI=10.1038/383707a0; Jourel A., Corpechot C., Ducros A., Vahedi K., Chabriat H., Mouton P., Alamowitch S., Domenga V., Cecillion M., Marechal E., Maciazek J., Vayssiere C., Cruaud C., Cabanis E.-A., Ruchoux M.M., Welssenbach J., Bach J.-F., Bousser M.-G., Tournier-Lasserve E.; M.M., Welssenbach J., "Notch3 mutations in CADASIL, a hereditary adult-onset condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT CADASIL 114-GLY--PRO-120 DEL.
MEDLINE=20264473; PubMed=10802807;
Joutel A., Chabriat H., Vahedi K., Domenga V., Vayssiere C.,
Suchoux M.M., Lucas C., Leys D., Bousser M.-G., Tournier-Lasserve E.;
"Splice site mutation causing a seven amino acid Notch3 in-frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS CADASIL TYR-49; CYS-71; CYS-90; CYS-110; CYS-133; CYS-141; ARG-146; CYS-153; CYS-169; CYS-171; CYS-182; ARG-185; SER-212; GLY-222; TYR-224; CYS-286; CYS-586; CYS-586; CYS-586; CYS-728; CYS-586; CYS-1006; CYS-1001; CYS-1231 AND ARG-1261, AND VARIANTS ARG-170; LEU-496; GLN-1133; MET-1183 AND ALA-2223. MEDLINE-98049753; PubMed=9388399; DOI=10.1016/S0140-6736(97)08083-5; Joutel A., Vahedi K., Corpechot C., Troesch A., Chabriat H., Wayssiere C., Cruaud C., Maciazek J., Weissenbach J., Bousser M.-G., Bach J.-F., Tournier-Lasserve E.;
                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NTC3_HUMAN STANDARD; PRT; 2321 AA.
Q9UM47; Q9UEB3; Q9UPL3; Q9YGLB;
28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last aguence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Neurogenic locus notch homolog protein 3 precursor (Notch 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Gunel M., Artavanis-Tsakonas S.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
causing stroke and dementia.";
Nature 383:707-710(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lancet 350:1511-1515(1997).
                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                           RESULT 43
NTC3_HUMAN
                       셤
```

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib.ch).

EMBL; EMBL; EMBL; EMBL; EMBL;

AF058884; AF058885; AF058886;

U97669; AAB91371.1; -.

EMBL;

EMBL;

AAC14346.1; JOINED. AAC14346.1; JOINED. AAC14346.1; JOINED. AAC14346.1; JOINED. AAC14346.1; JOINED. AAC14346.1; JOINED.

EMBL; EMBL; EMBL; EMBL; EMBL;

JOINED. JOINED

AAC14346.1; AAC14346.1; AAC14346.1;

JOINED

AAC14346.1; AAC14346.1; AAC14346.1;

AF058898;

EMBL;

EMBL;

AAC14346.1; JOINED

AF058892;

EMBL; EMBL;

EMBL;

```
MEDLINE=99180765; PubMed=10079256; Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L., Banks A., Leiman J., Ward D., 18h-Horowitz D., Artavanis-Tsakonas S.; Human Ilgands of the Notch receptor."; Am. J. Pathol. 154:785-794(1999).
                          deletion in CADASIL.";
Neurology 54:1874-1875(2000).
        IDENTIFICATION OF LIGANDS
```

```
Notch homolog.
Lytechinus variegatus (Sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euchinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97454256; PubMed-9310331;
Sherwood D.R., McClay D.R.;
"Identification and localization of a sea urchin Notch homologue:
insights into vegetal plate regionalization and Notch receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       025253 PRELIMINARY; PRT; 2653 AA.
025253;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
Notch homolog Scalloped wings.
Name=SC;
Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R InterPro; IPR00110; ANK.

RILGEPRO; IPR00110; ANK.

InterPro; IPR000121; Asx_hydroxyl_S.

R InterPro; IPR000143; EGF_Ca.

R InterPro; IPR001438; EGF_Ti.

R InterPro; IPR001438; EGF_Ti.

R InterPro; IPR001438; EGF_Ti.

R InterPro; IPR001438; EGF_Ti.

R InterPro; IPR000297; Notch.

R InterPro; IPR000297; Notch.

R Pfam; PF00006; EGF_Si.

R Pfam; PF00006; Notch; 3.

R PRINTS; PR01415; ANKXRIN.

R PRINTS; PR01415; ANKXRIN.

R PRINTS; PR01415; ANKXRIN.

R PRINTS; PR01452; NOTCH.

R SMART; SM0010; EGFELOOD.

R SMART; SM0014; ANK; 6.

R SMART; SM0014; ANK; 6.

R SMART; SM0014; ANK; 6.

R PROSITE; PS00101; EGF_Ti: 33.

R PROSITE; PS00106; EGF_Ti: 33.

R PROSITE; PS01186; EGF_Ti: 25.

R PROSITE; PS01186; EGF_Ti: 26.

R PROSITE; PS01186; EGF_TI: 27.

R PROSITE; PS01187; EGF_CA: 20.

R PROSITE; PS01187; EGF_CA: 20.

R PROSITE; PS01187; EGF_CA: 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2531;
                                                                       01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0016020; C:membrane; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0030154; P:cell differentiation; IEA.
GO; GO:0050793; P:regulation of development; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 54.2%; Score 65; DB 2;
Best Local Similarity 38.1%; Pred. No. 5.1e+02
Matches 8; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     661 NCEEDIDDCESRPCHNGGTCV 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        regulation.";
Development 124:3363-3374(1997).
BmBL; AF000634; AAB82088.1; -.
PIR; T31070; T31070.
HSSP; P01132; 1EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 XCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                     Lytechinus.
NCBI TaxID=7654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 45
Q25253
ID Q2525.
AC Q2525.
DT 01-NO
DT 01-MA.
DE NOMECH
GN NOMECH
GN NOMECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Forential.
Neurogenic locus notch homolog protein 3.
Notch extracellular truncation (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGF-like 9.
EGF-like 10, calcium-binding (Potential)
EGF-like 11, calcium-binding (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGF-like 4, calcium-binding (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGF-like B, calcium-binding (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGF-like 6, calcium-binding (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE: PSSO084; Nu, 3.

PROSITE: PSSO089, ANK REPEAT; 4.

PROSITE: PSSO089, ANK REPEAT; 4.

PROSITE: PSSO010; ASX HYDROXYL; 18.

PROSITE: PSSO026; EGF 1, 33.

PROSITE: PSSO026; EGF 3, 34.

PROSITE: PSSO026; EGF 3, 34.

PROSITE: PSSO187; EGF 3, 16.

Activator; ANK repeat; Developmental protein; Differentiation; Disease mutation; EGF-like domain, Glycoprotein;

Notch signaling pathway; Phosphorylation; Polymorphism; Receptor;

Repeat; Signal; Transcription regulation; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
Notch intracellular domain (By
similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytoplasmic (Potential),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 65; DB 1; Pred. No. 4.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.2%; Scor.
30.0%; Pred. No. 4...
13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300 CVCVNGWTGESCSQNIDDCATAVCFHGATC 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CXIXN----OXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                 Asx hydroxyl S.
ConA like_lec_gl.
EGF Z.
EGF Za.
EGF II.
EGF II.
EMBL, AF058999, AAC14346.1, JOINED.
EMBL, AC004257, AAC04897.1; -.
EMBL, AC004663, AAC15789.1; ALT_INIT.
PIR, S78549; S78549.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Potentia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPROJOGGO, NOD-
InterPro; IPROJOGGO, NOD-
InterPro; IPROJOGGO, NOCCh.
InterPro; IPROJOGGO, NOCCh.
InterPro; IPROJOGGO, NOCCh.
Ffam; PFOGOGO; EGF; 34.
Pfam; PFOGOGG; EGF; 34.
Pfam; PFOGOGG; NOCCh; 3.
PRINTS; PROJUTIS; NOCCH; 1.
PRINTS; PROJUTIS; ANKYRIN,
PRINTS; PROJUTIS; NOCCH; INTERPORTS; PROJUTIS; NOCCH; INTERPORTS; NOCCH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00248; ANK; 6.
SMART; SM00179; EGF_CA; 19.
SMART; SM00004; NL; 3.
                                                                                                                                                                                                              HGNC: 7883; NOTCH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                    P00740; 1EDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S:
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
TRANSMEM
                                                                                                                                                                HSSP; P(Genew; I
```

Gaps

ö

PRT; 2531 AA

PRELIMINARY;

O16004 ID 016004 RESULT 44

DOMAIN DOMAIN DOMAIN DOMAIN

CHAIN

DOMAIN DOMAIN DOMAIN

DOMAIN DOMAIN DOMAIN

```
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                           25-OCT-2004 (TrEMBLrel. 25-OCT-2004 (TrEMBLrel.
    Phytoxin-like SCR74.
                                                                                                                                                                                                                                                                                                                                                                              Phytoxin-like SCR74
                                                 NCBI_TaxID=4787;
                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phytophthora,
                                                                                                         Kamoun S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kamoun S.;
                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                    Q646V5
                                                                                                                                                                                                                                                                                                                                 0646V5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q646W1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 48
Q646W1
                                                                                                                                                                                                                                                                                              RESULT 47
    ઠે
                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                  STRAIN-SS seeking;
MEDLINE-98426367; PubMed=9753770; DOI=10.1016/S0965-1748(98)00032-0;
Chen Z., Newsome T., McKenzie J.A., Batterham P.;
"Molecular characterization of the Notch homologue from the Australian sheep blowfly, Lucilia cupinia.";
Insect Biochem. Mol. Biol. 28:601-612(1998).
EMBL: U58977; AAC36151.1;
HSSP; P07207; 1078.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
Calliphoridae; Lucilia.
NCBI_TaxID=7375;
                                                                    STRAIN=SS seeking,
MEDLINE=96400928; PubMed=8807304;
Davies A.G., Game A.Y., Chen Z., Williams T.J., Goodall S., Yen J.L.,
McKenzie J.A., Batterham P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                 "Scalloped wings is the Lucilia cuprina Notch homologue and a candidate for the modifier of fitness and asymmetry of diazinon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.2%; Score 65; DB 2; Length 265
29.2%; Pred. No. 5.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               285928 MW; 6AF2A058FEEC6329 CRC64;
                                                                                                                                                                                                                                                                              GO; GO:0016020; C:membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0030154; P:cell differentiation; IEA.
GO; GO:0030154; P:cell differentiation; IEA.
GO; GO:0030159; P:regulation of development; IEA.
InterPro; IPR00110; ANK.
InterPro; IPR001181; EGF 2.
InterPro; IPR001881; EGF 7.
InterPro; IPR001881; EGF 7.
InterPro; IPR001881; EGF 7.
InterPro; IPR001881; EGF 7.
InterPro; IPR001891; GO; NOCCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE, PSS0088; ANK_REPEAT; 5.

PROSITE; PSS0088; ANK_REPEAT; 5.

PROSITE; PSS0010; ASX_HYDROXYL; 22.

PROSITE; PS00121; EGF 1; 34.

PROSITE; PS01186; EGF 2; 28.

PROSITE; PS01186; EGF 2; 28.

PROSITE; PS01187; EGF 23; 36.

PROSITE; PS01187; EGF CA; 21.

ANK repeat; EGF-like domain.

SEQUENCE 2653 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   268 QGKNCEQNIDDCPGHLCQNGGTCI 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 XNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                 Notch_region.
                                                                                                                                                     Genetics 143:1321-1337(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 28, C
(TrEMBLrel. 28, I
(TrEMBLrel. 28, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIRSF; PIRSF002279; Notch; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00248; ANK; 7.
SMART; SM00179; EGF_CA; 24.
SMART; SM00004; NL; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00010; EGFBLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Jeam; PF07645; EGF_CA; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR01415; ANKYRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00066; Notch; 3
                                                                                                                                                                                                                                                                                                                                                                                                                         PEam; PF00023; Ank; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                 nterPro; IPR000800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
ses .7; Conserv
                                                          SEQUENCE FROM N.A
                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q646V4;
25-OCT-2004 (
25-OCT-2004 (
25-OCT-2004 (
                                                                                                                                           resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q646V4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 46
Q646V4
ID Q646V
AC Q646V
DT 25-OC
DT 25-OC
DT 25-OC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
```

```
ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                        "Patterns of Diversifying Selection in the Phytotoxin-like scr74 Gene Family of Phytophthora infestans."; Submitted (AUC-2004) to the EMBL/GenBank/DDBJ databases. EMBL, AY723713; AAU21454.1; SEQUENCE 74 AA; 7942 MW; CE020986B607E796 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Patterns of Diversifying Selection in the Phytotoxin-like scr74 Gene Family of Phytophthora infestans.";
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AY23711; AAU21452.1;
SEQUENCE 74 AA; 7825 MW; 537318AAFF612545 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                   SEQUENCE FROM N.A.
Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Liu Z., Bos'J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                53.8%; Score 64.5; DB 2; Length 74; 33.3%; Pred. No. 23; ive 11; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phytophthora infestans (Potato late blight fungus).
Eukaryota, stramenopiles, Oomycetes, Pythiales, Pythiaceae,
Phytophthora infestans (Potato late blight fungus).
Eukaryota, stramenopiles, Oomycetes, Pythiales, Pythiaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53.8%; Score 64.5; DB 2; Length 74; 33.3%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phytophthora infestans (Potato late blight fungus).
Eukaryota, stramenopiles, Oomycetes, Pythiales, Pythiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Phytoxin-like SCR74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 33.3%; Pred. No. 23; Matches 9; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 XCXQXLD-----DCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 XCXQXLD-----DCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :|:|::::|
45 KCCQAINADPIAFHDCCSKSCNTGSPC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 33.33
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
```

```
SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RC TISSUE-PERIPHEARIA N.A.

RX FEDILINE-22388227; PubMedia-12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE-22388237; PubMedia-12477932; DOI=10.1073/pnas.242603899;

RA Altachul S.F., Zeoberg B., Buetow K.H., Schamen C.M., Schuler G.D.,

RA Altachul S.F., Zeoberg B., Buetow K.H., Schamer C.F., Bhat N.K.,

RA Altachul S.F., Zeoberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S. I., Wang J., Hsieh F.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Uddin T.B., Toonhyuki S., Carninci P., Prange C.,

RA Bosak S.A., McChann P.D., McKernan K.J., Mallaly S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Bebey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schwutz J., Myers R.M., Butterfield Y.S.,

RA Gores S.J., Marra M.A.;

RG Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                   ;
                 "Parterns of Diversifying Selection in the Phytotoxin-like scr74 Gene Family of Phytophthora infestans."; Submity of Phytophthora infestans."; Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases..
EMBL; AY723705; AAUZ1446.1; -- SEQUENCE 74 AA; 7885 MW; 98D110005D613927 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
                                                                                                                                                                   / Match 53.8%; Score 64.5; DB 2; Length 74; Local Similarity 33.3%; Pred. No. 23, length 74; les 9; Conservative 11; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUB-Peripheral Nervous System;
Strausberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 14 EGF-like domains.
EMBL; BC063815; AAH63815.1; -- HSSP; P00743; IAPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                647 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0005509; F:calcium ion binding; IEA.
InterPro; IPR000152; Asx hydroxyl_S.
InterPro; IPR00042; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001438; EGF_II.
InterPro; IPR005209; EGF_IIke.
                                                                                                                                                                                                                                                               7 XCXQXLD-----DCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                              45 KCCQAINPDPIAFHDCCSKSCNTGSPC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWART; SM00181; BGF; 15.
SWART; SM00179; BGF_CA; 12.
PROSITE; PS00010; AŠX_HYDROXYL; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRODOLO; EGFBLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00008; EGF; 11.
Pfam; PF07649; EGF_CA; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                      Q6P3V5
Q6P3V5;
                                                                                                                                                                                                                                                                                                                                                                                  RESULT 49
O6623VG
DT O66-JUI
DE HYPOEL
OCC BURARY
OCC B
                                                                                                                                                                                               Best Loc
Matches
```

```
RADILINE-2196006; Pubbed=10731132; DOI=10.1126/science.287.5461.2185; RADILINE-2195006; Pubbed=10731132; DOI=10.1126/science.287.5461.2185; RADININE-2195006; Pubbed=10731132; DOI=10.1126/science.287.5461.2185; RADININE-2195006; Pubbed=10731132; DOI=10.1126/science.287.5461.2185; RADININE-2196006; RADININE-S.E., LiD P.W., Hoskins R.A., Galle R.F., Admans M.D., Celniker S.E., LiD P.W., Hoskins R.A., Galle R.F., Radicton G.G., Worteman J.R., Yandell M.D., Zhang Q., Chen L.X., Radicton G.G., Worteman J.R., Yandell M.D., Zhang Q., Chen L.X., Radicton G.G., Baxter E.G., Hell G., Nelson C.R., Baldwin D., RADILOR M.D., Ballew R.M., Basu A.M. Baxendale J., Baytaktaroglu L., Basaley E.M., RADILOR M., Baula M., Bauch G.J., Baytaktaroglu L., Basaley E.M., RADILOR M., Bothers J., Burchetein P., Bothiakov S., RADILOR M., Bouck J., Burchetein P., Bothiakov S., RADICHOR M., Boula M., Butler H., Cadicu E., Center A., Chandra I., RADICHOR M., Dugan-Rocha S., Dunkov B.C., Dunn P., RADICH K., Bungan D.A., Burler H., Gulan P., Harris M., Anderson M., Dugan-Rocha S., Dunkov B.C., Dunn P., RADICH K., Bangan C.C., Ferraz C., Ferraz C., Ferraz C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Adollan M., Harvey D., Heiman T.J., Hernandez J.R., Harris M., Harvey D., Heiman T.J., Harris M., Moushor K.A., Wollan P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Anderson D.L., Markulov G., Milshian N.V., Mobarry C., Morris J., Moshrefi A., Morleson D.L., Morris W., Moshrefi A., Moy M., Murphy B., Murphy L., Murshy D., Worles C., Worris J., Puris S., Shading X., Nadisan G., Stonder F., Shan H., Sping E., Spadling A.C., Stapen G., Morris G., Worley K., Walsen H., Shang C.Y., Wassarman D.A., Naison K., Mulliams S.M., WoodageT, Worley K.C., Worley K., Wolley M., Williams S.M., WoodageT, Worley K., Chu W. Stunger F., Shan H., Sping S., Yang S., Yang S., Yang S., Yang S., Zaveri J.S., Zaveri J.S., Zhan M., Zhong W., Zhong K., Zhan M., Zhong K., Wolley C., Worley K., Zhan M., Zhong K., Wolley C., Wolley C., Stepelecon S., Zhan M., Zhon
                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta, Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ebhydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                        Length 647;
                                                                                                                                   domain, Hyporhetical protein.
647 AA, 68068 MW; B71E79AA16E50CE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                             53.3%; Score 64; DB 2; Le:
33.3%; Pred. No. 1.9e+02;
ive 12; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY_2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-0CT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                            351 SCEENLDDCIAATCAPGSTCI 371
                                                                                                                                                                                                                                                                                                                                                                             7 XCXQXLDDCCSXXCNXXNXCV 27
                                                                 PS50026; EGF 3; 15.
PS01187; EGF CA; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 287:2185-2195(2000).
                                                                                                                                                                                                     Query Match
Best Local Similarity 33.3.
7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORFNames=CG15388;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                           SEQUENCE
                                                                                                                                          EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 50
Q9VQA9
```

```
Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PSS0923; SUSHI; 1.
EGF-like domain; Hypothetical protein.
SEQUENCE 1372 AA; 150561 MM; 0537FA79BA0576C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waterston R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WormBase Consortium;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases
EMBL; U00815; AAB37995.1; --
PIR; T25933; T25933.
01-MAR-2004 (TrEMBLRel. 03, Created)
01-MAR-2004 (TrEMBLRel. 03, Last sequence update)
Hypothetical protein W02C12.1.
Name=W02C12.1, ORFNames=W02C12.1;
Caenorhabditis elegans
Eukaryota, Metazo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.3%; Score 64; DB 2; I 25.0%; Pred. No. 3.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO, GO:0005509; F:calcium ion binding; IEA.
InterPro; IPR000152; Asx hydroxyl_S.
InterPro; IPR000152; Asx hydroxyl_S.
InterPro; IPR000142; EGF_Z.
InterPro; IPR00143; EGF_Z.
InterPro; IPR001438; EGF_II.
InterPro; IPR001438; EGF_II.
InterPro; IPR00150; EGF_III.
InterPro; IPR00170; Pentaxin.
InterPro; IPR001759; Pentaxin.
InterPro; IPR001759; Pentaxin.
InterPro; IPR000436; Sushi_SCR_CCP.
Pfam; PF00408; EGF; 10.
Pfam; PF00408; EGF; 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          elegans cosmid W02C12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; MiBmatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : ::|:|::|::| :::| :: :|: : :|: : :|: : :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 XNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP, Q12780, 1HAE.
WormBase, WBGene00020928, W02C12.1.
WormPep, W02C12.1; CE14412.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PROGOTO; EGPELOOD.
PRODOM; PRO10115; Pentaxin; 1.
SWART; SMO0179; EGF CA; 4.
PROSITE; PS000101, ASK HYDROXYL; 5.
PROSITE; PS000102; EGF L; 11.
PROSITE; PS01186; EGF Z; 8.
PROSITE; PS50022; EGF Z; 12.
PROSITE; PS01186; EGF Z; 8.
PROSITE; PS01186; EGF Z; 8.
PROSITE; PS01187; EGF Z; 12.
                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Bristol N2;
Murray J., Wohldmann P.;
"The sequence of C. elega
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WormBase Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Bristol N2
                                                                                                                                                                                                                                                                                                   NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                . d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                               Celliker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeifer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M., "Finishing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence.", Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDINE=22426069; PubMed=12537572;
Millara S., Crobby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.B., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Annotation of the Drosophila melanogaster euchromatic genome: a systematic review.";
Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 838 AA; 87786 MW; A654CDBE4FDF42B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53.3%; Score 64; DB 2; 28.0%; Pred. No. 2.3e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO, GO:0005509; F:calcium ion binding; IEA.
InterPro; IPR000152; Asx bydroxyl_S.
InterPro; IPR000142; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001438; EGF_II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :|: :|:::|:| |::| :::|
EIKGSNCEENVDECMSNPCQNGGLC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 XIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=22426070; PubMed=12537573;
                                                       MEDLINE=22426065; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00179; EGF_CA, 3.
PROSITE; PS00010; ASX HYDROXYL;
PROSITE; PS00020; EGF_1; 5.
PROSITE; PS01186; EGF_2; 3.
PROSITE; PS0026; EGF_3; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE003583; AAF51268.1; --
HSSP; P00740; 1EDM.
FlyBase; FBgn0031414; CG15388.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00008; EGF; S.
PRINTS; PR00010; EGFBLOOD.
SMART; SM00179; EGF_CA; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 28.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS01187
EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
```

FlyBаве;

RARARA BARARA BA

FlyBase;

ö

Gapa

ö

4; Indels

PRT; 1372 AA.

PRELIMINARY;

P91526 P91526; RESULT 51 P91526 ID P9152 AC P9152

ઠ 셤

Length 1372;

```
164951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genew;
MIM; 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
MEDLINES-99180765; PubMed-10079256;

MEDLINES-99180765; PubMed-10079256;

Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,
Barks A., Leinan J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.;
T. Human ligands of the Notch receptor.";
Am. J. Pathol. 154:785-794(1999).
C. - FUNCTION: Functions as a receptor for membrane-bound ligands
C. - Gomain (NICD) it forms a transfort cell-fate determination.
C. Upon ligand activation through the released notch intracellular
C. Gomain (NICD) it forms a transfortpitional activator complex with
RBF-J kappa and activates genes of the enhancer of split locus.
C. Affects the implementation of differentiation, proliferation and apoptotic programs. May regulate branching morphogenesis in the developing vascular system (By similarity).
C. SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EM) which are probably linked by disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isoid=Q99466-3; Sequence=VSP 001407;
TISSUE SPECIFICITY: Highly expressed in the heart, moderately in
the lung and placenta and at low levels in the liver, skeletal
muscle, kidney, pancreas, spleen, lymph node, thymus, bone marrow
and fetal liver. No expression was seen in adult brain or
peripheral blood leukocytes.
                                                                                                                                                                                                                                                                                                                                                   TISSUE=Placenta;
MEDLINE=97311416; PubMed=9168133; DOI=10.1016/S0378-1119(96)00857-8; Submayar K., Sasanuma S.-I., Nohata J., Kimura T., Fukagawa T., Nakamura Y., Ando A., Inoko H., Ikemura T., Mita K.; Gene organization of human NOTCH4 and (CTG)n polymorphism in this human counterpart gene of mouse proto-oncogene Int3.";
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1), AND POLYMORPHISM OF POLY-LEU REGION.
                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bonds (By similarity).
SUBCELLULAR LOCATION: Type I membrane protein. Following
Proteclytical processing NICD is translocated to the nucleus.
ALTERNAIUE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Bone marrow, and Heart, MEDLINE-98360091; PubMed=9693032; DOI=10.1006/geno.1998.5330; Li L., Huang G.M., Banta A.B., Deng Y., Smith T., Dong P., Friedman C., Chen L., Trask B.J., Spies T., Rowen L., Hood L.; Cloning, Characterization, and the complete 56.8-kilobase DNA genence of the human NOTCH4 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing, Named isoforms=3, Comment=Experimental confirmation may be lacking for some
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-503 FROM N.A., AND VARIANTS GLN-117 AND GLN-317.
Miyagawa T., Tokunaga K., Hojho H.;
"Human notch4 gene variant.";
                                           NTC4_HUMAN STANDARD; PRI; 2003 AA.
09946; 000306; 09948; 099940; 09H3S8; 09UI19; 09UIJ0;
28-FEB-2003 (Rel. 41, Created to the control of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=2;
IsoId=Q99466-2; Sequence=VSP_0014.06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=099466-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDENTIFICATION OF LIGANDS
                                                                                                                                                                                                                         Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isoforms;
                                                                                                                                                                                                    Name=NOTCH4;
      RESULT 52
NTC4_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -
```

```
control of the contro
```

```
SEQUENCE FROM N.A.
Hori S., Saitoh T., Matsumoto M., Makabe K.W., Nishida H.;
Hori S., Saitoh T., Matsumoto M., Makabe K.W., Nishida H.;
"Notch homologue from Halocynthia roretzi is preferentially expressed
in the central nervous system during ascidian embryogenesis.";
Dev. Genes Evol. 207.371-380(1997).
EMBL; AB001327; BAA25571.1; -.
PIR; T30201; T30201.
HSSP; P07207; L0T8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REINTS; PRO1452; NOTCH.

SMART; SM00248; ANK; 7.

SMART; SM000179; EGF_CA; 19.

REOSITE; PS50088; ANK REPEAT; 5.

PROSITE; PS50010; ASX-WPRGOXL; 18.

PROSITE; PS01016; EGF_1; 28.

PROSITE; PS01016; EGF_2; 22.

PROSITE; PS01186; EGF_2; 22.

PROSITE; PS01187; EGF_CA; 18.

REOSITE; PS01187; EGF_CA; 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53.3%; Score 64; DB 2; Length 2352; 26.9%; Pred. No. 6e+02; tive 13; Mismatches 6; Indels
                                                       Halocynthia roretzi (Sea squirt).
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Pyuridae; Halocynthia.
NCBI_TaxID=7729;
                                                                                                                                                                                                                                                                                                                                 O70244 PRELIMINARY; PRT; 3623 AA. 070244; CTEMBLrel. 07, Created) 01-ANG-1999 (TrEMBLrel. 09, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Intrinsic factor-B12 receptor precursor. Name=CUBILIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : EGFBLOOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 26.9
les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
                   HrNotch protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00010
                                       Name=HrNotch;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 54
070244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOW REAL TO THE REAL THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGF-like 2.
EGF-like 3.
EGF-like 3.
EGF-like 5.
EGF-like 6.
EGF-like 6.
EGF-like 6.
EGF-like 8. calcium-binding (Potential).
EGF-like 9. calcium-binding (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGF-like II, calcium-binding (Potential)
EGF-like 12, calcium-binding (Potential)
EGF-like I3, calcium-binding (Potential)
EGF-like I4, calcium-binding (Potential)
EGF-like I5, calcium-binding (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                            Potential.
Neurogenic locus notch protein homolog
Notch extracellular truncation (By
                                                                                             PROSITE; PSSO297; ANK REP REGION; 1.
PROSITE; PSSO089; ANK REPEAT; 5.
PROSITE; PSSO0010; ASX_HYDROXYL; 11.
PROSITE; PSO0010; ASX_HYDROXYL; 11.
PROSITE; PSO1086; EGF_2; 21.
PROSITE; PSO1186; EGF_2; 22.
PROSITE; PSO1187; EGF_3; 28.
PROSITE; PSO1187; EGF_67; 9.
Activator; Alternative splicing; ANK repeat; Developmental protein; Differentiation; EGF-1; PROSITE; PROSITE; PSO1187; PROSIDEOXYLation; Glycoprotein;
Differentiation; EGF-1; Phosphorylation; Polymorphism; Receptor;
Repeat; Signal; Transcription regulation; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Notch intracellular domain (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity).
Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytoplasmic (Potential).
EGF-like 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 64; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Pred. No. 5.26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Poly-Arg.
Lin/Notch 1.
                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGF-like 19.
EGF-like 20.
EGF-like 20.
EGF-like 21.
EGF-like 22.
EGF-like 23.
EGF-like 24.
EGF-like 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 2352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCEENLDDCIAATCAPGSTCI 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 XCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.3%;
33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 07, (TrEMBLrel. 07,
                                     SMART; SM00248; ANK; 5.
SMART; SM00179; EGF CA; 11.
SMART; SM00004; NL; 3.
                                                                                                                                                                                                                                                                                                                                 Triplet repeat expansion. SIGNAL 1 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1004
1044
1085
1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity :
                                                                                                                                                                                                                                                                                                                                                                                  24
1432
                                                                                                                                                                                                                                                                                                                                                                                                                                                1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O61240
O61240;
01-AUG-1998 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
TRANSMEM
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                  HAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 53
061240
ID 06124
AC 06124
DT 01-AU
```

ö

g

```
570 AA.
                                                                                                                                                                                                                             Cluster B.
Cluster B.
Cluster B.
Cluster B.
Cluster B.
Cluster A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CXIXNOXCXOXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                             6 CKCKNCRCRSCRKSCCSCCPAGCNNCV 32
                                                                                                                                                                                                                   Alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1996 (Rel. 33, Created)
                                                                                      EMBL; X62512; CAA44371.1; -.
                                                                                                                                                                                                                                                                                                                                                                           4429 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                               S33379; S18174.
                                                                                                        HSSP; P04355; 1MRT.
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strongylocentrotus.
NCBI_TaxID=7668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                          43 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FBP3_STRPU
P49013;
                                                                                                                                                                                                                                                                                                                                                              NON TER
SEQUENCE
                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 56
FBP3_STRPU
                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                             ô
          Moestrup S.K., Kozyraki R., Kristiansen M., Kaysen J.H., Rasmussen H.H., Brault D., Pontillon F., Goda F.O., Christensen B.I., Hammond T.G., Verroust P.J., Hammond T.G., Verroust P.J., "The intrinsic factor-vitamin Bl2 receptor and target of teratogenic antibodies is a megalin-binding peripheral membrane protein with homology to developmental proteins."; EMBL, AR022247; AAC71661.1; -. PIR; T08618; T08618.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Metallothionein B (MTB) (Fragment).
Colinus virginianus (Bobwhite quail) (Common bobwhite).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Odontophoridae; Colinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Liver,
MEDLINE=93247066; PubMed=8483164;
Shartzer K.L., Kage K., Sobieski R.J., Andrews G.K.;
"Evolution of avian metallothionein: DNA sequence analyses of the turkey metallothionein gene and metallothionein pheasant
                                                                                                                                                                                                                                                                                                                                                             .
0
MEDLINE=98148073; PubMed=9478979; DOI=10.1074/jbc.273.9.5235;
                                                                                                                                                                                                                                                                                                                                     53.3%; Score 64; DB 2; Length 3623; 29.2%; Pred. No. 8.9e+02; Live 13; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                              1 20 Potential.
21 3623 intrinsic factor-B12 receptor.
3623 AA, 398984 WW, 39FB792AC6545240 CRC64;
                                                                                            43 AA
                                                                                                                                                                                                                                                                                                                                                                                      : |:|::::|| |::| ::|:
425 SGQNCTENINDCSSNPCLNGGTCI 448
                                                                                                                                                                                                                                                                                                                                                                           4 XNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                            PROSITE; PS00022; EGF 1; 4.
PROSITE; PS01186; EGF 2; 2.
PROSITE; PS50026; EGF 2; 3; 6.
PROSITE; PS01187; EGF CA; 4.
EGF-like domain; Receptor; Signal.
                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 29.27
Period 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9014;
                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                             MTB COLVI P27087;
                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 55
MTB_COLVI
  ò
                                                                                                                                                                                                                                                                                                                                                                                            a
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Gastrula;
MEDLINE=93273088; PubMed=8500658; DOI=10.1006/dbio.1993.1155;
Bisgrove B.W., Raff R.A.;
"The SpEGF III gene encodes a member of the fibropellins: EGF repeat-containing proteins that form the apical lamina of the sea urchin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strongylocentrotus purpuratus (Purple sea urchin)
Bukaryota; Metazoa; Echinodermata; Bleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1996 (Rel. 3), Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Fibropellin C precursor (Epidermal growth factor-related protein (EGF III) (Fibropellin III).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.5%; Score 63; DB 1; Length 43; 33.3%; Pred. No. 20; ive 10; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         embryo."; -
Dev. Biol. 157:526-538(1993).
-1- FUNCTION: Forms the apical lamina, a component of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1612EB40EE6EB875 CRC64;
                                                                                                                                                                                                                                                   InterPro; 1PR000006; Metallthion.
InterPro; IPR000006; Metallthion.
InterPro; IPR001212; Somatomedin.B.
InterPro; IPR001313; Metallothio, 1.
PRINTS; PR00620; MTVERTERRATE.
PRINTS; PR00022; SOMATOMEDINB.
PROSITE; PS00203; METALLOTHIONEIN_VRT; PARTIAL.
NOW TER.
DOMAIN <1 1 16 Beta.
```

ô

```
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TROM N.A.

SEQUENCE TROM N.A.

STRAIN-25788.57; PubMed=1247932; DOI=10.1073/pnas.242603899;

KA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altechul S.P., Zeeberg B., Buetow K.H., Schnefer C.R., Schuler G.D.,

RA Altechul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Rapleton M., Soarse M.B., Bonaldo M.F., Carannor T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toohhyuki S., Carninci P., Frange C.,

RA Brownstein M.J., Usdin T.B., Toohhyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Wokernan R.J., Marason R.D., Mullahy S.J.,

RA Brownstein M.J., Wokernan R.J., Marason R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

RA Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Richards R.M., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Gones S.J., Marra M.A.;

RA Gones S.J., Marra M.A.;

RA Gones S.J., Marra M.A.;

RA Mannes C.M. Schmutz J., Myers R.M., Schein J.E.,

RA Gones S.J., Marra M.A.;

RA Gones S.J., Marra M.A.;

RA Mannes C.M. Schmutz J., Myers R.M., Butterfield Y.S.,

RA Mannes C.M. Saniska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Gones S.J., Marra M.A.;

RA Mannes C.M. Saniska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Mannes C.M. R. Saniska U., Smailus O. Full-length human A.M. Wang R.M., Butterfield M. S.,

RA Mannes C.M. Marka R.M., Smailus C.M. Schole R.D., Schmutz J. Schm
                                                                                                                                                                                                                                                                                            Gaps
By similarity.
N-linked (GLCNAC. ...) (Potential).
N-linked (GLCNAC. ...) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
1- SIMILARITY: Contains 6 EGF-like domains.
EMBL, BCG52002, AAH52002.1;
RSP; P00740; 1EDM.
RSP; P00740; 1EDM.
RGJ; GO:0005615; C:extracellular space; TAS.
RGJ; GO:0005615; C:extracellular specification; IMP.
R InterPro; IPR001438; EGF_1:
R InterPro; IPR001438; EGF_1:
R InterPro; IPR006209; EGF_1:
                                                                                                                                                                                                                                               Query Match 52.5%; Score 63; DB 1; Length 570; Best Local Similarity 26.9%; Pred. No. 2.1e+02; Matches 7; Conservative 12; Mismatches 7; Indels
                                                                                                                                                                                                             BE665E3E1C05E6EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Delta-like 3, isoform 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                585 AA
                                                                                                                                                                                                                                                                                                                                                      205 GFTGDNCETDIDECASAPCRNGGACV 230
                                                                                                                                                                                                                                                                                                                                   2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                             61116 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
  3363
344
3419
336
357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
354 33
370 33
3975 43
408 44
413 44
430 44
310 13
3157 3357 570 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=D113;
                     DISULFID
DISULFID
DISULFID
                                                                                 DISULFID
DISULFID
DISULFID
                                                                                                                                             CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q80W06
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 57
Q80W06
    511111111
                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
                                                                                                                                                                                                               SUBCELLULAR LOCATION: Extracellular.
DevELDOMBNYAL STAGE: Low levels in unfertilized eggs and during early cleavage, then rapidly increases in abundance between late morula and mesenchyme blastula stages to maximal levels maintained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE, PRO0010, ASK HYDROXYL, 8.
PROSITE; PRO1010, CUB. 1.
PROSITE; PS010180; CUB. 1.
PROSITE; PS01022; EGF 1; 8.
PROSITE; PS01086; EGF 2; 7.
PROSITE; PS01086; EGF 2; 7.
PROSITE; PS01187; EGF CA, 6.
Biotin, Calcium-binding; EGF-1ike domain; Glycoprotein; Repeat;
                                                                                                  through subsequent stages.

MISCELLANEOUS: Expressed both maternally and zygotically.
SIMILANITY: Contains 1 avidin domain.
SIMILANITY: Contains 1 CUB domain.
SIMILANITY: Contains 8 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 calcium-binding (
calcium-binding (
calcium-binding (
calcium-binding (
calcium-binding (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGF-like 5, calcium-binding
EGF-like 6, calcium-binding
EGF-like 7.
EGF-like 8, calcium-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Potential.
Fibropellin C.
EGF-like 1.
CUB.
EGF-like 2, calc
EGF-like 3, calc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR00152; Asx hydroxyl S. InterPro; IPR005469; Avidin. InterPro; IPR005469; Avidin/str. InterPro; IPR000859; CUB. InterPro; IPR0000859; CUB. InterPro; IPR001891; EGF_2. InterPro; IPR001891; EGF_II. InterPro; IPR001438; EGF_II. InterPro; IPR005209; EGF_II. Pfam; PP01382; Avidin; 1. Pfam; PP001008; EGF; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Avidin
                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L07045; AAA30045.1; -. PIR; A48836; A48836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00709; AVIDIN.
PRINTS; PR00010; EGFBLOOD.
  extracellular matrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P00740; 1EDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2114
2252
230
2336
2336
233
233
233
233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal.
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
```

```
TRANSMEM
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T., Sugiki Y., Nagai K., Sugano S., Ishii S., Kawai Hio Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K., Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N., Hattori A., Okumura K., Iwayanagi T., Ninomiya K.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

-I - SIMILARITY: Contains 6 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                          Query Match 52.5%; Score 63; DB 2; Length 585; Best Local Similarity 30.8%; Pred. No. 2.1e+02; Matches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 587;
                                                                                                                                                585 AA; 61125 MW; EB276F60899BD4E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                587 AA; .61144 MW; 2FF5E3EA66789B1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein FLJ90821.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52.5%; Score 63; DB 2; I 30.8%; Pred. No. 2.1e+02; vative 10; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                             587 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  589 AA
                                                                                                                                                                                                                                                       380 GFAGPRCEHDLDDCAGRACANGGTCV 405
            InterPro; IPR001005; Myb_DNA_binding. PERM, PF00008; RGF; 5.
PRINTS; PR00010; EGFBLOOD. SWART; SW00181; EGF; 6.
PROSITE; PS01082; EGF 1; 6.
PROSITE; PS01186; EGF 2; 6.
PROSITE; PS0026; EGF 3; 5.
PROSITE; PS0334; MYB=2; UNKNOWN_1.
                                                                                                                                                                                                                                    2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P00740; IEDM.
InterPro; IPR000742; EGF 2.
InterPro; IPR0001438; EGF 1.
InterPro; IPR006209; EGF like.
InterPro; IPR006210; IEGF.
InterPro; IPR0001005; Myb_DNA_binding.
Pfan; PP00009; EGF 5.
PRINTS; PR00010; EGFBLOOD.
BARNT; SM00101; EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           382 GFAGPRCEHDLDDCAGRACANGGTCV 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00022; EGF 1; 6.
PROSITE; PS01186; EGF 2; 6.
PROSITE; PS0026; EGF 3; 6.
PROSITE; PS00334; MYB 2; UNKNOWN 1.
EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLL3 RAT STANDARD;

ID DLL3 RAT STANDARD;

AC 088671;

DT 16-OCT-2001 (Rel. 40, Created)
InterPro; IPR006210; IEGF
                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                  PROSITE; PS00334
EGF-like domain.
SEQUENCE 585 A
                                                                                                                                                                                                                                                                                                                                         Q8NBS4
Q8NBS4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 59:
                                                                                                                                                                                                                                                                                                            RESULT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                           Q8NBS4
ò
                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                            -!-DISEASE: A truncating mutation in Dl13 is the cause of the pudgy (pu) phenotype. Pudgy mice exhibit patterning defects at the earliest stages of somitogenesis. Adult pudgy mice present severe vertebral and rib deformities.
-!-SIMILARITY: Contains 1 DSL domain.
-!-SIMILARITY: Contains 6 EGF-like domains.
      TISSUE SPECIFICITY: Predominantly expressed in the neuroectoderm
                                                                                                                                                                                                                                                                                                                                                                                                                                              REMBL; ALBOS; LAMA33716.1; -.

REMBL; AB013440; BAA33716.1; -.

R HSSP; P00740; IEDM.

R GO; GO:0005112; F:Notch binding; NAS.

GO; GO:0007386; P:cell fate determination; NAS.

GO; GO:0007386; P:cell fate determination; IMP.

GO; GO:0007399; P:neubryonic development (sensu Mammalia); NAS.

GO; GO:0007399; P:neubryonic development; IMP.

GO; GO:0007219; P:Notch signaling pathway; NAS.

GO; GO:0007501; P:Rold, Signaling pathway; NAS.

R GO; GO:000742; EGF 2.

R InterPro; IPR001438; EGF 1.

R InterPro; IPR001438; EGF 1.

R PROSTIE; PR00010; EGFE 2.

R PROSTIE; PR00106; EGF 2.

R PROSTIE; PR01166; EGF 3; 6.

R PROSTIE; PS01186; EGF 3; 6.

R Alternative splicing; Developmental protein; Differentiation;

M EGF 11ke domain; Notch signaling pathway; Repeat; Signal;
                         and paraxial mesoderm during embryogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Potential.
Delta-like protein 3.
Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytoplasmic (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGF-like 1.
EGF-like 2.
EGF-like 3.
EGF-like 4.
EGF-like 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Potential
                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF068865; AAC40170.1; -. EMBL; AF068865; AAC40169.1; -. EMBL; Y11895; CAA72637.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pransmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDILINE=98324780; PubMed=9662403; DOI=10.1038/961; Kusumi K., Sun E.S., Kerrebrock A.W., Bronson R.T., Chi D.-C., Blulotesky M.S., Spencer J.B., Birren B.W., Frankel W.N., Lander E.S.; "The mouse pudgy mutation disrupts Delta homologue Dll3 and initiation of early somite boundaries.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nakayama K., Nakayama N., Tomooka Y., Hayashi Y., Takahashi M.;
"Specific expression of a divergent type of Delta in a set of earliest generated neurons including the prospective subplace neurons.";
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Inhibits primary neurogenesis. May be required to divert neurons along a specific differentiation pathway. Play a role in the formation of somite boundaries during segmentation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DLL3 MOUSE

ID DLL3 MOUSE

O88516; 035675; 090WL2;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 25-JAN-2005 (Rel. 46, Last annotation update)

DD DE Delta-like protein 3 precursor (Drosophila Delta homolog 3) (M-Delta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6 X DBA; TISSUE=Embryo;
STRAIN=C57BL/6 X DBA; TISSUE=Embryo;
MEDLINE=97417575; PubMed=9272948;
Dunwoodie S.L., Henrique D.M.P., Harrison S.M., Beddington R.S.P.;
"Mouse D113: a novel divergent Delta gene which may complement the
function of other Delta homologues during early pattern formation in
                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               paraxial mesoderm.
SUBUNIT: Can bind and activate Notch-1 or another Notch receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Type I membrane protein (Probable).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                52.5%; Score 63; DB 1; Length 589; 30.8%; Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                         8; Indels
                                                                                                                                                                                                          A17B3BF9B95EC17F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
                                                                                similarity.
similarity.
                                                               similarity
                           similarity
                                          similarity
                                                                                                                           similarity
                                                                                                                                            similarity
                                                                                                                                                                                                                                                                                         10; Mismatches
                                                                                                                                                                    similarity
                                                                                                                                                                                     similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=088516-2; Sequence=VSP_001376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=088516-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                         384 GFAGPRCEHDLDDCAGRACANGGTCV 409
                                                                                                                                                                                                                                                                                                                                 2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
      Development 124:3065-3076(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                          61424 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nat. Genet. 19:274-278(1998).
                                                                                                                                                                                                                                                                   Local Similarity 30.8
1es 8; Conservative
    Mus musculus (Mouse).
  tube;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mouse embryo.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=129/SvJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Probable)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Neural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=Dll3;
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                               DISULFID
DISULFID
DISULFID
                                                                                                                                                                                  DISULFID
                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                           Matches
  FT
FT
FT
FT
FT
SO
                                                                                                                                                                                                                                                                                                                                                                       용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DDJJJAC
DDJJAC
DD
```

```
Genew; HGNC:2909; DLL3.
H-InvDB; HIX0015121; -.
MIM; 602768; -.
MIM; 277300; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26
618
618
513
2213
310
310
331
231
231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal; Transmembrane.
SIGNAL 1 26
CHAIN 27 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27
493
514
176
216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
TRANSMEM
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
DISULFID
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULENCE-22386357; Pubbmed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Harberg E., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Bachenko L., Marusina K., Farmer A.A., Rubin G.M., Hnon L.,
Bacheron M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
Rablecon M., Jodin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Robards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Nichards S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.M., Blakesley R.W., Touchman M., Madan A., Rodrigues S., Sanchez A.M., Blakesley R.W., Touchman J.W., Grewchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Grewchenko Y., Bouffard G.G.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Generation and initial analysis of moze than 15,000 full-length human mouse cDNA sequences.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor:

JERBARS: Defects in DLL3 are the cause of autosomal recessive spondylocostal dysostosis type 1 (SCDO1) [MIM:277300]. SCDO1 is characterized by multiple hemivertebrae, rib fusions and deletions with a non-progressive kyphoscoliosis.
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND VARIANT SCDO1 ASP-385.
MEDLINE=20206573; PubMed=10742114; DO1=10.1038/74307;
Bulman M.P., Kusumi K., Frayling T.M., McKeown C., Garrett C.,
Lander E.S., Krumlauf R., Hattersley A.T., Ellard S., Turnpenny P.D.;
defects in the human delta homologue, DLL3, cause axial skeletal
Nat. Genet. 24:438-441(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99.16899-16903 (2002).
-!- FUNCTION: Inhibits primary neurogenesis. May be required to divert neurons along a specific differentiation pathway. Play a role in the formation of somite boundaries during segmentation of the
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                paraxial mesoderm (By similarity).
SUBUNIT: Can bind and activate Notch-1 or another Notch receptor
                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Type I membrane protein (Probable).
DOMAIN: The DSL domain is required for binding to the Notch
                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Delta-like protein 3 precursor (Drosophila Delta homolog 3)
                                                                              Length 592;
  DWLIQVLF -> A (in isoform 1)
                                                                       1 S2.5%; Score 63; DB 1; Length 592 Similarity 30.8%; Pred. No. 2.2e+02; 8; Conservative 10; Mismatches 8; Indels
             /FTIG=VSP_001376.
E -> K (in Ref. 3).
G -> A (in Ref. 1).
: 1A84F8022E7E7DCC CRC64;
                                                                                                                                                                                                                618 AA
                                                                                                                                      380 GFAGPRCEHDLDDCAGRACANGGTCV 405
                                                                                                                         2 XIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                PRT;
                                    401 G
62069 MW;
                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                592 AA;
                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (By similarity)
                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                          94
                                                                                                                                                                                                         DLL3 HUMAN
Q9NY<u>J</u>7;
                                                                                                                                                                                                                                                                                     Name=DLL3;
                       CONFLICT
                                                SEQUENCE
 VARSPLIC
                                                                        Query Match
                                                                                                                                                                                               HUMAN
                                                                                     Best Loc
Matches
                                                                                                                                                                                   RESULT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -
FT FT S
                                                                                                                                             g
                                                                                                                                                                                                            ò
```

```
Dev. Dyn. 225:384-391(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences.
                                                                         Xenopodinae; Xenopus
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P00740; 1EDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PSS0026;
PROSITE; PS01187;
EGF-like domain.
SEQUENCE 642 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   initiative.";
     SOW SORRY STREET STREET
                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                               52.5%; Score 63; DB 1; Length 618; 30.8%; Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 642;
                                                                                                                                    8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52.5%; Score 63; DB 2; Length 642
30.8%; Pred. No. 2.38+02;
ive 11; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to the EMBL/GenBank/DDBJ databases.
/FTId=vAR_016776.
G -> D (in_SCDO1).
/FTId=vAR_009952.
; 58A9BC0A7DEAD1A0_CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              642 AA; 70667 MW; D7DC31EB9D92820C CRC64;
                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Jen W.C., Wettstein D.A., Chitnis A.B., Kintner C.;
Jen W.C., Wettstein D.A., Chitnis A.B., Kintner C.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ datab
EMBL; U70843; AAB37131.1;
HSSP; P00740; 1EDW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0016020; C:membrane; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:000754; P:call communication; IEA.
INCERPO; IPR00172; Asx hydroxyl_S.
INCERPO; IPR001774; DSL.
INCERPO; IPR00181; EGF Z.
INCERPO; IPR00181; EGF Z.
INCERPO; IPR00181; EGF Z.
INCERPO; IPR00181; EGF Z.
                                                                                                                                                                                                                                                                                                             642 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  642 AA
                                                                                                                                    10; Mismatches
                                                                                                                                                                                                382 GFAGPRCEHDLDDCAGRACANGGTCV 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     415 GFSGPRCELNIDDCASSPCANGGTCV 440
                                                                                                                                                                          2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                             01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequ-
01-MAR-2004 (TrEMBLrel. 26, Last anno-
Notch Jagand X-Delta-2.
Name=X-Delta-2;
Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00010; ASX HYDROXYL; 2. PROSITE; PS00022; EGF 1; 8. PROSITE; PS01186; EGF 3; 6. PROSITE; PS01187; EGF 3; 6.
                                                         618 AA; 64617 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 24, (TrEMBLrel. 24, I
                                                                                                                Best_Local Similarity 30.8%
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF07645; EGF CA; 1.
PRINTS; PR00010; EGFBLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00051; DSL; 1.
SMART; SM00179; EGF_CA; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 30.8
                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01414; DSL; 1.
Pfam; PF00008; EGF; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopodinae; Xenopus
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGF-like domain
SEQUENCE 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2003 (
01-JUN-2003 (
01-MAR-2004 (
                                                         SEQUENCE
                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                   VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q7ZXT4
                                                                                                                                                                                                                                                                     RESULT 62
P79941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 63
Q72XT4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
 FF F S
                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                           22555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
```

```
Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Alausmer R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casrainci P., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Robark S.A., McZwan P.J., McKernan R.J., Malek J.A., Gunarane P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Embryo;
MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia; Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                           TISSUE-Embryo;
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.5%; Score 63; DB 2; Length 642; 30.8%; Pred. No. 2.3e+02; ive 11; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Klein S., Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC044262; AAH44262.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     642 AA; 70655 MW; S6AFB4013E1C2AE2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0016020; C:membrane; IEA.
GO; GO:0005509; F:calcium ion binding; IEA
GO; GO:0007154; P:cell communication; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INCEPPO: IPRODO152; ABX hydroxyl_S.
INCEPPO: IPROD0152; ABX hydroxyl_S.
INCEPPO: IPROD0174; DSL.
INCEPPO: IPROD188; EGF_Ca.
INCEPPO: IPROD188; EGF_Ca.
INCEPPO: IPROD188; EGF_II.
INCEPPO: IPROD188; EGF_II.
FEam; PFO01414; DSL; 1.
FEam; PFO0008; EGF; 5.
FEAM; PFO0008; EGF; 5.
FRANTS; PROD10; EGFBLOOD.
SWART; SWO010; EGFBLOOD.
SWART; SWO0119; EGF CA; 1.
FROSITE; PSO0012; EGF_CA; 3.
PROSITE; PSO0012; EGF_CA; 1.
```

```
EGF-like 1.

EGF-like 2.

EGF-like 3.

EGF-like 4.

EGF-like 4.

EGF-like 6, calcium-binding (Potential).

EGF-like 7, calcium-binding (Potential).

EGF-like 8.

EGF-like 9.

EGF-like 10.

EGF-like 11.

EGF-like 11.

EGF-like 12.

EGF-like 13.

EGF-like 14.

EGF-like 14.

EGF-like 15.

EGF-like 16.

EGF-like 16.

EGF-like 17.

EGF-like 18.

EGF-like 19.

EGF-like 19.

EGF-like 19.

EGF-like 19.

EGF-like 10.

EGF-like 
                                                                     protein; EGF-like domain; Glycoprotein;
                                                                                                                 Extracellular (Potential)
                                                                                                                             Potential.
Cytoplasmic (Potential).
DSL.
      By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Potential.

Potential.

By similarity.

By similarity.
                                                                                                              DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                    DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULPID
                                                                                                                                                         DOMAIN
                                                                                                                                                                                                               DOMAIN
         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics institute. There are no restrictions on its web by non-profit institutions as long as its content is in no way modified and this statement is nor removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REMBLY UNGOSO, AACE2946.1; --
REMBLY UNGOSO, AACE2946.1; --
R GD; 2938; Jag2.
R GO; GO:0008083; Egrowth factor activity; ISS.
R GO; GO:0008083; Egrowth factor activity; ISS.
R GO; GO:0007049; P:cell differentiation; NAS.
R GO; GO:0007049; P:cell differentiation; NAS.
R GO; GO:0007049; P:cell differentiation; NAS.
R GO; GO:0007099; P:cell differentiation; NAS.
R GO; GO:0007099; P:cell differentiation; NAS.
R GO; GO:0007099; P:limb morphogenesis; NAS.
R GO; GO:0007219; P:limb morphogenesis; NAS.
R GO; GO:0007219; P:regulation of cell migration; ISS.
R GO; GO:0007283; P:regulation of cell migration; ISS.
R GO; GO:000438; P:T-cell differentiation; ISS.
R InterPro; IPR000142; RGF_2.
R InterPro; IPR000143; RGF_1I.
R InterPro; IPR001881; RGF_2.
R InterPro; IPR001881; RGF_2.
R InterPro; IPR001881; RGF_2.
R InterPro; IPR001891; PMP_SGCI.
R Ffam; PP01414; DPMP_SGCI.
                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
29-JAN-2005 (Rel. 46, Last annotation update)
Jagged 2 (Jagged2) (Fragment).
                                                                                                      PRT; 1.202 AA
               2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01414; DSL; 1.
Pfam; PF00008; EGF; 14.
PRINTS; PR00010; EGFBLOOD.
PROSITE; PS00010; ASX_HYDROXYL; 10.
                                                                                                    STANDARD;
                                                                                                                                                                                                        Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                            TISSUE=Brain;
                                                                                                                                                                                          Name=Jag2;
                                                                                                   JAG2 RAT
                                                                                                               P97607
```

```
-i- SIMILARITY: Contains 1 DSL domain.
-i- SIMILARITY: Contains 16 EGF-like domains.
-i- SIMILARITY: Contains 1 VWFC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Potential
                                                                                                                                                                                                                  EMBL, AF020201; AAB71189.1; BMBL, AF020201; AAB61285.1; BMBL, AF029778; AAB84215.1; EMBL, AF029778; AAB84216.1; EMBL, AF111170; AAD15562.1; BMBL; X14330; CAA74706.1; HSSP; P01132; 1GKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11080
11105
11080
1238
2240
2240
3345
421
421
459
634
634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01414; DSL; 1.
Pfam; PF00008; EGF; 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27
27
1081
1106
178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM LONG).

MEDLINE=97459705; PubMed=9315665;
Luo B., Aster J.C., Hasserjian R.P., Kuo F., Sklar J.;

Lao B., Aster J.C., Hasserjian R.P., Kuo F., Sklar J.;

Isolation and functional analysis of a cDNA for human Jagged2, a gene encoding a ligand for the Nocchi receptor.";

Mol. Cell. Biol. 17:6057-6067(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Short; Synonyma=HJAG2.del-E6; Isol=G9Y19-2; Sequence=VSP 001395; Isol=G9Y19-2; Sequence=VSP 001395; TISSUE SPECIFICITY: Expressed in heart, placenta and skeletal muscle and to a lesser extend in pancreas. Very low expression in brain, lung, liver and kidney.

DISBASE: May be associated to Usher syndrome type IA (USHAIA) which describes a congenital sensory deafness associated with retinitis pigmentosa and feeble-mindedness.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUB=Fetal brain;
MEDLINE=99180765; PubMed=10079256;
Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,
Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.;
"Human ligands of the Notch receptor.";
                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Characterization, chromosomal localization, and the complete 30-kb DNA sequence of the human Jagged2 (JAG2) gene.";
Genomics 63:133-138(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Bone marrow;
MEDLINE=20130121; PubMed=10662552; DOI=10.1006/geno.1999.6045;
Deng Y., Madan A., Banta A.B., Friedman C., Trask B.J., Hood L.,
                                                                                                                 ö
                                                                        Query Match 52.5%; Score 63; DB 1; Length 1202; Best Local Similarity 23.1%; Pred. No. 4.1e+02; Matches 6; Conservative 13; Mismatches 7; Indels
 791 806 By similarity.
808 817 By similarity.
1202 AA, 129703 MW; 09CB44E5271FF8BE CRC64;
                                                                                                                                                                                                                                                                              UAG2 HUMAN STANDARD; PRT; 1238 AA. 09Y219; 09YED9; 09UEB9; 09UEB9; 09VED0; 09YEB-2003; 09Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 17-1238 FROM N.A. (ISOFORM LONG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=Q9Y219-1; Sequence=Displayed;
                                                                                                                                                                         582 GFTGTYCHENIDDCMGQPCRNGGTCI 607
                                                                                                                                                  2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                            Jagged 2 precursor (Jagged2) (HJ2)
Name=JAG2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM LONG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Am. J. Pathol. 154:785-794 (1999).
                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=Long;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Heart;
DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -
                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                     셤
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS: PROBLES PROBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MINI, 60270;

R MINI, 60270;

R MINI, 60270;

R GO; GO: 0005887; C: integral to plasma membrane; ISS.

R GO; GO: 0000503; F:growth factor activity; IDA.

R GO; GO: 0000512; F:Notch binding; IPI.

R GO; GO: 00007049; P:cell cycle; NAS.

R GO; GO: 00007049; P:cell differentiation; IDA.

R GO; GO: 00007267; P:cell differentiation; NAS.

R GO; GO: 00007267; P:cell-cell signaling; ISS.

R GO; GO: 00007219; P:nimb morphogenesis; ISS.

R GO; GO: 0007219; P:Notch signaling pethway; NAS.

R GO; GO: 0007219; P:Notch signaling pethway; NAS.

R GO; GO: 0007219; P:Precupation of cell migration; IDA.

R GO; GO: 0007219; P:requiation of cell migration; IDA.

R GO; GO: 0004217; P:requiation of cell migration; IDA.

R GO; GO: 0004207; P:requiation of cell migration; IDA.

R GO; GO: 0004207; P:requiation of cell migration; IDA.

R GO; GO: 0004207; P:requiation of cell migration; IDA.

R GO; GO: 0004207; P:requiation of cell migration; IDA.

R InterPro; IPR00174; BGF Z.

R InterPro; IPR00174; BGF Z.

R InterPro; IPR00184; EGF Z.

R InterPro; IPR00184; EGF Z.

R InterPro; IPR00184; PMP_SGCI.

R InterPro; IPR00143; PMP_SGCI.

R Pfam: PR01414; DSL: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGF-like 3.
EGF-like 3.
EGF-like 4.
EGF-like 5.
EGF-like 6, calcium-binding (PEGF-like 7, calcium-binding (PEGF-like 9.
EGF-like 9.
EGF-like 9.
EGF-like 10 (atypical).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jagged 2.
Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytoplasmic (Potential). DSL.
```

ò

```
calcium-binding (Potential)
calcium-binding (Potential)
                                                      (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Missing (in isoform Short).

/FIGH-VSP (001395.

RLPRR -> KIPPPA (in Ref. 1).
L -> F (in Ref. 1).
L -> F (in Ref. 1).
L -> SA (in Ref. 1).
L -> SA (in Ref. 1).
K -> E (in Ref. 1).
ANE -> VND (in Ref. 1).
X -> E (in Ref. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Potential).
(Potential).
(Potential).
(Potential).
(Potential).
                                                  calcium-binding calcium-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GlcNAc. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GlcNAc. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 63; DB 1; Le
Pred. No. 4.2e+02;
1; Mismatches 7;
                                                                                   By similarity.
By sim
   EGF-like 11, c
EGF-like 12, c
EGF-like 13.
EGF-like 14.
EGF-like 16, c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-linked
N-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.5%; 23.1%;
  Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                   DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                               DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                            DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                              DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
DISULFID
DISULFID
                                                                                                                                                              DISULFID
                                                                                                                                                                         DISULFID
                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
```

```
MEDLINE=97459705; PubMed=9315665;

MEDLINE=97459705; PubMed=9315665;

Luo B., Aster J.C., Hasserlian R.P., Kuo F., Sklar J.;

Luo B., Aster J.C., Hasserlian R.P.

Toolation and functional analysis of a cDNA for human Jagged2, a gene conding a ligand for the Notch1 receptor.";

Mol. Cell. Biol. 17:607-667(1997).

The Mol. Cell. Biol. 17:607-667(1997).

Thymic development way be involved in myogenesis and in the signaling. Plays an essential role during limb, craniofacial and cevelopment of peripheral and central nervous systems.

Thymic development of peripheral and central nervous systems.

Thymic SPECIFICITY: Found to be highest in fetal thymus, epidermis, foregut dorsal root ganglia and inner ear. In 2-week.

Cla mice, abundant in heart, lung, thymus, skeletal muscle, brain and thesetis. Expression overlaps partially with Notch1 expression.

Cloral root ganglia. At 13 dpc, found in paravertebral vessels and developing thymus and in the muscles of the tongue. By 15 dpc, in many tisning them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lan Y., Jiang R., Shawber C., Weinmaster G., Gridley T.; "The Jagged2 gene maps to chromosome 12 and is a candidate for the lgl and sm mutations.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Brain;
MEDLINE=98145947; PubMed=9486542; DOI=10.1016/S0925-4773(97)00146-9;
Valsecchi C., Ghezzi C., Ballabio A., Rugarli E.I.;
"JAGGED2: a putative Notch ligand expressed in the apical ectodermal ridge and in sites of epithelial-mesenchymal interactions.";
Mech. Dev. 69:203-207(1997).
                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                     UAG2_MOUSE STANDARD; PRT; 1247 AA. 2070XE2, 055139; 07019; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 25-JAN-2005 (Rel. 46, Last annotation update) Name=Jag2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMÎLARITY: Contains 1 DSL domain.
SIMÎLARITY: Contains 16 EGF-like domains.
                     627 GFTGTYCHENIDDCLGQDCRNGGTCI 652
2 XIXNOXCXQXLDDCCSXXCNXXNXCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 302-819 FROM N.A. TISSUE-Brain; MEDLINE-98051918; PubMed-9341252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF038572; AAF16411.1; -. EMBL; AF010137; AAC14010.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [3]
SEQUENCE OF 325-759 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mamm. Genome 8:875-876(1997)
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=Swiss Webster / NIH;
                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       many tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                Tsai S.;
                                                                                                                                         셤
```

ö

Gaps

ö

13;

Conservative

Length 1238; Indels

```
061204 PRELIMINARY; PRT; 1687 AA.
061204;
061204;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
EGF repeat transmembrane protein.
EGF repeat (Mouse),
Mus musculus (Mouse),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
11]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302 L -> M (in Ref. 2).
461 N -> T (in Ref. 2).
478 CQHGGTCKDL -> VSAWGHLQGP (in Ref. 2).
549 G -> V (in Ref. 2).
549 G -> V (in Ref. 2).
549 A -> V (in Ref. 2).
549 A -> V (in Ref. 2).
549 A -> V (in Ref. 2).
690 N -> H (in Ref. 2).
600 N -> H (in Ref. 2).
610 N -> H (in Ref. 2).
611 N -> A (in Ref. 2).
612 N -> A (in Ref. 2).
613 N -> A (in Ref. 2).
613 N -> A (in Ref. 2).
613 N -> A (in Ref. 2).
614 N -> A (in Ref. 2).
615 N -> A (in Ref. 2).
616 N -> A (in Ref. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Potential).
(Potential).
(Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.5%; Score 63; DB 1; Length 1247; 23.1%; Pred. No. 4.2e+02; 7; Indels ive 13; Mismatches
            By similarity.
By sim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :::|:::|| ::|::|| 652 GFTGTYCHENIDDCMGQPCRNGGTCI 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A
              DISCULTO
DIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
(Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGF-like 1.
EGF-like 2.
EGF-like 3.
EGF-like 4.
EGF-like 4.
EGF-like 5. calcium-binding (Pot EGF-like 6. calcium-binding (Pot EGF-like 9.
EGF-like 10.
EGF-like 10.
EGF-like 11.
EGF-like 12.
EGF-like 13.
EGF-like 13.
EGF-like 14.
EGF-like 15.
EGF-like 16.
EGF-like 17.
EGF-like 18.
EGF-like 19.
EGF-like 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24
110
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
11085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
10085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
```

ö

Gaps

```
Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=6491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGF-like domain.
                                                                                                                                                                                                                                                                                  PF00084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                  Pfam;
                                                                                                                                                                                                                                                                                    Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 69
CXO7_CONGE
                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAC
DITAL PAC
DI
RC STRAIN=CS7BL/6J; TISSUE=Whole embryo;

RA MEDLINE=98142023; PubMed=9473344; DOI=10.1006/excr.1997.3865;

RA HOFF H.B. III, Tresini M., Li S., Sell C.;

RT response to insulin-like growth factor l.";

RI response to insulin-like growth factor l.";

REMBL, US7368; AAB01338-1; -.

REMBL, US7368; AAB01338-1; -.

REMBL, US7368; AAB01338-1; -.

ROS GO:0016021; C:integral to membrane; IEA.

GO; GO:0016021; C:integral to membrane; IEA.

ROS GO:000509; F:calcium ion binding: IEA.

ROS GO:000509; F:calcium ion binding: IEA.

RICHEPTO: IPR000152; DEAD box.

BR InterPro: IPR000189; BGF_1ike.

BR InterPro: IPR000629; BGF_1ike.

BR InterPro: IPR000629; BGF_1ike.

BR InterPro: IPR000639; BGF_1ike.

BR Ffam; PF00008; EGF_5.

BR PROSITE; PS000019; EGF_7; S.

BR PROSITE; PS00010; ASX HYDROXYL; 2.

BR PROSITE; PS00010; ASX HYDROXYL; 2.

BR PROSITE; PS001016; ASX HYDROXYL; 2.

BR PROSITE; PS001016; ASX HYDROXYL; 2.

BR PROSITE; PS00118; EGF_7; 5.

BR PROSITE; PS01186; EGF_7; 5.

BR PROSITE; PS01186; EGF_7; 5.

BR ROSITE; PS01186; EGF_7; 5.

BR ROSITE; PS01187; ASY HYDROXYL; 2.

RW BGF-1ike domain; Transmembrane.

SAMTENCR 1687 AA: 188528 WW: DA3B5302B67545D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AgCP1653 (Fragment).
Name=agCG50053; ORFNames=ENSANGG0000007782;
Anophales gambiae str. PEST.
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1687 AA; 188528 MW; DA3B5302B67545D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAR-2004 (TrEMBLrel. 26, Created)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52.5%; Score 63; DB 2; I 26.9%; Pred. No. 5.6e+02; ive 13; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 3523 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : : : : : | | | ::: | | ... | | 180 GFEGSTCERNIDDCPNHKCQNGGVCV 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000152; Asx hydroxyl S. InterPro; IPR008985; ConA like_lec_gl. InterPro; IPR000859; CUB. InterPro; IPR00142; EGF_2. InterPro; IPR001891; EGF_C. InterPro; IPR001438; EGF_II. InterPro; IPR001438; EGF_II. InterPro; IPR001438; EGF_II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 26.97
Ti Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=PEST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q70CP4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 68
Q7QCP4
            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
```

```
Science 230:1338-1343[1985].
-!- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind and block voltage-sensitive calcium channels (VSCC).
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expersed by the venom duct.
-!- MISCELLANEOUS: The sequence shown is that of conotoxin GVIIA.
-!- SIMILARITY: Belongs to the conotoxin O-superfamily. Omega-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CXO7_CONGE STANDARD; PRT; 29 AA.
P05483;
01-NOV-1988 (Rel. 09, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Omega-conotoxins GVIIA/GVIIB (Shaker peptides GVIIA/GVIIB) (SNX-178).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A43620; A43620.
PIR; B43620; B43620.
Calcium channel inhibitor; Direct protein sequencing; Hydroxylation; Calcium channel inhibitor; Neurotoxin; Presynaptic neurotoxin; Toxin. MOD_RES 4 + 4-hydroxyproline.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Mollusca, Gastropoda, Orthogastropoda,
Apogastropoda, Caenogastropoda, Sorbeoconcha, Hypsogastropoda,
Neogastropoda, Conoidea, Conidae, Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=86070213; PubMed=4071055;
Olivera B.M., Gray W.R., Zeikus R.D., McIntosh J.M., Varga J.,
Rivier J.E., de Santos V., Cruz L.J.;
"Peptide neurotoxins from fish-hunting cone snails.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.5%; Score 63; DB 2; Length 3523; 33.3%; Pred. No. 1.1e+03; tive 11; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3523 AA; 385001 MW; B58BB588E2A484EG CRC64;
InterPro; IRR000421; FASB_C.
InterPro; IRR009309; Grow_fac_recept.
InterPro; IRR003410; Hyallin.
InterPro; IRR002172; LDL_receptor_A.
InterPro; IRR001304, Lectin_C.
InterPro; IRR000436; Sushi_SCR_CCP.
Perm. PR00411; CUB; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2247 TGKNCQHTVDDCESAPCQNGGTCV 2270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 XNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE, PS00010; ASX HYDROXYL, 11.
PROSITE: PS01180; CUB; 3.
PROSITE: PS50041; C TYPE LECTIN_2;
PROSITE; PS00022; EGF 1; 15.
PROSITE; PS00186; EGF 2; 13.
PROSITE; PS50026; EGF 2; 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conus geographus (Geography cone)
                                                                                                                                                                                                                                           Pfam; PF07645; BGF_CA; 2.
Pfam; PF07645; FS_F8 Lype_C; 2.
Pfam; PF02494; HYR; 3.
Pfam; PF00057; Ldl recept a; 1.
Pfam; PF00059; LecTin_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00010; EGFBLOOD.
PROSITE; PS00010; ASX HYDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS50068; LDLRA_2
PS50923; SUSHI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            Sushi
```

```
22
72
72
72
72
72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 7; Conserv
                                                                                                                                      HSSP; P05484; 1DW4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phytophthora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kamoun S.;
                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                     PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q646U4;
                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                           PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q646U3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q646U4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            064604
10 QQ
10 QQ
007 25
007 25
000 BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2646U3
  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCOUNT TO THE SECOND TO THE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Venow, and Venom duct;

MEDLINE=20519630; PubWed=10938268; DOI=10.1074/jbc.M002252200;
Lewis R.J., Nielsen K.J., Craik D.J., Loughnan M.L., Adams D.A.,
Sharpe I.A., Luchian T., Adams D.J., Bond T., Thomas L., Jones A.,
Matheson J.-L., Drinkwater R., Andrews P.R., Alewood P.F.;
"Novel omega-conotoxins from Conus catus discriminate among neuronal
calcium channel subtypes.";
J. Biol. Chem. 275:35335-35344(2000).
-I-FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind
and block voltage-sensitive calcium channels (VSCC) (By
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., SEQUENCE OF 46-72, SYNTHESIS, AND STRUCTURE
                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                us-Jul-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Four-loop conctoxin preproprotein (Fragment).
Conus tulipa (Fish-hunting cone snail) (Tulip cone).
Eukaryota; Metazoa, Mollusca; Gastropoda, Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda; Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
                                                                                                                                                                                              Score 62; DB 1; Length 29;
Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 62; DB 2; Length 62;
Pred. No. 35;
                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Duda T.F. Jr., Palumbi S.R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF480316; AAQ05868.1; -.
                                                                                                            L -> S (in GVIIB).
57307C69583FB1E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  four-loop conotoxin.
916B1EB16D6A5085 CRC64;
4-hydroxyproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Omega-conotoxin CVID precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 AA.
                                                                                                                                                                                                                                                   13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
                                                                                                                                                                                                                                                                                                                                           1 CKSPGTPCSRGMRDCCTSCLLYSNKC 26
                                                                                                                                                                                                                                                                                                           1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CXIXNQXCXQXLDDCCSXXCNXXNX 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                              51.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 AA; 7083 MW;
                                                                                                                                   3290 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 32.09
les 8; Conservative
                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conus catus (Cat cone)
                                                                                                                                                           Query Match
Best Local Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=6495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONCT
                                                 DISULFID
                                                                                                            VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q71KS8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         071KS8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 71
CXOD_CONCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 70
071KS8
10 071KS
AC 071KS
AC 071KS
DT 05-JUI
DT
FT
FT
SO
                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Patterns of Diversifying Selection in the Phytotoxin-like scr74 Gene Family of Phytophthora infestans "; Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases. EMBL, AY021465.1; -2004 IVAN 17910 MW; C925922881E5EA3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                         Pfam; PF02950; Conotoxin; 1.
Amidation; Calcium channel inhibitor; Direct protein sequencing;
Ionic channel inhibitor; Neurotoxin; Presynaptic neurotoxin; Signal;
similarity). This toxin blocks N-type calcium channels.
-!- SUBCELULAR LOCATION: Secreted.
-!- TISSUE SPECIFULTY: Expressed by the venom duct.
-!- SIMILARITY: Belongs to the conotoxin O-superfamily. Omega-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cysteine amide (G-73 provides amide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-0CT-2004 (TrEMBLrel. 28, Created)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Phytoxin-like SCR-2004 (Presentation update)
Phytoxin-like SCR-2004 (Potato late blight fungus).
Eukaryota, stramenopiles; Oomycetes; Pythiales; Pythiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phytoxin-like SCR74.
Phytophthora infestans (Potato late blight fungus).
Eukaryota, stramenopiles, Oomycetes, Pythiales, Pythiaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 62; DB 1; Length 73; Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 51.7%; Score 62; DB 2; Length 74; Local Similarity 25.8%; Pred. No. 41; nes 8; Conservative 14; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           group).
C4CEBD30C77DAEC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 28, Last sequence update) (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                Omega-conotoxin CVID.
By similarity.
By similarity.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 XIXNOXCXQ-----XLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 KVTSKCCKAINADPIAFHDCCSKSCNTGSPC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                               Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-OCT-2004 (TrEMBLrel. 28, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CXIXNQXCXQXLDDCCSXXCNXX 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 CKSKGAKCSKLMYDCCSGSCSGT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
                                                                                                                                                                    InterPro, IPR004214; Conotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7748 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
```

54

us-10-627-685a-1.rup

```
EMBL; AY723703; AAU21444.1; -.
SEQUENCE 74 AA; 7817 MW; 5373030B547B94FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phytoxin-like SCR74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
Les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phytophthora,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kamoun S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2S albumin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                    Q646W6
                                                                                                                                                                                                                                                                                                                                                                                                                0646W6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9AUD1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9AUD1
                                                                                                                                                                                                                                                                                                                                   RESULT 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 77
                                                                                                                                                                                                                                                                                                                                                              Q646W6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9AUD1
                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ï
                                                                                                                                         "Patterns of Diversifying Selection in the Phytotoxin-like scr74 Gene Family of Phytophthora infestans.";
Submitted (ANG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY723723; AAU31464.1;
SEQUENCE 74 AA, 7879 WW; FP19FPA1F67DBADD CALCAL
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Patterns of Diversifying Selection in the Phytotoxin-like scr74 Gene Family of Phytophthora infestans.";
Submitted (Aug-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AY723704; AAUJ1445.1; -9D10BA1F26FCSB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kamoun S.;
"Patterns of Diversifying Selection in the Phytotoxin-like scr74 Gene
"Family of Phytophthora infestans.";
Submitted (AUG-2004) to the EMBL/GenBark/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                         SEQUENCE FROM N.A.
Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
                                                                                                                                                                                                                                                                                                                                                                                 .
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha I.,
Tortœ-Alalibó T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Phytoxin-like SCR74.
Phytophthora infestans (Potato late blight fungus).
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Phytoxin-like SCR74.
Phytophthora infestans (Potato late blight fungus).
Phytophthora, Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae; NCBL TaxID=4787;
                                                                                                                                                                                                                                                                                                          Query Match 51.7%; Score 62; DB 2; Length 74; Best Local Similarity 25.8%; Pred. No. 41; Matches 8; Conservative 14; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 51.7%; Score 62; DB 2; Length 74; Best Local Similarity 25.8%; Pred. No. 41; Matches 8; Conservative 14; Mismatches 3; Indels
                                                                                                                                                                                                                                                              7879 MW; FF19FBALF67B8A3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D9D10BA1F26FC5B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 AA
                                                                                                                                                                                                                                                                                                                                                                                                                     2 XIXNQXCXQ-----XLDDCCSXXCNXXIVXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 DVVSKCCKAINADPIAFHDCCSKSCNTGSPC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 XIXNOXCXQ-----XLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 DVVSKCCKAINADPIAFHDCCSKSCNTGSPC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
NCBI_TaxID=4787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phytophthora.
NCBI_TaxID=4787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q646W2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q646W2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q646W3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 74
10646W
AC 0646W
AC 0646W
DT 25-0C
DT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 75
0646W3
AC 0646W
DD 25-0C
DT 25-0C
DT 25-0C
DB Phyto
OC Phyto
OX NCBI
RN SEQUE
RN SEQUE
RN KAMOU
셤
                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
```

```
ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sesamum indicum (Oriental sesame) (Gingelly).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicocyledons; core eudicots; asterids;
lamiids; Lamiales; Pedaliaceae; Sesamum.
NCBI_TaxID=4182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Patterns of Diversifying Selection in the Phytotoxin-like scr74 Gene Family of Phytophthora infestens.";
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY723700; AAU2141.1;
                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No. 141
No. 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phytophthora infestans (Potato late blight fungus).
Eukaryota, stramenopiles, Oomycetes, Pythiales, Pythiaceae,
                     Length 74;
                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.7%; Score 62; DB 2; Length 74; 25.8%; Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 AA; 7851 MW; D9D10BA1F67B94F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Query Match 51.7%; Score 62; DB 2; Best Local Similarity 25.8%; Pred. No. 41; Matches 8; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 AA.
                                                                                                                                                                 2 XIXNOXCXQ-----XLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                            41 DVVSKCCKAINADPIAFHDCCSKSCNTGSPC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 XIXNQXCXQ-----XLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 DVVSKCCKAINADPIAFHDCCSKSCNTGSPC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.8%; Pred. No. 41;
iive 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AY723701, AU21442.1;
EMBL, AY723702, AAU21443.1;
EMBL, AY723699, AU21440.1;
SEQUENCE 74 AA, 7851 Mm. r.v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DER PER PACE OF THE PACE OF T
```

```
or send an email to license@isb-sib.ch)
                         EMBL; BC019431; AAH19431.1; -.
EMBL; AB011019; BAA88686.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Missing
                                                               PROSITE; PS00010; AGK HYDROXYL; PROSITE; PS00010; AGX HYDROXYL; PROSITE: PS00022; EGF 1: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           060Y11; Q9BQ54;
25-0CT-2004 (Rel. 45, Created)
25-0CT-2004 (Rel. 45, Last and
25-0CT-2004 (Rel. 45, Last and
                                                                                                                                                                                                                                                                                 Repeat; Signal; Transmembrane
SIGNAL 1 26
CHAIN 27 382 E
DOMAIN 27 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40404 MW;
                                                                                                                                                       Pfam; PF00008; EGF; 5. -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                3382
3305
3326
3326
3326
1172
1172
400
400
711
1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              382 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EFL9 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                            RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 79
EFL9_HUMAN
 ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGEPTPA
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1).

STRAIN=FVBDN; TISSUE-Salivary gland;

MEDLINE=2238825; PubMed=12477932; DoI=10.1073/pnas.242603899;

MEDLINE=2238825; PubMed=12477932; DoI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Alachul S.F., Zebebrg B., Buerow K.H., Schamen C.M., Schuler G.D.,

A Hopkins R.F., Jordan H., Moore T., Max S.L., Mang J., Heiseh F.,

A plachul S.F., Zebebrg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.L., Mang J., Heiseh F.,

B plachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B roase M.H., Moore T., Morkernan R.J., Maruson R.D., Mullahy S.J.,

B Roase S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

B Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

B short and show and show analysis of more than 15,000 full-length human
                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                 ö
                                                                                                                                                                                                                                     QBKIE3; Q9QYP3; 25-0CT-2004 (Rel. 45, Created) 25-0CT-2004 (Rel. 45, Last sequence update) 25-0CT-2004 (Rel. 45, Last sequence update) 25-0CT-2004 (Rel. 45, Last annotation update) Multiple EGF-like-domain protein 9 precursor (Endothelial cell specific protein 5-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 259-182 FROM N.A. (ISOFORM 2).
Fukudome K., Tsuneyoshi N., Kimoto M.;
"Endothelial cell specific protein S-1.";
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-!- ALTERNATIVE PRODUCTS:
                                                                   51.7%; Score 62; DB 2; Length 153; 39.1%; Pred. No. 79;
                                                                                                 5; Indels
                          SMART; SM00499; AAI; 1.
SEQUENCE 153 AA; 17504 MW; 6A8F9117DAB81568 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note=No experimental confirmation available; SIMILARITY: Contains 6 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                              382 AA
                                                                                                 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isold=Q8K1E3-2; Sequence=VSP 011768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=Q8K1E3-1; Sequence=Displayed;
                                                                                                                                             GNQQSEQSLRDCCQQLRNVDERC 102
                                                                                                                           4 XNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and mouse cDNA sequences.";
PRINTS; PR00211; GLUTELIN PRINTS; PR00496; NAPIN.
                                                                                 Local Similarity 39.1
les 9; Conservative
                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                            Name=Egfl9;
                                                                                                                                                                                                                              EFL9 MOUSE
                                                                     Query Match
                                                                                                 Matches
8288
                                                                                                                                                      g
                                                                                                                             ઠે
```

```
ö
                                                                                                                                                                                                                                    EGF-like 2.
EGF-like 3.
EGF-like 4.
EGF-like 5, calcium-binding (Potential).
EGF-like 6, calcium-binding (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (in isoform 2).
PROSITE; PS01186; EGF_2; 6.
PROSITE; PS50026; EGF_3; 6.
PROSITE; PS01187; EGF_CA; 2.
Alternative splicing; Calcium; Calcium-binding; EGF-like domain;
                                                                                                                          Multiple EGF-like-domain protein 9. Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Multiple EGP-like-domain protein 9 precursor (UNQ2903/PRO28633).
Name=EGFL9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F2C82AD649CA0B3C CRC64;
                                                                                                                                                                                            Cytoplasmic (Potential).
EGF-like 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.7%; Score 62; DB 1; 32.0%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-linked (GlcNAc.
                                                                                                                                                                                                                                                                                                                                         By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      383 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 32.0%; Pred. no. -...
Marches 8; Conservative 11; Mismatches
                                                                                                                                                                           Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTId=VSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203 GFAGRFCTINLDDCASRPCQRGARC 227
```

```
Memanian Butherios; Concidet; Crainting; Moninidae, Nono.

Wennalian Butherios; Concidet; Crainting; Moninidae, Nono.

Wennalian Butherios; Concidet; Crainting; Moninidae, Nono.

Well-TaxID-8060;

III

RA GROUNGE FROW NA. (ISOPONN 1).

RA GROUNGE STAND CRIMINIAN STAND STA
```

```
EGF-like 3.

EGF-like 4.

EGF-like 5, calcium-binding (Potential).

EGF-like 6, calcium-binding (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anopheles gambiae str. PEST.
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterrygota, Diptera, Nematocera, Culicoidea, Anopheles.
NCBI_TaxID=180454;
                              SWART; SMO0181; EGF, 6.
SWART; SMO0181; EGF, 6.
SWART; SMO0179; EGF CA, 4.
PROSITE; PSO0100; ASX HYDROXYL; 2.
PROSITE; PSO0102; EGF 1, 6.
PROSITE; PSO026; EGF 2, 6.
PROSITE; PSO1187; EGF CA, 2.
Alternative splicing; Calcium, Calcium-binding; EGF-like domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-linked (GlcNAc. .) (Potential). Missing (in isoform 2).
                                                                                                                                                Multiple EGF-like-domain protein Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51.7%; Score 62; DB 1; Length 383; 32.0%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anopheles Genome Sequencing Consortium;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          701AC6B043863EA7 CRC64;
                                                                                                                                                                                 Cytoplasmic (Potential).
EGF-like 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O7PM27;
01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 1.8e+02;
                                                                                                                                                                                                                                                             By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            638 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Pred. No. 1.8e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d=VSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 GFAGRFCTINLDDCASRPCQRGARC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 XIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
InterPro; IPR001841; Znf_ring
                                                                                                                          Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         383 AA; 40547 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENSANGP0000014402 (Fragment)
Name=ENSANGG0000011913;
                      EGFBLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
          Pfam; PF00008; EGF; 5.
PRINTS; PR00010; EGFBL
                                                                                                                                       Local Similarity
es 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                         Repeat; Signal;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=PEST
                                                                                                                                                                                                                                                                                              DISULFID
DISULFID
                                                                                                                                                                    FRANSMEM
                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                         DOMAIN
                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                       DOMAIN
                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q7 PM27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 80
Q7PM27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
```

```
DOMAIN
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Podocoryne carnea.
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
Hydractiniidae; Podocoryne.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                   Length 638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bauer F., Plickert G.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF397902; AAK92130.1; -.
HSSP; P00740; IEDM.
                                                                                                                                                                                        638 638
638 AA; 69390 MW; 026DB44846AB483F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           713 AA; 76908 MW; 980E392B533E42D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                 51.7%; Score 62; DB 2; I
28.0%; Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51.7%; Score 62; DB 2; I 26.9%; Pred. No. 3.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; QUO'40; IEDM.

GO, GO:0005509; F:calcium ion binding; IEA.
InterPro; IPR000152; Aax_hydroxyl_S.
InterPro; IPR00152; Aax_hydroxyl_S.
InterPro; IPR001439; EGF_Ca.
InterPro; IPR001439; EGF_II.
InterPro; IPR001439; EGF_II.
FROM: PF000009; EGF_II.B.
FRINTS; PR00010; EGFBLOD.
SWART; SW00179; EGF_CA; 16.
PROSITE; PS00010; ASX_HYDROXYL; 17.
PROSITE; PS000129; EGF_I: 18.
PROSITE; PS001186; EGF_I: 18.
PROSITE; PS01186; EGF_I: 18.
PROSITE; PS01187; EGF_CA; 16.
PROSITE; PS01187; EGF_CA; 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    713 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
                                                                                                                                                                                                                                                                                       12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   489 GFTGETCEIEIDECSSSPCQNAGTCV 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                               2 XIXNOXCXOXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                   30 RLSNHRCIPHCDDCDNGICTKPGYC 54
    EMBL, Veritourist

preliminary data.

EMBL, AAABO1008980; EAA14483.2; -.

HSSP; P19438; IEXT.

InterPro; IPR003341; DUF139.

InterPro; IPR006209; EGF like.

Pfam; PF02363; C_triplex; 15.

Pfam; PF00188; EGF; 1.

PROSITE; PS01186; EGF 2: 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGF-like protein (Fragment).
                                                                                                                                                                                                                                                                   Local Similarity 28.0%
les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=6096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 82
DLL1_RAT
ID DLL1_RAT
AC P97677,
DT 01-NOV-199
DT 01-NOV-199
                                                                                                                                                                    NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q962W9
SSERERREFFS
                                                                                                                                                                                                                                                                                                                                                                 요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC DOT THE PRINCIPLE OF THE PRINCIPLE OF
```

```
Data-2008 (Reil, 46, Lase amocation update)

Data-114e protein Jrecursor (Crosophila Delta homolog 1) (Deltai).

Marmenlia Subthers; Robertis, Sciurognathi Muridae; Murinae; Ratus.

Marmella Subthers; Robertis, Sciurognathi; Muridae; Murinae; Ratus.

NCDI Taxil-101016; Brobertis, Robertis, Sciurognathi; Muridae; Murinae; Ratus.

MIJ Taxil-101016; Brobertis, Robertis, Sciurognathi; Muridae; Murinae; Ratus.

MIJ Taxil-101016; Brobertis, Robertis, Sciurognathi; Muridae; Murinae; Ratus.

MIJ Taxil-101016; Brobertis, Robertis, Robertis, Sciurognathi; Muridae; Murinae; Ratus.

MIJ Taxil-101016; Brobertis, Robertis, Robertis, Sciurognathi; Muridae; Murinae; Ratus.

MIJ Taxil-101016; Brobertis, Robertis, Robertis, Sciurognathi; Muridae; Murinae; Ratus.

CC 1: SURCELLIST; Contains 1054 Genain.

1: SURLIARITY; SURLIARITY; SURLIARITY; Recourse 1054 Genain.

1: SURLIARITY; SURLIARITY; SURLIARITY; Recourse 1054 Genain.

1: SURLIARITY; SURLIARITY; SURLIARITY; SURLIARITY; SURLIARITY
```

```
between the Swiss Institute of Bioinformatics and the EWBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00008; ECF; U. S. PRINTS; PROMOID; BGFBLOOD.
PRINTS; PR00010; ASX HYDROXYL; 3.
PROSITE; PR00010; ASX HYDROXYL; 3.
PROSITE; PS0108; EGF_1; 8.
PROSITE; PS01187; EGF_2; 8.
PROSITE; PS01187; EGF_CA; 2.
PROSITE; PS01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGF-like 1.
EGF-like 2.
EGF-like 3.
EGF-like 4, calcium-binding (Potential).
EGF-like 5.
EGF-like 6.
EGF-like 7, calcium-binding (Potential).
                                                                                                                                                                                                                H HASEY; POOT4074 JEDM.

H HASEY; POOT4074 JEDM.

R MGD; MGI:104659; D111.

R GO; GO:0005576; C:extracellular; ISS.

GO; GO:0005125; F:Notch binding; IPI.

R GO; GO:0005125; F:Protein binding; IPI.

R GO; GO:0007346; P:conpartment specification; ISS.

R GO; GO:0007346; P:conpartment specification; IMP.

R GO; GO:0007346; P:conpartment specification; IMP.

R GO; GO:0007346; P:conpartment specification; IMP.

R GO; GO:0007346; P:nembryonic development (sensu Mammalia); NAS.

R GO; GO:0007349; P:hinner ear morphogenesis; NAS.

R GO; GO:0007399; P:nemcyonesis; ISS.

R GO; GO:0007399; P:nemcyonesis; ISS.

R GO; GO:0007399; P:newcyonesis; NAS.

R GO; GO:0007399; P:newcyonesis; Rensu Vertebrata); NAS.

R GO; GO:0007399; P:newcyonesis; Rensu Vertebrata); NAS.

R GO; GO:0007399; P:regulation of cell adhesion; ISS.

R InterPro; IPR001475; P:regulation of cell adhesion; ISS.

R InterPro; IPR00143; EGF 2.

R InterPro; IPR00143; EGF 2.

R InterPro; IPR00149; EGF 2.

R InterPro; IPR00149; EGF 2.

R InterPro; IPR00149; EGF 1.

R InterPro; IPR00149; EGF 1.

R Pfam; PF01414; DSL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Delta-like protein 1.
Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Potential
                                                                                                                                                               EMBL; X80903; CAA56865.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          545
568
722
722
722
723
3324
4401
4439
747
742
                                                                                                                                                                                     PIR; 148324; 148324.
HSSP; P00740; 1EDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CSTBL/6 X MALB/C; TISSUB=Embryo;

WEDLINE=95401858; PubMed=7671806;
WEDLINE and restricted expression during mouse embryogenesis of public, a murine gene closely related to Drosophila Delta.";
DIII, a murine gene closely related to Drosophila Delta.";
DEVELORINE MAY be involved in cell-to-cell communication in mammalian embryos. May have a role in cellular interactions underlying somitogenesis and development of the nervous system.
C-1-SUBUNIT: Interacts with Notch receptors.
C-1-SUBUNIT: Interacts with the embryo, expressed in the paraxial mesoderm and nervous system. Expressed at high levels in adult heart and at lower levels, in adult lung.
C-1-SUBCOPMENTAL STAGES: Expressed until day 15 in the embryo.
Expression then decreases and increases again in the adult.
C-1-SIMILARITY: Contains 1 DSL domain.
C-1-SIMILARITY: Contains 8 EGF-like domains.
                              calcium-binding (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Delta-like protein 1 precursor (Drosophila Delta homolog 1) (Deltal).
Name=Dlli;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linked (GlcNAc. .) (Potential) 4B8EE2272BAEA27E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 3.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
    EGF-like 6.
EGF-like 7, cal
EGF-like 8.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              722 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.7%; Score 62; DB 28.0%; Pred. No. 3.2e iive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 433 GFSGRYCEDNVDDCASSPCANGGTC 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 XIXNOXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77378 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity Zb.v.,
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                           3351
3362
3380
3390
4401
4419
4419
4466
504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     714 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 83
DLL1 MOUSE
ID DLL1 MOUSE
AC Q61483;
DOMAIN
DOMAIN
DOMAIN
DISULFID
DISULFID
DISULFID
                                                                                                                          DISULFID
DISULFID
DISULFID
                                                                                                                                                                                     DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                         DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                    DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SULFID
  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
```

```
ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  쉽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DAT DDT TABLE THE STATE OF STA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MISTAL STATE S
                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                          .) (Potential)
                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                        DB 1; Length 722
                                                                                                                                                                                                                                                                                                                                                                               6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=CS78L/6; TISSUE=Mouse;
Strausberg R.,
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nagaraja R., Waeltz P., Brathwaite M.E.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                          95F581B56DCEC9B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                     . 3.2e+02;
                                                                                           similarity.
similarity.
similarity.
similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    722 AA
                                                                                                                                                                                                                                                                                                                                                                                   12; Mismatches
                                                                 similarity
                                                                                                                                                                                                                                                                                                                 51.7%; Score 62; 28.0%; Pred. No.
By similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : ::||: ::|| | | :: | : : | 433 GFSGRYCEDNVDDCASSPCANGGIC 457
                                                                                                                                                                                                                                                                                                                                                                                                                                             2 XIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                       78448 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 27, (TrEMBLrel. 27, I
                                                                                                                                                                                                                                                                                                                                                  Local Similarity 28.0 1es 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q6PFV7;
05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-OCT-2004 (TrEMBLrel. Delta-like 1.
   Mus musculus (Mouse).
                                                                                                                                                                                                                                                          722 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [5]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J;
   4446
4446
4468
4484
476
506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=Dlll
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                        DISULFID
DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q6PFV7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 84

106 PFV7

107 PFV7

108 PFV7

109 P
   FT FT FT 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        유
```

```
SECUENCE FROM N.A.
MEDLINE=99180765; PubMed=10079256;
Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,
Banks A., Leiman J., Ward D., Ish Horowitz D., Artavanis-Teakonas S.;
"Human ligands of the Notch receptor.";
Am. J. Pathol, 154:785-794(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Han W., Ye Q., Moore M.A.S.;
As soluble form of human delta-like-1 inhibits differentiation of
hematopoietic progenitor cells ";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                 R GO; GO:0005615; C:extracellular space; TAS.
R GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0005615; C:integral to membrane; TAS.
R GO; GO:0005386; P:compartment specification; IMP.
GO; GO:00017386; P:compartment specification; IMP.
GO; GO:0001737; P:somite specification; IMP.
R GO; GO:0001777; P:somite specification; IMP.
R InterPro; IPR00174; DSL.
R InterPro; IPR00144; DSL.
R InterPro; IPR00144; EGF_Ca.
R InterPro; IPR00148; EGF_I.
R InterPro; IPR00148; EGF_II.
R InterPro; IPR00148; EGF_II.
R InterPro; IPR00148; EGF_II.
R PR001414; DSL.
R PF0018; EGF; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DILLI HUMAN STANDARD; PRT; /23 AM.
000548; QSNU41; QSUUVZ;
15-JUL-1998 (Rel. 36, Leated)
15-JUL-1998 (Rel. 36, Lest sequence update)
25-JAN-2005 (Rel. 46, Lest annotation update)
Delta-like protein 1 precursor (brosophila belta homolog 1)
(H-Delta-1) (UNQ146/PR0172).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
Brathwaite M., Waeltz P., Dudekula D., Nagaraja R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      722 AA; 78449 MW; 9D570B9DC7EEC75E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.7%; Score 62; DB 2; I 28.0%; Pred. No. 3.2e+02; ive 12; Mismatches 6;
                                                             -! - SIMILARITY: Contains 8 EGF-like domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : ::|::|| |::|
433 GFSGRYCEDNVDDCASSPCANGGIC 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 XIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00010; ASX HYDROXYL; PROSITE; PS00022; BGF 1; 8. PROSITE; PS01186; BGF 2; 8. PROSITE; PS01187; BGF GA; 2.
                                                                                     EMBL, BC057400; AAH57400.1; -. EMBL, BC055053, AAH65063.1; -. EMBL, AY497019; AAR30869.1; -. HSSP, P00743; 1APO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00010; EGFBLOOD.
SMART; SM00051; DSL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 28.0%
les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00181; EGF;
SMART; SM00179; EGF C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS01187;
EGF-like domain.
SEQUENCE 722 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 85
DLL1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loca
Matches
```

; 0

```
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 86
Q66S04
         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropan Bioinformatics Institute: There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                          SEQUENCE FROM N.A.

MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
Baton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
Huang A., Xim H.S., Klimwoski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagets A.,
A vandlen R., Watenabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
Godowski P., Gray A.,
The secreted protein discovery initiative (SPDI), a large-scale
effort to identify novel human secreted and transmembrane proteins: a
bioinformatics assessment.";
Li Genome Res. 13:2265-2270(2003).
                                                                                                                                                                                                                                                                               R MIM, 606582; -.
R GG) GC:0005576; C:extracellular; NAS.
R GC) GC:0005877 C:integral to plasma membrane; NAS.
R GC) GC:0005187; C:integral to plasma membrane; NAS.
R GC) GC:00031054; F:NOtch binding; IPI.
R GC) GC:00031054; P:cell differentiation; TAS.
R GC) GC:0001709; P:cell fate determination; NAS.
R GC) GC:0001709; P:cell fate determination; NAS.
R GC) GC:0005912; P:hair cell fate commitment; ISS.
R GC; GC:0005912; P:hair cell fate commitment; ISS.
R GC; GC:0007309; P:neurogenesis; ISS.
R GC; GC:0007309; P:neurogenesis; ISS.
R GC; GC:0007309; P:Notch signaling pathway; NAS.
R GC; GC:00042475; P:coduncogenesis (sensu Vertebrata); ISS.
R GC; GC:00042475; P:cegulation of cell adhesion; TAS.
R GC; GC:000522; Asx_hydroxyl_S.
Oda T., Chandrasekharappa S.C.;
"Human Delta 1 gene sequence.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                          Almeida J.,
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF003522; AAB61286.1; --
EMBL; AF196571; AAF05834.1; --
EMBL; AF222310; AAG09716.1; --
EMBL; AX358892; AAQ8251.1; --
EMBL; AL078605; CAB89569.1; --
GENSW, HGNC: 2908; DLL1.
                                                                                                                                                                                                                              SEQUENCE FROM N.A. Almeida J.;
```

```
ö
                                                                                                                                                                                                             PRINTS; PRO0010; EGFELOD.
SWART; SM00051; DSL; 1.
SWART; SM00051; DSL; 1.
PROSITE; PS00010; ASK HYDROXYL; 3.
PROSITE; PS00022; EGF 1; 8.
PROSITE; PS01186; EGF 2; 8.
PROSITE; PS01187; EGF 2; 7.
PROSITE; PS01187; EGF 2; 7.
PROSITE; PS01187; EGF 2; 1.
PROSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGF-like 1.
EGF-like 2.
EGF-like 3.
EGF-like 4.
EGF-like 5.
EGF-like 6.
EGF-like 6.
EGF-like 7.
EGF-like 7.
EGF-like 7.
EGF-like 7.
EGF-like 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 By similarity.
By similarity.
N-linked (GlCNAc. . .) (Potential).
E -> Q (in Ref. 2.
G -> R (in Ref. 4 and 5).
G -> S (in Ref. 2.)
MW, B4EC455FFA32A12B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.7%; Score 62; DB 1; Length 723; 28.0%; Pred. No. 3.3e+02; iive 12; Mismatches 6; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Delta-like protein 1.
Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytoplasmic (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         By similarity. By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity.
similarity.
similarity.
similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 XIXNOXCXQXLDDCCSXXCNXXNXC 26
InterPro; IPR001481; EGF Ca.
InterPro; IPR001481; EGF Ca.
InterPro; IPR0061439; EGF II.
Pfam; PF01414; DSL; 1.
Pfam; PF00008; EGF; 6.
PRINTS; PR00010: FGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77956 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 28.0*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4447
469
5490
507
477
510
510
723 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q66S04
Q66S04;
```

```
Name=IA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=IB;
                                                                                                                                                                                                                 urchin.";
                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                         SEQUENCE FROM N.A.
PubMed=1534333; DOI=10.1038/nature02709;
Seo H.C., Edvardsen R.B., Maeland A.D., Bjordal M., Jensen M.F.,
Hansen A., Flaat M., Weissenbach J., Lehrach H., Wincker P.,
Reinhardt R., Chourrout D.;
Frox cluster disintegration with persistent anteroposterior order of
expression in Oikopleura dioica.";
Nature 431:67-71(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
Echinoidea, Euechinoidea, Echinacea, Echinoida, Strongylocentrotidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIJNE=90112459; PubMed=2514273; Mersh D.A., Raff R.A.; Delgadillo-Reynoso M.G., Rollo D.R., Hursh D.A., Raff R.A.; Delgadillo-Reynoso M.G., Rollo D.R., Hursh D.A., Raff R.A.; Extructural analysis of the uEGF gene in the sea urchin strongylocentrotus purpuratus reveals more similarity to vertebrate than to invertebrate genes with EGF-like repeats."; Mol. Evol. 29:314-327(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-1989 (Rel. 10, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Fibropellin I precursor (Epidermal growth factor-related protein 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Notch receptor-like protein.
OKRNAmes=008-50;
OKRNAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 51.7%; Score 62; DB 2; Length 824; Best Local Similarity 30.8%; Pred. No. 3.7e+02; Matches 8; Conservative 12; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         824 AA; 89253 MW; 955AEAE53CCFC86A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1064 AA.
                                                                                                                                                                                                                                                                                                                                    |:|: :|:|: :| CEIEKSFCEQFPNYCENGDCNDGGFC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CXIXNOXCXQXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PERINTS, PRO0010; EGF, 11.
PRINTS, PR00010; EGFBLOOD.
SMART; SM00118; EGF, 17.
SMART; SM00118; EGF, 17.
PROSITE; PS01010; ASX HYDROXYL; 10.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01186; EGF 2; 17.
PROSITE; PS01186; EGF 2; 14.
PROSITE; PS01187; EGF 2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strongylocentrotus.
NCBI TaxID=7668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=EGF1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P10079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FBP1_STRPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 87
              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensealsib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isold=P10079-2; Sequence=VSP_000451;
DEVELOPMENTAL STAGE: Moderate levels in unfertilized eggs and DEVELOPMENTAL STAGE: Moderate levels in and abundance between late morula and mesenchyme blastula stages to maximal levels maintained through subsequent stages. Expressed both maternally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dev. Biol. 146:89-99(1991).

-!- FUNCTION: Forms the apical lamina, a component of the

-!- sextracellular matrix.

-!- SUBCELULIAR LOCATION: Extracellular. In vesicles in the cytoplasm

of unfertilized eggs, then to the base of the hyalin layer
throughout development and finally in the apical lamina in late
                                                                                                                                                                                                                                                                                                        MEDLINE-89196806; PubMed=2784773;
Hunt L.T., Barker W.C.;
"Avidin-like domain in an epidermal growth factor homolog from a sea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARACTERIZATION.
MEDLINE=91285284; PubMed=2060714;
Bisgrove B.W., Andrews M.E., Raff R.A.;
Bisgrove I.W., Andrews M.E., Raff R.A.;
Withbropellins, products of an Ed's repeat-containing gene, form a unique extracellular matrix structure that surrounds the sea urchin
SEQUENCE OF 279-476 AND 781-1064 FROM N.A.
MEDLINE=87319677; PubMed=3498216;
Hursh D.A., Andrews M.E., Raff R.A.;
Ha sea urchin gene encodes a polypeptide homologous to epidermal growth factor.";
Science 237:1487-1490(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Contains 1 avidin domain.
-!- SIMILARITY: Contains 1 CUB domain.
-!- SIMILARITY: Contains 21 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=P10079-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000142; EGF 2.
InterPro; IPR00181; EGF 2.
InterPro; IPR00181; EGF 7.
InterPro; IPR001819; EGF 11.
InterPro; IPR006209; EGF 11.
InterPro; IPR006209; EGF 11.
InterPro; IPR006309; EGF 11.
Pfam; PP00181; EGF; 21.
PRINTS; PR00109; EGFB: 21.
PRINTS; PR00100; EGFB: 21.
PROSITE; PS00010; ASX HYDROXYL; 19.
PROSITE; PS00577; AVIDIN; 1.
PROSITE; PS01180; CUB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000152; Asx hydroxyl_S.
InterPro; IPR005469; Avidin.
InterPro; IPR005468; Avidin/str.
InterPro; IPR000859; CUB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, L08692; AAA62164.1; --
EMBL, L08692; AAA62163.1; --
EMBL, X17330; CAA35571.1; --
EMBL, M17421; AA30050.1; --
EMBL, X17533; CAA35573.1; --
PIR, A40136; A40136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  embryos and early larvae. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FASEB J. 3:1760-1764(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and zygotically.
                                                                                                                                                                                                                                                                            AVIDIN-LIKE DOMAIN.
```

```
Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'S STRAIN=PEST;
An Anopheles Genome Sequencing Consortium;
Anopheles Genome Sequencing Consortium;
Anopheles Genome Sequencing Consortium;
L'Submitted (MAR-2002) to the EMBL/Genbank/DDBJ databases.
C -!- CAUTION: The sequence shown here is derived from an BMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
C EMBL; AAAD1000859; EAAO7783.1; -..
DR HSSP; P00740; IEDM.
DR HSSP; P00740; IEDM.
DR HSSP; P00740; IEDM.
DR InterPro; IPR000152; Asx hydroxyl S.
DR InterPro; IPR000152; Asx hydroxyl S.
DR InterPro; IPR00143; EGF-2.
DR InterPro; IPR00143; EGF-2.
DR InterPro; IPR00143; EGF-3.
DR InterPro; IPR00143; EGF-11.
DR InterPro; IPR001501; LRR.
DR InterPro; IPR00151; LRR.
                                                                                                                                                                                                             (Potential).
(Potential).
(Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13
                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                               t; Score 62; DB 1; Length 1064;
t; Pred. No. 4.6e+02;
13; Mismatches 6; Indels ...
                                                                                                                                                                                                                                                              2E569CA012ED6D09 CRC64;
                                                                                                                                                                                                                                    Missing (in isoform IB)
/FTId=VSP 000451.
L -> S (in Ref. 2).
                                                                                                                                                                                                               (GlcNAc. . .)
                                                                                                                                                                                                                                                                                                                                                        By similarity.
                                                                                                                                                                                                                                                                                                                          205 GFTGRNCEIDIDECASDPCQNGGACV 230
                                                                                                                                                                                                                                                                                                               2 XIXNOXCXOXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                              112072 MW;
                                                                                                                                                                                                                                                                             Query Match 51.7%;
Best Local Similarity 26.9%;
Matches 7; Conservative 1
                     279 27
1064 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                   DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                        DISULFID
DISULFID
DISULFID
                                                                                                                  DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                    CONFLICT
                    ò
                                                                                                                                                                                                                                                                                                                               원
                                                                                                   EGF-like 2, calcium-binding (Potential).

EGF-like 3, calcium-binding (Potential).

EGF-like 4, calcium-binding (Potential).

EGF-like 6, calcium-binding (Potential).

EGF-like 6, calcium-binding (Potential).

EGF-like 9, calcium-binding (Potential).

EGF-like 9, calcium-binding (Potential).

EGF-like 10, calcium-binding (Potential).

EGF-like 11, calcium-binding (Potential).

EGF-like 12, calcium-binding (Potential).

EGF-like 13, calcium-binding (Potential).

EGF-like 14, calcium-binding (Potential).

EGF-like 15, calcium-binding (Potential).

EGF-like 16, calcium-binding (Potential).

EGF-like 16, calcium-binding (Potential).

EGF-like 18, calcium-binding (Potential).

EGF-like 19, calcium-binding (Potential).

EGF-like 19, calcium-binding (Potential).

EGF-like 21, calcium-binding (Potential).

EGF-like 21, calcium-binding (Potential).

EGF-like 21, calcium-binding (Potential).

EGF-like 21, calcium-binding (Potential).
PROSITE; PS00022; EGF_1; 19.
PROSITE; PS0186; EGF_2; 19.
PROSITE; PS50026; EGF_3; 11.
PROSITE; PS01187; EGF_GA; 11.
Alternative splicing; Biotin; Calcium-binding; EGF-like domain; Glycoprotein; Repeat; signal.
                                                                   Potential.
Fibropellin I.
EGF-like 1.
CUB.
                                                                                                                                                                                                                                                                                         similarity.
similarity.
similarity.
similarity.
similarity.
similarity.
similarity.
similarity.
similarity.
                                                                                                                                                                                                                                                                                                                                                                                                          similarity.
similarity.
similarity.
similarity.
similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity,
similarity,
similarity,
similarity,
similarity,
similarity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity.
similarity.
similarity.
                                                                                                                                                                                                                                                                                                                                                                                 similaritý.
similarity.
similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity.
similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similaritý.
similarity.
similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similaritý.
similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity.
similarity.
similarity.
similarity.
similarity.
similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity
                                                                                                                                                                                                                                                                                          7746
88620
88620
88620
88620
88620
88620
88620
88650
88650
88650
88650
88650
88650
88650
88650
88650
88650
                                                                                                                                                                                                                                                                                DOMAIN
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                    DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                             DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
DISULFID
DISULFID
DISULFID
                                                                         CHAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                     DOMAIN
```

Gaps

```
SEQUENCE FROM N.A.
MEDLINE=20144115; PubMed=10677532; DOI=10.1073/pnas.040545897;
MEDLINE=20144115; PubMed=10677532; DOI=10.1073/pnas.040545897;
Smith J.D., Graig A.G., Kriek N., Hudson-Taylor D., Kyes S., Fagen T.,
Pinches R., Baruch D.I., Mawbold C.I., Miller L.H.;
"Identification of a Plasmodium falciparum intercellular adhesion molecule-1 binding domain: a parasite adhesion trait implicated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium falciparum.
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 51.7%; Score 62; DB 2; Length 1515; Best Local Similarity 33.3%; Pred. No. 6.4e+02; Matches 8; Conservative 10; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 51.7%; Score 62; DB 2; Length 1685; Best Local Similarity 29.6%; Pred. No. 7e+02; Matches 8; Conservative 13; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1515 AA; 166871 MW; 12FD111277D18D5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 1685 AA; 193671 MW; D1FD426666B0551E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Variant surface protein PfEMPI (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cerebral malaria.";

proc. Natl. Acad. Sci. U.S.A. 97:1766-1771(2000).

EMB., AF19424; AAF18980.1;

GO; GO:0005539; F:glycosaminoglycan binding; IEA.

GO; GO:0009405; P:pathogenesis; IEA.

InterPro: IPR00454; Eub_ATPase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1685 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |: ::::|: : || |:::| ::|:
1048 CKTKDKKCTNKSDDCNTCTEACTAYNR 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CXIXNOXCXQXLDDC--CSXXCNXXNX 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1059 VGQQCEQDYNDCLENKCQHGAECV 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEAM; PF03011; PPEMP; 1.
PROSITE; PS00605; ATPASE_C; UNKNOWN_1.
NON TER 1685 1685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 XNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS01186; ECF 2; 7.
PROSITE; PS01026; EGF 3; 8.
PROSITE; PS01187; EGF CA; 2.
PROSITE; PS0025; LAW_G_DOMAIN; 1.
                                                                                                                                                                                                                                                                     SMART; SM00082; LRRCT; 4.
SMART; SM00013; LRRCT; 4.
SMART; SM00369; LRR TYP; 9.
PROSITE; PS00010; ASX HYDROXYL;
            Laminin G 2; 1.
                                                                                                                        LEURICHRPT
                                                                                                                                                   CT; 1.
EGF CA; 1.
FOLN; 3.
LamG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                 PRINTS; PRO0019; I
SMART; SM00041; CT
SMART; SM0179; EC
SMART; SM0179; EC
SMART; SM00282; Li
SMART; SM0082; Li
                                 Pfam; PF01463; I
Pfam; PF01462; I
Pfam; PF00560; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGF-like domain
SEQUENCE 1515
                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; 1
         Pfam;
Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-Michigan;

X MEDLINE-21098742; PubMed=11161558; DOT=10.1006/dbio.2000.0105;

A FO S.Y., Little M.H., Yamada T., Miyashita T., Halloran M.C.,

Kuwada J.Y., Huh T.L., Okamaco H.;

"Overexpression of a slit homologue impairs convergent extension of
The mesoderm and causes cyclopia in embryonic zebrafish.";

Dev. Biol. 230:1-17(2001).

R RSDP; PO1132: 16K5.

Z PIN; ZDB-GRNE-010306-4; slit3.

R GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:0005155; P:call adhesion; IEA.

R GO; GO:0005155; P:call adhesion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Ostariophysi, Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.7%; Score 62; DB 2; Length 1286; 33.3%; Pred. No. 5.5e+02; ive 10; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1286 AA; 144156 MW; EE919D876B21BB3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9DE37;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1515 AA
                                                                                                                                                                                                                                                            PS01185; CTCK 1; 1.

PS01225; CTCK 2; 1.

PS01225; EGF 1; 7.

PS01186; EGF 2; 4.

PS50026; EGF 2; 7.

PS50026; EGF 2; 7.

PS50025; LAM G DOMAIN; 1.

PS00119; PA2 ASP; UNKNOWN 1.
InterPro; IPR003591; LRR typ.
InterPro; IPR001211; PhospholipaseA2.
                                                       Pfam; PP00008; EGF; 7.
Pfam; PP01463; LRRCT; 3.
Pfam; PP01462; LRRCT; 3.
Pfam; PP00560; LRR 1; 14.
PRINTS; PR00010; EGFBLOOD.
PRINTS; PR00019; LEBRICHRPT.
PROSITE; PS0010; ASX HYDROXYL; 3.
PROSITE; PS01185; CTCK 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *|:::||| :::||
882 NCTDNIDDCVNHMCQNGGTCV 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 XCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR006207; Cys knot c
InterPro; IPR00142; EGF 2.
InterPro; IPR001881; EGF Ca.
InterPro; IPR006209; EGF Inke.
InterPro; IPR006465; Fol N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laminin G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000483; LRR Cterm.
InterPro; IPR000372; LRR Nterm.
InterPro; IPR003591; LRR Lyp.
InterPro; IPR003129; TSP N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 33.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00008; EGF; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nterPro; IPR001791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nterPro; IPR001611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cyprinidae; Danio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGF-like domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=slit3;
                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                          PROSITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9DE37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 89
Q9DE37
      DORANGE SERVICE OF SER
```

ò 임

ô

ä

```
(AUG-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 2524 AA.
                                                                                                                                                                       InterPro; IPR00110; ANK.
InterPro; IPR00110; ANK.
InterPro; IPR000152; ASK.hydroxyl_S.
InterPro; IPR001481; EGF_Ca.
InterPro; IPR001438; EGF_II.
InterPro; IPR006209; EGF_II.
InterPro; IPR006209; EGF_II.
InterPro; IPR006209; ASK.hydroxyl_S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 XNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00023; An; 6.
Pfam; PF00023; An; 6.
Pfam; PF00008; EGF; 29.
Pfam; PF00066; Notch; 3.
PIRSF; PIRSF00279; Notch; 1.
PRINTS; PR001415; ANKRIN.
PRINTS; PR0010; EGFBLOOD.
                                            EMBL; AF537369; AAN06819.1;
HSSP; P07207; 10T8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00248; ANK; 7.
SMART; SM00179; EGF_CA; 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=notch;
                      Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9GPA5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9GPA5
                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                      Anopheles gambiae str. pEST.

Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,

Neoptera, Endopterrygota, Diptera, Nematocera, Culicoidea, Anopheles.

NCBI_TaxID=180454,
                                                                                                                                                                                                                                                                                                                                            Anotheles Genome Sequencing Consortium,
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boophilus microplus (Cattle tick),
Eukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Acari,
Parasitiformes, Ixodida, Ixodidae, Boophilus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.7%; Score 62; DB 2; Length 2037;
26.9%; Pred. No. 8.3e+02;
Live 14; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2037 AA; 221100 MW; 7D925FCB7D7AC776 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO, GO:0005199; F:calcium ion binding; IEA.
GO; GO:0005198; F:calcium ion binding; IEA.
GO; GO:0005198; F:calcium ion binding; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPR000152; Asx hydroxyl S.
InterPro; IPR000182; Asx hydroxyl S.
InterPro; IPR00184; EGF Z.
InterPro; IPR00184; EGF Z.
InterPro; IPR001438; EGF II.
InterPro; IPR001791; Laminin G.
                                                                01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
AgCP13744 (Fragment).
Name=agCG44966; ORFNames=EMSANGG0000015360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Notch-like protein.
                                PRT; 2037 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 2428 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          670 GMTGRLCEIDIDDCESQPCQNGGRCI 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 XIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                          preliminary data.
EMBL; AAAB01008844; EAA06013.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00010; ASX HYDROXYL; 17.
PS00022; EGF 1; 24.
PS01186; EGF 2; 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PSSO026; EGF_3; 27.
PROSITE; PSSO025; EGF_CA; 13.
PROSITE; PSSO025; LAM_G_DOMAIN; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE=Whole ticks;
Whitfeld P.L., McNicholas P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Query Match
Best Local Similarity 26.39,
And 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00008; EGF; 24.
Pfam; PF07645; EGF CA; 2.
Pfam; PF02210; Laminin G 2
PRINTS; PR00010; EGFBLÖOD
                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P00740; 1EDM.
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=6941;
                                                                                                                                                                                                                                                                                                                                STRAIN-PEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=BOTCH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q816X6
Q816X6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 92
0816X6
1D Q816X1
AC Q816X1
DT 01-MAJ
070FS2
                        TAMES OF THE PROPERTY OF THE P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Branchiostoma floridae (Florida lancelet) (Amphioxus).
Bukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
Branchiostoma.
MCBI_TaxID=7739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 51.7%; Score 62; DB 2; Length 2428; Local Similarity 29.2%; Pred. No. 9.8e+02; ies 7; Conservative 11; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Whole larvae,
Holland L.Z., Burgtorf C., Holland N.D., Lehrach H., Tamme
Abi-Rached L., Pontarotti P., Lardelli M.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE, PSS0088, ANK REPEAT; 4.
PROSITE; PSS0029; ANK_REP REGION; 1.
PROSITE; PS00010; ASX_HPNEOXYL; 22.
PROSITE; PS01186; EGF_2; 27.
PROSITE; PS01186; EGF_2; 27.
PROSITE; PS01187; EGF_3; 35.
PROSITE; PS01187; EGF_3; 35.
ANK repeat; EGF_1ike Gomain.
SEQUENCE 2428 AA; 260842 MW; 766A9362CE37CB9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUB=Whole larvae;
Lardelli M.T.;
Submitted (ARR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; Y125.9; CAC19873.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Putative notch receptor protein.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO:0030154; P:call differentianion; IEA.
GO; GO:0050793; P:regulation of development; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0016020; C:membrane; IEA.
GO; GO:0005509; F:calcium ion binding; IEA
```

```
QBLAG1;
01-OCT-2002 (TrEMBLrel. 22, Created)
 SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: Expressed b
                                                                                                                                                                                                                                                                                                  51.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conotoxin scaffold VI/VII,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 51.23
Best Local Similarity 27.65
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                              8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=89451;
                                                                                                                    DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                         DISULFID
                                                                                                                                                               MOD RES
                                                                                                                                                                           STRAND
                                                                                                                                                                                                      STRAND
                                                                                                                                                                                                                                STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9BP77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8LAG1
                                                                                                                                                                                                                                                          STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9BP77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 96
Q8LAG1
ID Q8LAG
AC Q8LAG
DT 01-OC
                                                                                                                                                                                        TURN
                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9BP7
 ò
                                                                                                                                                                                                                                                                                                                                                                               엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Venom;
MEDLINE-89123282; PubMed=2914898;
Skinner W.S., Adams M.E., Quistad G.B., Kataoka H., Cesarin B.J.,
Skinner W.S., Adams O.A.;
Enderlin F.E., Schooley D.A.;
"Purification and characterization of two classes of neurotoxins from
the funnel web spider, Agelenopsis aperta.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96182019; PubMed=8608119; DOI=10.1021/bi952605r; Omecinsky D.O., Holub K.E., Adams M.E., Reily M.D.; "Three-dimensional structure analysis fun-datoxins: further evidence for comnon motifis among neurotoxins with diverse ion channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             specificities.";
Biochemistry 35:2836-2844(1996).
-I- FUNCTION: Causes irreversible paralysis in lepidopterous insects
by massive transmitter release (which is mediated by glutamate
receptors) from presynaptic stores at neuromuscular junctions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Agelenopsis aperta (Funnel-web spider).
Eukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Araneae,
Araneomorphae, Entelegynae, Agelenidae, Agelenopsis.
NCBI_TaxID=6908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 62; DB 2; Length 2524; Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00022; EGF_1; 34.—
PROSITE; PS01166; EGF_2; 28.
PROSITE; PS50026; EGF_3; 36.
PROSITE; PS510167; EGF_CA; 22.
ANK repeat; EGF-like Gomain; Receptor.
SEQUENCE 2524 AA; 270970 MW; C2CA57E306D23EC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 · 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-1989 (Rel. 11, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
F:receptor activity; IEA.
P:cell differentiation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Mismatches
                                                                                                                                                                                                                                                                           PROSITE; PSS0088; ANK REPEAT; 4.
PROSITE; PSS0297; ANK REP REGION; 1.
PROSITE; PS00010; ASX_HYDROXIL; 23.
PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
                       InterPro; IPR008985; Con like lec_gl.
InterPro; IPR00045; Cytc_heme_BS.
InterPro; IPR000742; EGF_Z.
InterPro; IPR001881; EGF_Z.
InterPro; IPR001483; EGF_II.
InterPro; IPR001438; EGF_II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           925 GFGGTNCEEDIDECYSNPCQNGGQCI 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                       Interpro; IPRN001881; EGF_Ca.
Interpro; IPRN01438; EGF_II.
Interpro; IPRN06209; EGF_II.ke.
Interpro; IPRN00800; Notch_region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1989 (Rel. 11, Created)
                                                                                                                                                           Pfam; PF00008; EGF; 34.
Pfam; PF00066; NGF; 2.
Pfam; PF00066; NOCCD; 3.
PRINTS; PR01415; ANKYRIN.
PRINTS; PR00010; EGFBLOOD.
PRINTS; PR01452; NOTCH.
SMART; SM00248; ANK; 6.
SMART; SM0019; EGF CA; 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 23.1 tes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                              Pfam; PF00023; Ank;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRUCTURE BY NMR.
GO; GO:0004872;
GO; GO:0030154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mu-agatoxin 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TXM1 AGEAP
P11057;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                       SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TXM1_AGEAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 94
 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

```
ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Mechanisms for evolving hypervariability: the case of conopeptides."; Mol. Biol. Evol. 18:120-131(2001).
BMBL; AP215061; AAG6489.1; ---
GO, GO:0005576; C:extracellular; IEA.
GO; GO:0008200; F:ion channel inhibitor activity; IEA.
                                             PIR; A32038; A32038.
PIR; A32038; A32038.
PDB; 1EIT; NMR; @=1.36.
Interpreto; 1FR009243; Toxin_7.
Pfam; PF05980; Toxin 7; 1.
3D-structure; Amidation; Direct protein sequencing; Neurotoxin; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ë.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conus arenatus (Sand-dusted cone).
Bukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoldea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21105969; PubMed=11158371;
Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
Fainzilber M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels

    I-SSUE SPECIFICITY: Expressed by the venom gland.
    SIMILARITY: Belongs to the mu-agatoxin family.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR04214; Conctoxin.
Pfam; PPC2950; Conctoxin; 1.
SEQUENCE 81 AA; 8697 MW; 99EB0139D26851D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4273 MW; 3B973A605B90DE85 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                 Asparagine amide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     471 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51.2%; Score 61.5; I 27.6%; Pred. No. 50; iive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CXIXNQXCXQXLDDCCS---XXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 CVPENGHCRDWYDECCEGFYCSCRQPPKCI 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CXIXNQXCXQXLDDCCSXXC---NXXNXC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |:::::|::|||||::|
46 CTVDSDFCDPDNHDCCSGRCIDEGGSGVC 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 61.5;
Pred. No. 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
```

.

```
Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones 'Mamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki J. Davis R.W., Ecker J.R., Theologis A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AY065014; AAL57658.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AY096601; AAM20251.1; -. EMBL; AY142043; AAM98307.1; -. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 22.2 Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T25N20.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9ZVZ7;
                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,

Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,

Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,

Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,

Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Sacu M.,

Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
                                                                                            Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Satou M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B. Lee J.M., Lin J., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou P.
Saki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
Palammura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=22088475; PubMed=12093376;
Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
"Full-length messenger RNA sequences greatly improve genome annotation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell Feldmann K.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY087835; AAM5388.1;
Hypothetical protein.
SEQUENCE 471 AA; 53428 MW; 3573C789C54FB28A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.2%; Score 61.5; DB 2; Length 4 22.2%; Pred. No. 2.5e+02; ive 12; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ecker J.R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seki M., Shinn P., Southwick A., Surmormorm. Theologis A.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                  Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last amotation update)
At1905410/T25N20_5 (Hypothetical protein At1905410)
           Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |::|::|::||
150 CKAGNEKCRSLMPQCEAETL.PAMPCDICCGERKFCV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CXIXNOXCXQXLDDC-----CSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                              Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
01-OCT-2002 (TrEMBLrel. 22, Last sequenc
01-WAR-2003 (TREMBLrel. 23, Last annotat
Hypothetical protein.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 22.2
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=At1g05410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QBVZES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
089/ZES
100/ZES
100/Z
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
```

```
Kim C.J., Chen H., Cheuk R., Shinn P., Boweer L., Carninci P., Chan M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y., Hsuan V.W., Ishida J., Jones T., Kamiya A., Karlin-Nemann G., Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C., Yamada K., Yu G., Yuan S., Davis R.W., Theologis A., Ecker J.R., Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mikharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. Checks S., Buehler E., Chao Q., Johnson-Hopson C., Cheuk R., Shinn P., Brooks S., Buehler E., Chiou J., Choi E., Conn L., Comway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Johnson-Hopson C., Brooks S., Buehler E., Chao Q., Khan S., Kim C., Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Ecker J.R., Vaysberg M., Yu G., Federspiel N.A., Theologis A., Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
Υ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ٠.
د
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                ll protein.
471 AA; 53368 MW; 582512E495010DDA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |::|::|::|
150 CKAGNEKCRSLMPQCEAETLPAMPCDICCGERKFCV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.2%; Score 61.5; DB 2; 22.2%; Pred. No. 2.5e+02; ive 12; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CXIXNOXCXQXLDDC-----CSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481 AA
```

ä

```
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
             %+++++++++
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                        ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDZINE=2255705; PubMed=12368864; DOI=10.1038/nature01097; Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K., Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.S., Nene V., Shallon S.J., Suh B., Peterson J., Angluoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., Werfaden G.I., Cummings L.M., Subramanian G.M., Mungall C., Vorucci D.J., Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=94150815; PubMed=8107968; DOI=10.1016/0028-3908(93)90008-Q;
Monje V.D., Haack J.A., Naisbitt S.R., Miljanich G., Ramachandran J.,
Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .,
e
                                                                                                                                                                                                                                                                                                                                                        ٠.
م
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 61.5; DB 2; Length 2050;
Pred. No. 9.4e+02;
                                                                                                                                                                                                                                                               Length 481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium faĪciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome seguence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                    Indels
                                                 Theologis A., Ecker J.;
Submirted-(JUN-2200) to the EMBL/GenBank/DDBJ databases.
EMBL; AC005106; AAF9739.1; -
SEQUENCE 481 AA; 54484 MW; 409BE67FF55068E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2050 AA; 243182 MW; 0A0586A5B42A3B8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-DEC-1998 (Rel. 37, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Omega-conotoxin MVIId precursor (SNX-238) (Fragment).
Conus magus (Magus cone).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                          51.2%; Score 61.5; DB 2;
22.2%; Pred. No. 2.5e+02;
ive 12; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CXIXNQXCXQXLDDC-----CSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 2050 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CXIXNQXCXQ---XLDDCCSXXCNXXNX 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last seq
05-JUL-2004 (Rel. 44, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE014829; AAN35235.1; -.
HSSP; Q93IC2; 1MWX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51.2%;
32.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, Hypothetical manal man
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 32.19 les 9; Conservative
                                                                                                                                                                                                                                                                                                                                                    8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 419:498-511 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
SEQUENCE 2050 AA; 2
                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=36329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI TaxID=6492;
Thaveri A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      falciparum
                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CXOD CC
026350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QBIK03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 100
CXOD CONNA
LO CXOD CONNA
LO CXOD CONNA
DT 15-DEC
DT 15-DEC
DT 05-UIL
DE OMEGA-
CO APOGAE
OC APO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 99
1081803
100181803
1001-MA
DT 01-MA
DT 
                                                                                                                                                                                                                                                                                                                                                        Matches
        Sarrs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                                             ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       쉽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                        two-dimensional 1H NMR of omega-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                    Civera C., Vazquez A., Sevilla J.M., Bruix M., Gago F., Garcia A.G.,
                                                                                                                                                                                                                                     "Solution structure determination by two-dimensional 1H NMR of omega conctoxin MVIID, a calcium channel blocker peptide.";
Biochem. Biophys. Res. Commun. 254:32-35(1999).

-1- FUNCTION: Omega-concloxins act at presynaptic membranes, they bi and block voltage-sensitive calcium channels (VSCC). This toxin
                                                                                                                                                                                                                                                                                                                                                                                           blocks channels of the N-type as well as other types.
-!- SUBCELDIAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom duct.
-!- SIMILARITY: Belongs to the conotoxin O-superfamily. Omega-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cysteine amide (G-29 provides amide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P05484; 1FEO.
IncerPro; 198004214; Conotoxin.
Amidation; Calcium channel inhibitor; Ionic channel inhibitor;
Neurotoxin; Presynaptic neurotoxin; Toxin.
                                                                                                                            STRUCTURE BY NMR.
MEDLINE=99121185; PubMed=9920728; DOI=10.1006/bbrc.1998.9878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 29; 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Indels
Nasdasdi L., Olivera B.M., Hillyard D.R., Gray W.R.; "A new Conus peptide ligand for Ca channel subtypes."; Neuropharmacology 32:1141-1149(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9E04B2EA3779CB22 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Omega-conotoxin MVIId
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 61;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CXIXNQXCXQXLDDCCSXXCNXXNX 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: April 18, 2005, 20:37:46 Job time : 121 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 COGRGASCRKTMYNCCSGSCNRGRC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.8%;
28.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; S69322; AAB29902.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3104 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28
23
28
28
28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR, A58537; A58537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 AA;
                                                                                                                                                                                                                      Sevilla P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
```

This page Blank (uspto)

1

Snail Conus Conus Conus Conus Conus Conus Conus	Conus Snail Snail Snail Snail Conus Conus Conus		ARI37766 SVIB/SNX-ARV12941 OWEGA CON-ARV12971 OWEGA CON-ARV25410 OWEGA-CON-ARV26480 NATURAL O AARV26480 NATURAL O AARV26480 NATURAL O AARV36480 NATURAL O AARV36481 NATURAL O AARV2641 OWEGA-CON-ARV2641 OWEGA-CON-ARV6689 TYCOBIAB BET ABD96872 OWEGA-CON-ARV6689 TYCOBIAB ABD9677 CONB BET ABD9677 CONB SENAI ABA13762 SNX-231. AARI37762 SNX-231. AARI37761 MVIIC/SNX AARI9552 NATURAL O AARV2613 CONUB GEN AARV2613 CONUB GEN AARV2613 CONUB GEN AARV2613 CONUB GEN AARV2613 OWEGA-CON AAV2613 OWEGA-CON AAV2613 OWEGA-CON AAV2613 OWEGA-CON AAV26141 OMEGA-CON AAV2613 OMEURAL OMEGA-CON AAV2613 OMEGA-CON AAV2
4 0 0 0 0 0 0 0 0	0 4 4 4 4 4 4 6 6 6 6	• • • • • • • • • • • • • • • • • • •	26 2 AARX37612 26 2 AARX37612 26 2 AARX37612 26 2 AARX36480 26 3 AAX56480 26 4 AAB19449 26 4 AAB19449 26 4 AAB19449 27 5 ABB9668 26 5 ABB9668 27 5 ABB96776 27 5 ABB96776 27 5 ABB96776 27 5 ABB96776 27 5 ABB96776 27 5 ABB96774 27 5 ABB96774 27 5 ABB96774 27 5 ABB96774 27 5 ABB96774 26 2 AAR37761 26 2 AAR37761
155 96. 155 96. 155 96. 155 96. 155 96. 155 96.	155 96. 153 95. 153 95. 153 95. 153 95. 153 95. 153 95.		6 6 1 3 3 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7
nn 5.1.6 Compugen Ltd. Search time 125 Seconds (without alignments)	nillion cell updates/sec	2105692	ccted by chance to have a score distribution. Description Aaw35723 Kappa-con Aaw10218 Snail Kap Aaw38358 Conus pur Aaw10205 Snail Kap Aaw38358 Conus pur Aaw38343 Conus pur Aaw38343 Conus pur Aaw38343 Conus pur Aaw38343 Conus pur Aaw38347 Conus pur Aaw38347 Conus pur Aaw38347 Conus pur Aaw38357 Conus pur Aaw38336 Conus pur Aaw38338 Conus pur Aaaw38338 Conus pur Aaw38338 Conus pur Aaw38338 Conus pur Aaw38338
GenCore version 5.1.6 GenCore version 5.1.6 Copyright (c) 1993 - 2005 Comput protein - protein search, using sw model	US-10-627-685A-26 161 1 CRIXNQKCFQHLDDCCSRKCNRFNN BLOSUM62DX Gapop 10.0 , Gapext 0.5 2105692 seqs, 386760381 res	Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries Listing first 100 summaries A Geneseqp1980s:* 2: geneseqp1980s:* 2: geneseqp2000s:* 4: geneseqp2001s:* 5: geneseqp2001s:* 6: geneseqp2003s:* 7: geneseqp2003s:* 8: geneseqp2003s:* 7: geneseqp2003s:*	Lits predictive score the total summaries summaries summaries size size size size size size size s

Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; 04A.

Snail Kappa-conotoxin PVIIA analogue O4A.

(first entry)

16-JAN-2002

AAU10218;

AAU10218 standard; peptide; 27 AA.

/note= "The C-terminus is either a carboxyl group or an

amide group"

WO200121648-A1.

29-MAR-2001.

'note= "Hyroxyproline"

Location/Qualifiers

Key Modified-site

Modified-site

purpurascens

Conus purp Synthetic.

Mccabe RT;

Layer RT,

Temple DL,

Cornell-Bell AH, Pemberton KE,

Jones RR;

WPI; 2001-648090/74.

(COGN-) COGNETIX INC.

22-SEP-1999; 99US-0155135P. 20-JUL-2000; 2000US-0219438P.

21-SEP-2000; 2000WO-US025827

~

```
/note= "Optionally 4-trans-hydroxyproline, hydroxyproline or proline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a new kappa-conotoxin PVIIA which targets potassium channels and can be used to augment neurotransmitter release in pathological situations such as autoimmune diseases, e.g. Alzheimer's disease, Lambert-Eaton syndrome or myasthenia gravis. This peptide inmobilize fish which are injected with the two peptides. Injection of kappa-conotoxin PVIIA and synergistically to rapidly kappa-conotoxin PVIIA alone results in different symptoms with an injected fish becoming hyperactive and then contracting and suddenly extending all major fins. This "fin-popping" occurs repeatedly resulting in a series of jerky movements, but injection of only kappa-conotoxin PVIIA does not immobilize or kill the fish
        Aay43715 Amino aci
Aab14377 Omega-con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New kappa-conotoxin peptides - which target potassium channels and can be used to augment neurotransmitter release in e.g. autoimmune diseases.
                                                                                                                                                                                                                          Kappa-conotoxin PVIIA; potassium channel; neurotransmitter release;
cone snail; venom; goldfish; delta-conotoxin PVIIA; disulphide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Olivera BM;
                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                      'note= "disulphide bond"
                                                                                                                                                                                                                                                                                                                                                                                     note= "disulphide bond"
                                                                                                                                                                                                                                                                                                                                                                                               15. 26
/note= "disulphide bond"
     AAY43715
AAB14377
                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                          Ä
                                                                                                                        27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shon K, Grilley MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 23; 29pp; English.
                                                                                                                   AAW35723 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97WO-US003483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-00619936
     m m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UTAH .) UNIV UTAH RES FOUND.
                                                                                                                                                                         (first entry)
     26
                                                                                                                                                                                                    Kappa-conotoxin PVIIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-480162/44.
                                                                                                                                                                                                                                                                  Conus purpurascens.
    37.9
37.9
                                                                                                                                                                                                                                                                                           Key
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                      Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                              Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9734925-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-MAR-1996;
                                                                                                                                                                        03-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-SEP-1997.
    61
                                                                                                                                             AAW35723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Terlau H,
99
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (Kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappaconotoxin PVIIA peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              psed: No. 1e-10;
if Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRIANOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 28; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 100.0%;
Local Similarity 96.3%; Res 26; Conservative 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
```

AAE38358 standard; peptide; 27 AA.

AAE38358 ID AAE3

ö

Gaps ; 0

100.0%; Score 161; DB 2; Length 27; 96.3%; Pred. No. 1e-10; Live 1; Mismatches 0; Indels

Local Similarity 96.3

Query Match Matches 1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27

ò 유

CRIPNOKCFQHLDDCCSRKCNRFNKCV

2,3

```
cerebral ischaemia; ocular ischaemia; asthma; S17A.
                                                                                                                                                                                                                                                                    Cornell-Bell AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 27 AA;
                                                                                                                                        WO200121648-A1
                                                                   Modified-site
                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-JAN-2002
                                                                                                                                                              29-MAR-2001
                                    Synthetic
                                                                                                                                                                                                                                                                                Jones RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU10206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5 ·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matchès
  요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral evesoppens accompanying subarachnoid haemorrhage, anxiety disorder, cerebral ischaemia, coronary artery bypass graft (GASG) surgery, ischaemic heart disease, asthma, and congestive heart failure. The present
                                                                             Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                              Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 161; DB 6; Length 27;
                                                                                                                                                                                                                                                                                                    Temple DL, Mcintosh JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                        Conus purpurascens kappa-PVIIA analogue peptide, Q4A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Snail Kappa-conotoxin PVIIA analogue S17A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRIANQKCFQHLDDCCSRKCNRFNKCV
                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 8; 32pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ą
                                                                                                                                                                                                                                                                                                       Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU10212 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
96.3%; E
                                                                                                                                                                                                                      28-JAN-2003; 2003WO-US002384.
                                                                                                                                                                                                                                             29-JAN-2002; 2002US-0352219P.
                                                                                                                                                                                                                                                                  (COGN-) COGNETIX INC.
(UTAH ) UNIV UTAH RES FOUND.
                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 96.3
les 26; Conservative
                                                                                                                                                                                                                                                                                                     Pemberton-Goodman KE,
                                                                                                                                                                                                                                                                                                                                       WPI; 2003-679464/64.
                                                                                                                                                  Conus purpurascens
                                                                                                                                                                        WO2003063782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-JAN-2002
                                 20-NOV-2003
                                                                                                                                                                                               07-AUG-2003
                                                                                                                                                                                                                                                                                                                Olivera BM;
            AAE38358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU10212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
```

```
The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with channel, especially cardiac ischaeme by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-conotoxin PVIIA peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; F9Y.
                                                                                                                                                                                                    /note= "The C-terminus is either a carboxyl group or an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating disorders associated with radical depolarization of excitable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mccabe RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Layer RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 158; DB 4;
Pred. No. 2.2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Snail Kappa-conotoxin PVIIA analogue F9Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRIXNOKCFQHLDDCCARKCNRFNKCV 27
                                                                                                                                            /note= "Hyroxyproline"
                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 28; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-SEP-1999; 99US-0155135P, 20-JUL-2000; 2000US-0219438P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                  21-SEP-2000; 2000WO-US025827
                                                                                                                                                                                                                                      amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU10206 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 Similarity 96.3
26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (COGN-) COGNETIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-648090/74.
Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conus purpurascens.
Synthetic.
```

4

```
28-JAN-2003; 2003WO-US002384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE38352
                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular analogue of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    excitable
na comprises
                                                                                 /note= "The C-terminus is either a carboxyl group or an amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
cerebral ischaemia; ocular ischaemia; asthma; R2K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "The C-terminus is either a carboxyl group or an
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treating disorders associated with radical depolarization of excitab
membrane e.g. cardiac, cerebral and ocular ischemia and asthma compractivating a KATP channel by administering to an individual a kappa-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                    Mccabe RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 98.1%; Score 156; DB 4; Length 27; Best Local Similarity 96.3%; Pred. No. 2.2e-10; Matches 26; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                    Layer RT,
                                                                                                                                                                                                                                                                                                                                                            Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Snail Kappa-conotoxin PVIIA analogue R2K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRIXNOKCPOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "Hyroxyproline"
    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU10203 standard; peptide; 27 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 28; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                            Pemberton KE,
                                                                                                                                                                                                                  21-SEP-2000; 2000WO-US025827
                                                                                                                                                                                                                                                            22-SEP-1999; 99US-0155135P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conotoxin PVIIA peptide
                                                                                                                                                                                                                                                                                                                  (COGN-) COGNETIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-648090/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           purpurascens
                                                                                                                                                                                                                                                                                                                                                      Cornell-Bell AH,
                                                                                                                                     WO200121648-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 27 AA;
                  Modified-site
                                                          Modified-site
                                                                                                                                                                                                                                                          22-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                             29-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                             Jones RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU10203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU10203
ID AAU.
XX AC AAU.
XX DT 16-1
XX CW PUR KW CAR KW
```

d ò

```
The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprishing administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-conotoxin PVIIA peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertenaton; angina; retlinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                Mccabe RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98.1%; Score 158; DB 4; Length 27; 96.3%; Pred. No. 2.2e-10; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                          Layer RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conus purpurascens kappa-PVIIA analogue peptide, S17A.
                                                                                                                                                                                                                                                                                                                                                                       Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CKIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 27; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                           Cornell-Bell AH, Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE38352 standard; peptide; 27
                                                                                                                                                                21-SEP-2000; 2000WO-US025827.
                                                                                                                                                                                                                      22-SEP-1999; 99US-0155135P, 20-JUL-2000; 2000US-0219438P.
amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Hyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            analogue of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                       (COGN-) COGNETIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-648090/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conus purpurascens.
                                                WO200121648-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003063782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                         29-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-AUG-2003.
                                                                                                                                                                                                                                                                                                                                                                                         Jones RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
```

ô

us-10-627-685a-26.rag

```
ö
                                                                                                                                                                                                                                                                            organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conocoxins. The conocoxins can also be used for arresting, protecting or preserving an organ of a mammal using kappa-PVIIA-related conocoxins. The conocoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral ecrebral schemata, coronary artery bypass graft (CABG) surgery, ischemic heart disease, asthma and congestive heart failure. The present sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                   invention relates to kappa-PVIIA-related conotoxins and their use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypase graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 158; DB 6; Length 27;
Pred. No. 2.2e-10;
                                                                                                  Mcintosh JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conus purpurascens kappa-PVIIA analogue peptide, F9Y.
                                                                                                    Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRIPNOKCFQHLDDCCARKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                  Disclosure; Page 7; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE38346 standard; peptide; 27 AA
                                                                                                    Jones RM,
               29-JAN-2002; 2002US-0352219P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.1%;
92.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JAN-2002; 2002US-0352219P
                                              (COGN-) COGNETIX INC.
(UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JAN-2003; 2003WO-US002384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (COGN-) COGNETIX INC. (UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 92.00,
Best Acad Similarity 92.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Hyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                  Pemberton-Goodman KE,
                                                                                                                                               WPI; 2003-679464/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2003063782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-NOV-2003
                                                                                                                  Olivera BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE38346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
AAE38346
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
```

```
Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                         The invention relates to kappa-PVIIA-related conotoxins and their use ar organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral wasospasm accompanying subarachnoid haemorrhage, anxiety disorder, cerebral ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ischaemic heart disease, cerebral ischaemia, anxiety disorder, diabetes, organ protectant, arryhthmia, reperfusion injury; hypertension, angina, retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; ABG.
                                                                                                                                                                                                                                                                                                                                                            sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
               Mcintosh JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                          98.1%; Score 158; DB 6; Length 27; 92.6%; Pred. No. 2.2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mcintosh JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conus purpurascens kappa-PVIIA analogue peptide, R2K.
               Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRIPNOKCYOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                             Disclosure; Page 7; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ź
               Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE38343 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JAN-2003; 2003WO-US002384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JAN-2002; 2002US-0352219P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (COGN-) COGNETIX INC.
(UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Hyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 92.6
Matches 25; Conservative
               Pemberton-Goodman KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pemberton-Goodman KE,
                                                               WPI; 2003-679464/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-679464/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conus purpurascens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2003063782-A2
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-AUG-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Olivera BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE38343;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                              Olivera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
```

ö

φ

ö

Gaps

. 0

```
WPI; 2001-648090/74.
                                                                Best Local Similarity
                                                                                                                             Conus purpurascens.
Synthetic.
                                                                                                                                                                                        Cornell-Bell AH,
                                                       Sequence 27 AA;
                                                                                                                                                         WO200121648-A1
                                                                                                                                      Key
Modified-site
                                                                                                                                              Modified-site
                                                                                                       16-JAN-2002
                                                                                                                                                               29-MAR-2001
                                                             Query Match
                                                                                                  AAU10207:
                                                                                                                                                                                            Jones RR;
                                                                                      RESULT 10
ò
                                                                                              유
```

```
The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conctoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with channel, especially cardiac ischaemia, cerebral ischaemia, KATP ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
cerebral ischaemia; ocular ischaemia; asthma; V27A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappaconotoxin PVIIA peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "The C-terminus is either a carboxyl group or an
  activating a KATP channel by administering to an individual a kappa-conotoxin PVIIA peptide.
                                                                                                                                                                                                                                                                                                                                Length 27;
                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Layer RT,
                                                                                                                                                                                                                                                                                                                            Score 157; DB 4;
Pred. No. 2.8e-10;
                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Snail Kappa-conotoxin PVIIA analogue V27A.
                                                                                                                                                                                                                                                                                                                                                                                                                         1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU10217 standard; peptide; 27 AA.
                                                        Claim 1; Page 28; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cornell-Bell AH, Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 28; 46pp; English
                                                                                                                                                                                                                                                                                                                          97.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-SEP-1999; 99US-0155135P.
20-JUL-2000; 2000US-0219438P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-SEP-2000; 2000WO-US025827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                            26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (COGN-) COGNETIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-648090/74.
                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conus purpurascens.
                                                                                                                                                                                                                                                                                    Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200121648-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU10217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jones RR;
                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
  à
                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                    present
              a mammal comprises
                                                                                      The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, treatment of arrivthima, urinary incentinence, reperfusion injury, daabetes, retinopathy, neuropathy, nephropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral esebspara accompanying subarachnoid haemorrhage, anxiety disorder, eschamal ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The presensequence is comes purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
cardioactive; antiasthmatic; KATP charnel activation; cardiac ischaemia;
cerebral ischaemia; ocular ischaemia; asthma; R2Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        п
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "The C-terminus is either a carboxyl group or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Layer RT, Mccabe RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                   Score 158; DB 6; Length 27;
Pred. No. 2.2e-10;
2; Mismatches 0; Indels
Protection and preservation of an organ e.g. heart of a use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Snail Kappa-conotoxin PVIIA analogue F.2Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                          Disclosure; Page 7; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU10207 standard; peptide; 27 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                         98.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-SEP-1999; 99US-0155135P.
20-JUL-2000; 2000US-0219438P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-SEP-2000; 2000WO-US025827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                           25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (COGN-) COGNETIX INC.
```

Mccabe RT;

```
ö
The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-concorain PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conctoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant, arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to kappa-PVIIA-related conotoxins and their use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conctoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                         97.5%; Score 157; DB 4; Length 27; 100.0%; Pred. No. 2.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Temple DL, Mcintosh JM;
                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conus purpurascens kappa-PVIIA analogue peptide, V27A.
                                                                                                                                                                                                                                     100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                   56
                                                                                                                                                                                                                                                                                                   1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                      CRIXNQKCFQHLDDCCSRKCNRFNKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 8; 32pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                              AAE38357 standard; peptide; 27 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pemberton-Goodman KE, Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JAN-2003; 2003WO-US002384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JAN-2002; 2002US-0352219P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (COGN-) COGNETIX INC.
(UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Hyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                     analogue of the invention
                                                                                                                                                                                                                                                               26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-679464/64.
                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003063782-A2
                                                                                                                                                                                       Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Olivera BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE38357;
                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conus
                                                                                                                                                                                                                                                                                                                                                                                        Matches
       8888888888888888
                                                                                                                                                                                                                                                                                                                                   셤
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                               Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a mammal comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to kappa-PVIIA-related conotoxins and their use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organ protectants The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conocoxins. The conocoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, peripheral circulation disturbances, hopertension injury, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, cerebral ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The present sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue peptide
cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
ischaemic heart disease, asthma and congestive heart failure. The preser
sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                        Gaps
                                                                                                                                                        ö
                                                                                                                      Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mcintosh JM;
                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protection and preservation of an organ e.g. heart of use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                    Conus purpurascens kappa-PVIIA analogue peptide, R2Q.
                                                                                                                      Score 157; DB 6;
Pred. No. 2.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jones RM, Temple DL,
                                                                                                                                                        Mismatches
                                                                                                                                                                                          56
                                                                                                                                                                                                                          1 CRIPNOKCFÓHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                          1 CRIXNQKCFQHLDDCCSRKCNRFNKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 7; 32pp; English.
                                                                                                                                                                                                                                                                                                              AAE38347 standard; peptide; 27
                                                                                                                  97.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JAN-2003; 2003WO-US002384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JAN-2002; 2002US-0352219P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Hyp
                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (COGN-) COGNETIX INC. (UTAH ) UNIV UTAH RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pemberton-Goodman KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-679464/64.
                                                                                                                                  Local Similarity
les 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conus purpurascens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003063782-A2
                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                     Sequence 27
                                                                                                                                                                                                                                                                                                                                                                                  20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Olivera BM;
                                                                                                                                                                                                                                                                                                                                                AAE38347;
                                                                                                                        Query Match
                                                                                                                                        Best Loc
Matches
                                                                                                                                                                                                                                                                              RESULT 13
                                                                                                                                                                                                                                                                                                AAE38347
   8X33333
                                                                                                                                                                                                                        원
```

ω

Page

Ą,

Sequence 27

g

Gaps

;

```
Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; 112A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conctoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for trearing disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-
                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "The C-terminus is either a carboxyl group or an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mccabe RT:
 97.5%; Score 157; DB 6; Length 27; ilarity 92.6%; Pred. No. 2.8e-10; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Layer RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Temple DL,
                                                                                                                                                                                                                                                 Snail Kappa-conotoxin PVIIA analogue L12A.
                                                            1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                           note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                     Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cornell-Bell AH, Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 28; 46pp; English.
                                                                                                                                                            AAU10214 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-SEP-2000; 2000WO-US025827.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-SEP-1999; 99US-0155135P.
20-JUL-2000; 2000US-0219438P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conotoxin PVIIA peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (COGN-) COGNETIX INC
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-648090/74.
                                                                                                                                                                                                                                                                                                                                         Conus purpurascens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200121648-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                             25;
                                                                                                                                                                                                                        16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-MAR-2001.
                                                                                                                                                                                            AAU10214;
                              Matches
                                                                                                                                   RESULT 14
                                                                                                                                                                a
                                                          à
```

```
The invention relates to treating disorders associated with radical comprisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-contoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia, and asthma. The present sequence is a kappa-conotoxin PVIIA
                                                                                                                                                                                                    Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
cerebral ischaemia; ocular ischaemia; asthma; I3A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappaconotoxin PVIIA peptide.
                                                                                                                                                                                                                                                                                                                                                        C-terminus is either a carboxyl group or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mccabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Temple DL, Layer RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96.9%; Score 156; DB 4; I
96.3%; Pred. No. 3.6e-10;
11ve 0; Mismatches 1;
                    27
                                                                                                                                                                           Snail Kappa-conotoxin PVIIA analogue I3A.
    27
                                                                                                                                                                                                                                                                                                                             'note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CRAXNQKCFQHLDDCCSRKCNRFNKCV 27
CRIXNOKCFOHLDDCCSRKCNRFNKCV
                 CRIXNOKCFOHADDCCSRKCNRFNKCV
                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cornell-Bell AH, Pemberton KE, Jones RR;
                                                                                               27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 27; 46pp; English.
                                                                                         AAU10198 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-SEP-2000; 2000WO-US025827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-JUL-2000; 2000US-0219438P
                                                                                                                                                                                                                                                                                                                                                       /note= "The
                                                                                                                                                                                                                                                                                                                                                                    amide group"
                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      analogue of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 96.3
1es 26, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (COGN-) COGNETIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-648090/74.
                                                                                                                                                                                                                                                          Conus purpurascens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                              WO200121648-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 27 AA;
                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                              16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                        29-MAR-2001
 -
                                                                                                                      AAU10198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                            Best Loca
Matches
                    g
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                    ö
```

an

. 0

ö

Gaps

ö

Length 27; 1; Indels

96.9%; Score 156; DB 4; 96.3%; Pred. No. 3.6e-10; iive 0; Mismatches 1;

Conservative

Query Match Best Local Similarity Matches 26; Conserv

Location/Qualifiers

/label= Hyp

```
ischaemic heart disease, cerebral ischaemia, anxiety disorder, diabetes, organ protectant, arrhythmia, reperfusian injury, hypertension, angina, retinopathy, coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
                                                      Conus purpurascens kappa-PVIIA analogue peptide, L12A
                                                                                                                                                                                                                                                                                                      28-JAN-2003; 2003WO-US002384.
                           20-NOV-2003 (first entry)
                                                                                                                                                                  Conus purpurascens.
                                                                                                                                                                                                                                                 WO2003063782-A2
                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                            07-AUG-2003
 AAE38354;
엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                              Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to kappa-PVIIA-related conotoxins and their use as organ of a mammal using kappa-PVIIA-protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, neptropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, ecerbral ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The presensequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 156; DB 6; Length 27; Pred. No. 3.6e-10; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mcintosh JM;
                                                                                                                        Conus purpurascens kappa-PVIIA analogue peptide, I3A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRAPNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                              Location/Qualifiers
                                      AAE38338 standard; peptide; 27 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 6; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pemberton-Goodman KE, Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 92.6%;
Matches 25; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                          28-JAN-2003; 2003WO-US002384
                                                                                                                                                                                                                                                                                                                                                                                                     29-JAN-2002; 2002US-0352219P
                                                                                                                                                                                                                                                                                                                                                                                                                              (COGN-) COGNETIX INC.
(UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                      /label= Hyp
                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-679464/64.
                                                                                                                                                                                                                                    Conus purpurascens.
                                                                                                                                                                                                                                                                                                                   WO2003063782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 27 AA;
                                                                                                                                                                                                                                                                          Modified-site
                                                                                             20-NOV-2003
                                                                                                                                                                                                                                                                                                                                               07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Olivera BM;
                                                                  AAE38338,
            RESULT 16
                         AAE38336
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present
                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythma, utinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral usosopasm accompanying subarachnoid haemorrhage, anxiety disorder, cerebral ischaemia, coronary artery bypass graft (GABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The present sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                              Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                               Mcintosh JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96.9%; Score 156; DB 6; 92.6%; Pred. No. 3.6e-10;
                                                                                                                               Jones RM, Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Snail Kappa-conotoxin PVIIA analogue R2A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 8; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU10200 standard; peptide; 27
29-JAN-2002; 2002US-0352219P.
                                                                          FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 92.6
Matches 25, Conservative
                                               (COGN-) COGNETIX INC.
                                                                                                                                  Pemberton-Goodman KE,
                                                                                                                                                                                                            WPI; 2003-679464/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JAN-2002
                                                                                                                                                             Olivera BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU10200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8X4X5X8
```

AAE38354 standard; peptide; 27 AA.

RESULT 17 AAE38354 ID AAE3 XX

ઠ

/note= "The C-terminus is either a carboxyl group or an amide group"

note= "Hyroxyproline"

Location/Qualifiers

us-10-627-685a-26.rag

```
The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active radical depolarisation of excitable membrane by activating the conocoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
               Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
cerebral ischaemia; ocular ischaemia; asthma; R2A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Snail Kappa-conotoxin PVIIA analogue Q1.0A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAIXNQKCFQHLDDCCSRKCNRFNKCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU10216 standard; peptide; 27 AA.
                                                                                                                                                                                                                                                                                                                                                                              Cornell-Bell AH, Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 27; 46pp; English.
                                                                                                                                                                                                                                                                                                          22-SEP-1999; 99US-0155135P.
20-JUL-2000; 2000US-0219438P.
                                                                                                                                                                                                                                                                             21-SEP-2000; 2000WO-US025827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conotoxin PVIIA peptide.
                                                                                                                                                                                                                                                                                                                                                  (COGN-) COGNETIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-648090/74.
                                                                        Conus purpurascens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 26; Conserv
                                                                                                                                                                                                                    WO200121648-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 27 AA;
                                                                                                                              Modified-site
                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                         22-SEP-1999;
                                                                                                                                                                                                                                                29-MAR-2001,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                 Jones RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU10216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU10216
ID AAU1
XX
AC AAU1
XX
DT 16-J
XX
KW Snai
KW Purp
KW Card
KW Cere
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ठ
```

Mccabe RT;

Temple DL, Layer RT,

```
The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprishing administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active radical depolarisation of excitable membrane by activating a specially cardical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular analogue of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
cerebral ischaemia; ocular ischaemia; asthma; F9M.
                                                                                                                                                                                                                                                                                                                                                  Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprise activating a KATP channel by administering to an individual a kappa-conotoxin PVIIA peptide.
                                                                                                     or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                           C-terminus is either a carboxyl group
                                                                                                                                                                                                                                                                                          Mccabe RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 96.3%; Score 155; DB 4; Length 27; Best Local Similarity 96.3%; Pred. No. 4.7e-10; Matches 26; Conservative 0; Mismatches 1: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                          Layer RT,
                                                                                                                                                                                                                                                                                        Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Snail Kappa-conotoxin PVIIA analogue F9M.
                                                                  note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU10205 standard; peptide; 27 AA.
                                                                                                                                                                                                                                                                                      Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 28; 46pp; English.
                                                                                                                                                                                                                 22-SEP-1999; 99US-0155135P.
20-JUL-2000; 2000US-0219438P.
                                                                                                                                                                                       21-SEP-2000; 2000WO-US025827.
                                                                                                              amide group"
                                                                                              /note= "The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-JAN-2002 (first entry)
                                                                                                                                                                                                                                                         (COGN-) COGNETIX INC.
 Conus purpurascens.
Synthetic.
                                                                                                                                                                                                                                                                                                                           WPI; 2001-648090/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conus purpurascens.
Synthetic.
                                                                                                                                                                                                                                                                                  Cornell-Bell AH,
                                                                                                                                  WO200121648-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 27 AA;
                                        Key
Modified-site
                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Modified-site
                                                                                                                                                             29-MAR-2001
                                                                                                                                                                                                                                                                                                   Jones RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU10205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU10205
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
```

ö

ö

ö

1; Indels

96.3%; Score 155; DB 4; Length 27; 96.3%; Pred. No. 4.7e-10;

0; Mismatches

Purple cone snall; kappa-conotoxin PVIJA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; Q10A.

```
21-SEP-2000; 2000WO-US025827.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                              (COGN-) COGNETIX INC.
                                                                                                                                                    WPI; 2001-648090/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conus purpurascens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 26; Conserv
                                                                                                                   Cornell-Bell AH,
                                                                                                                                                                                                                                                                                                                                                        Sequence 27 AA;
   WO200121648-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200121648-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                22-SEP-1999;
                        29-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU10196;
                                                                                                                               Jones RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU10196
   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                 The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-concoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                                                                                                                                                                           depolarization of excitable ischemia and asthma comprises to an individual a kappa-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
                   /note= "The C-terminus is either a carboxyl group or an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "The C-terminus is either a carboxyl group or amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gape
                                                                                                                                                                         Mccabe RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 155; DB 4; Length 27; Pred. No. 4.7e-10; O; Mismatches 1; Indels
                                                                                                                                                                         Temple DL, Layer RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cerebral ischaemia; ocular ischaemia; asthma; K19A
                                                                                                                                                                                                                                      membrane e.g. cardiac, cerebral and ocular activating a KATP channel by administering conotoxin PVIIA peptide.
                                                                                                                                                                                                                            Treating disorders associated with radical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Snail Kappa-conotoxin PVIIA analogue K19A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRIXNOKCMOHLDDCCSRKCNRFNKCV 27
/note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ź
                                                                                                                                                                                                                                                                                Claim 1; Page 28; 46pp; English.
                                                                                                                                                                        Cornell-Bell AH, Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU10199 standard; peptide; 27
                                                                                                                   22-SEP-1999; 99US-0155135P.
20-JUL-2000; 2000US-0219438P.
                                                                                               21-SEP-2000; 2000WO-US025827
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 96.3%;
Matches 26; Conservative
                                  amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-JAN-2002 (first entry)
                                                                                                                                                    (COGN-) COGNETIX INC
                                                                                                                                                                                                       WPI; 2001-648090/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 27 AA;
                                                      WO200121648-A1
            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                           29-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                    Jones RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU10199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU10199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
```

```
The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                                                                                                                                                                                                                                                                                                                                   Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-conctoxin PVIIA peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Purple cone snail, kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; R18A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "The C-terminus is either a carboxyl group or an amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gape
                                                                                                                                                                                                                         Mccabe RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                             Layer RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96.3%; Score 155; DB 4;
llarity 96.3%; Pred. No. 4.7e-10;
Conservative 0; Mismatches 1.
                                                                                                                                                                                                                         Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Snail Kappa-conotoxin PVIIA analogue R18A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRIXNOKCFOHLDDCCSRACNRFNKCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CRIXNOKCFQHLDDCCSRKCNRFNKCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ź
                                                                                                                                                                                                                             Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 27; 46pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27
21-SEP-2000; 2000WO-US025827
                                                               99US-0155135P
                                                                                             20-JUL-2000; 2000US-0219438P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU10196 standard; peptide;
```

```
ö
                                                                                                                                                                                                                      The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conctoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active radical depolarisation of excitable membrane by activating a depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular analogue of the invention
                                                                                                                                              excitable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; K25A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             an
                                                                                                                                    Treating disorders associated with radical depolarization of excitablemembrane e.g. cardiac, cerebral and ocular ischemia and asthma compractivating a KATP channel by administering to an individual a kappa-
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "The C-terminus is either a carboxyl group or
                                                                                Mccabe RT;
                                                                                                                                                                                                                                                                                                                                                                                                         o;
                                                                                                                                                                                                                                                                                                                                                                           Score 155; DB 4; Length 27;
Pred. No. 4.7e-10;
0; Mismatches 1; Indels
                                                                               Layer RT,
                                                                            Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Snail Kappa-conotoxin PVIIA analogue K25A.
                                                                                                                                                                                                                                                                                                                                                                                                                          1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                            CRIXNQKCFQHLDDCCSAKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU10202 standard; peptide; 27 AA:
                                                                                                                                                                                                 Claim 1; Page 27; 46pp; English.
                                                                        Pemberton KE,
             22-SEP-1999; 99US-0155135P.
20-JUL-2000; 2000US-0219438P.
                                                                                                                                                                                                                                                                                                                                                                          96.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-SEP-1999; 99US-0155135P.
20-JUL-2000; 2000US-0219438P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-SEP-2000; 2000WO-US025827
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 96.38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                             conotoxin PVIIA peptide
                                               (COGN-) COGNETIX INC.
                                                                                                            WPI; 2001-648090/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (COGN-) COGNETIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   purpurascens.
                                                                       Cornell-Bell AH,
                                                                                                                                                                                                                                                                                                                                                 Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200121648-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-MAR-2001.
                                                                                      Jones RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU10202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

```
ö
                                                                                                                                                                         The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conctoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular analogue of the invention
                                                                              membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-conotoxin PVIIA peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
cerebral ischaemia; ocular ischaemia; asthma; Q6A.
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                      Mccabe RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "The C-terminus is either a carboxyl group amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mccabe RT;
                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                              Length 27;
                                                                                                                                                                                                                                                                                                                                      96.3%; Score 155; DB 4; Length 27 larity 96.3%; Pred. No. 4.7e-10; Conservative 0; Mismatches 1; Indels
                     Layer RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Layer RT,
                    Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Snail Kappa-conotoxin PVIIA analogue Q6A.
                                                                                                                                                                                                                                                                                                                                                                                          1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                             1 CRIXNQKCFQHLDDCCSRKCNRFNACV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
              Cornell-Bell AH, Pemberton KE,
                                                                                                                                                Claim 1; Page 27; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cornell-Bell AH, Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU10210 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-SEP-2000; 2000WO-US025827.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-SEP-1999; 99US-0155135P.
20-JUL-2000; 2000US-0219438P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                     WPI; 2001-648090/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (COGN-) COGNETIX INC.
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-648090/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conus purpurascens.
                                                                                                                                                                                                                                                                                                              Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200121648-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-MAR-2001
                            Jones RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU10210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jones RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 24
ò
                                                                                                                                                                                                                                                                                                                                                                                                                  셤
```

Gaps

ö

1; Indels Length

27

X44444X8X2CCCCCCCCX8X4444X8X

ઠે

```
The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KAPP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KAPP channel, especially cardiac isochemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; K7A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "The C-terminus is either a carboxyl group or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel
                                                                                                                                                                                                                                                   Score 155; DB 4;
Pred. No. 4.7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Temple DL,
                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Snail Kappa-conotoxin PVIIA analogue K7A.
                                                                                                                                                                                                                                                                                                                    1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                         1 CRIXNQKCFQHLDDCCSRKCNAFNKCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                          Ź
              Claim 1; Page 27; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 28; 46pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU10204 standard; peptide; 27
                                                                                                                                                                                                                                                   96.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-SEP-1999; 99US-0155135P.
20-JUL-2000; 2000US-0219438P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-SEP-2000; 2000WO-US025827
                                                                                                                                                                                  analogue of the invention
                                                                                                                                                                                                                                                                                    26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conotoxin PVIIA peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (COGN-) COGNETIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-648090/74.
                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conus purpurascens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cornell-Bell AH,
                                                                                                                                                                                                                   Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200121648-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU10204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jones RR;
                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 26
XXXUUUUU
                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                           The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
          disorders associated with radical depolarization of excitable e.g. cardiac, cerebral and ocular ischemia and asthma comprises a KATP channel by administering to an individual a kappa-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-conotoxin PVIIA peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; R22A.
                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "The C-terminus is either a carboxyl group or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mccabe RT
                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                    96.3%; Score 155; DB 4; Length 27; 96.3%; Pred. No. 4.7e-10;
                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Layer RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Temple DL,
                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Snail Kappa-conotoxin PVIIA analogue R22A
                                                                                                                                                                                                                                                                                                                                                                                                         1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                          CRIXNAKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Z
                                                                                             Claim 1; Page 28; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cornell-Bell AH, Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU10197 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-SEP-2000; 2000WO-US025827.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-SEP-1999; 99US-0155135P
20-JUL-2000; 2000US-0219438P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                    Local Similarity 96.3
les 26; Conservative
                                                           conotoxin PVIIA peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (COGN-) COGNETIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-648090/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    purpurascens
                                                                                                                                                                                                                                                                                                    Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200121648-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-Bite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-MAR-2001
                                               activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                             membrane
                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU10197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jones
```

an

Mccabe RT;

Layer RT,

us-10-627-685a-26.rag

sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue peptide

ó

Gaps

; 0

Length 27 1; Indels

Score 155; DB 6; Pred. No. 4.7e-10;

96.3%;

Ouery Match Best Local Similarity Thes 25; Conserv?

Sequence 27 AA;

ន្តដ្ឋប្រ

1; Mismatches

Conservative

1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27

Ś a

CRIPNQKCFQHLDDCCSRKCNRFNACV

AAE38344 standard; peptide; 27 AA.

RESULT 28

27

```
ö
      kappa-conotoxin PVIIA (kappa-
                                                                                                                                                                                                                                                                                                          ischaemic heart disease; caretaria ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
          PVIIA) peptide or its analogue, derivative or physiologically active radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular analogue of the invention
                                                                                                                                Gaps
                                                                                                                                ;
0
                                                                                                           Length 27;
                                                                                                                                                                                                                                                                                                       snail; kappa-PVIIA-related conotoxin; urinary
                                                                                                                               .1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Temple DL, Mcintosh JM;
                                                                                                                                                                                                                                                                                 Conus purpurascens kappa-PVIIA analogue peptide, K25A.
                                                                                                       Score 155; DB 4;
Pred. No. 4.7e-10;
0; Mismatches 1.
 comprising administering to an individual
                                                                                                                                              1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                    27
                                                                                                                                                            CRIXNQACFQHLDDCCSRKCNRFNKCV
                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                          Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jones RM,
                                                                                                                                                                                                                   AAE38342 standard; peptide; 27
                                                                                                    Query Match 96.3%;
Best Local Similarity 96.3%;
Matches 26; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JAN-2003; 2003WO-US002384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JAN-2002; 2002US-0352219P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (COGN-) COGNETIX INC.
(UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                             /label= Hyp
                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pemberton-Goodman KE,
                                                                                                                                                                                                                                                                                                                                                                    Conus purpurascens,
                                                                                 Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003063782-A2
                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                             20-NOV-2003
                                                                                                                                                                                                                                                                                                         cone
                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Olivera BM;
                                                                                                                                                                                                                                          AAE38342;
                                                                                                                                                                                                 RESULT 27
AAE38342
ð
                                                                                                                                                                  g
```

Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia, reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.

Location/Qualifiers

Conus purpurascens

Conus purpurascens kappa-PVIIA analogue peptide, K7A.

(first entry)

20-NOV-2003

AAE38344;

```
The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protection and preservation of an organ e.g. heart of a mammal comprises
use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, treatment of arrhythmia, urinary incontinence, reperfusion is for the diabetes, retinopathy, neuropathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral esospanying subarachnoid haemorrhage, anxiety disorder, cerebral isohaemia, coronary artery bypass graft (CABG) surgery, isothaemia, coronary artery bypass graft (CABG) surgery, sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mcintosh JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Page 7; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pemberton-Goodman KE, Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JAN-2002; 2002US-0352219P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JAN-2003; 2003WO-US002384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (COGN-) COGNETIX INC. (UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Hyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-679464/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003063782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Olivera BM;
AAE38344

XX
 AAE38344

XX
 AAE3

XX
 CON

XX
 CON

XX
 AAE3

XX
 CON

XX
 CON

XX
 AAE3

XX
 CON

XX
 AAE3

AAE3
```

a mammal comprises

Protection and preservation of an organ e.g. heart of use of a compound binding to kappa-PVIIA-binding site.

WPI; 2003-679464/64.

Disclosure; Page 7; 32pp; English.

The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, paripheral circulation disturbances, hypertension, angina, cerebral vasospasm accompanying subarachhoid haemorrhage, anxiety disorder, vasospasm accompanying subarachhoid haemorrhage, anxiety disorder, ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The present

```
The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, cerebral ischaemia, coronary artery bypass graff (CABG) surgery, ischaemic heart disease, and congestive heart failure. The present sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a mammal comprises
                                                                                                                                                                                                                                                                                                             Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                     Gaps
                                     ö
     DB 6; Length 27; 4.7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Temple DL, Mcintosh JM;
                                   1; Indels
                                                                                                                                                                                                                                                                                  Conus purpurascens kappa-PVIIA analogue peptide, R18A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protection and preservation of an organ e.g. heart of use of a compound binding to kappa-PVIIA-binding site.
96.3%; Score 155; DB
92.6%; Pred. No. 4.7e
tive 1; Mismatches
                                                                    1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                     CRIPNOACFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                    Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 6; 32pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pemberton-Goodman KE, Jones RM,
                                                                                                                                                                                   AAE38336 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-JAN-2003; 2003WO-US002384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JAN-2002; 2002US-0352219P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (COGN-) COGNETIX INC.
(UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Hyp
                                                                                                                                                                                                                                                  (first entry)
                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-679464/64.
                                                                                                                                                                                                                                                                                                                                                                                                                    Conus purpurascens.
                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003063782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Modified-site
                                                                                                                                                                                                                                                20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-AUG-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Olivera BM;
                                                                                                                                                                                                                   AAE38336;
     Query Match
                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide
                    Best Loc
Matches
                                                                                                                                                  RESULT 29
                                                                                                                                                                   AAE3833
                                                                                                 셤
                                                                                                                                                                                   ò
```

```
Purple cone snail, kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, escheral ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The presen sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mcintosh JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96.3%; Score 155; DB 6; Length 27; 92.6%; Pred. No. 4.7e-10; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                        Conus purpurascens kappa-PVIIA analogue peptide, K19A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jones RM, Temple DL,
                 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRIPNOKCFQHLDDCCSRACNRFNKCV 27
CRIPNOKCFQHLDDCCSAKCNRFNKCV
                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                     Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 7; 32pp; English.
                                                                                                    AAE38339 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JAN-2003; 2003WO-US002384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JAN-2002; 2002US-0352219P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                /label= Hyp
                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (COGN-) COGNETIX INC.
(UTAH ) UNIV UTAH RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pemberton-Goodman KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-679464/64.
                                                                                                                                                                                                                                                                                                                                                Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003063782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                Key
Modified-site
                                                                                                                                                                        20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Olivera BM;
                                                                                                                                      AAE38339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
                                                                  RESULT 30
                   유
                                                                                                       8XCCCCCCCCCCCCX8X44X8X11X44X4X6X6X6X6X144X8X8X8X8X8X6X6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
```

ö

Gaps

ö

Score 155; DB 6; Length 27; Pred. No. 4.7e-10; 1; Mismatches 1; Indels

96.3%;

Query Match Best Local Similarity 92.67 Marches 25; Conservative

ö

1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27

us-10-627-685a-26.rag

Page 16

AAE38345

```
Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conctoxins. The conotoxins can also be used for arresting, protecting or preserving sometoxins. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, peripheral circulation disturbances, hypertension, anglia, cerebral vasospasm accompanying subarachnoid haemorrhage, a mixiety disorder, cerebral ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The preser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention relates to kappa-PVIIA-related conotoxins and their
                                      Conus purpurascens kappa-PVIIA analogue peptide, R22A.
                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 6; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                      28-JAN-2003; 2003WO-US002384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE38340 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JAN-2002; 2002US-0352219P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FOUND.
                                                                                                                                                                                                                                                                                  /label= Hyp
    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
hes 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (COGN-) COGNETIX INC. (UTAH ) UNIV UTAH RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pemberton-Goodman KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-679464/64.
                                                                                                                                                                                                     Conus purpurascens
                                                                                                                                                                                                                                                                                                                      WO2003063782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 27 AA;
                                                                                                                                                                                                                                                          Modified-site
  20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Olivera BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE38340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 33
AAE38340
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XXEX BXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related contotxins. The invention also relates to a method of arresting, protecting or preserving somatic cells. The invention is for the protecting or preserving somatic cells. The invention is for the readment of arrhythmia, urinary incontinence, reperfusion injury, peripheral circulation disturbances, hypertension, angina, cerebral vasospasm accompanying subarachnoid haemorrhage, arxiety disorder, cerebral ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The present of conus purpurascens (purple cone snail) kappa PVIIA analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                ischaemic heart disease, cerebral ischaemia, anxiety disorder; diabetes, organ protectant, arrhythmia, reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to kappa-PVIIA-related conotoxins and their use as
                                                                                                                                                           Purple cone snail, kappa-PVIIA-related conotoxin, urinary incontinence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mcintosh JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
96.3%; Score 155; DB 6; Length 27;
Best Local Similarity 92.6%; Pred. No. 4.7e-10;
Matches 25; Conservative 1; Mismatches 1; Indels
                                                                                                                    Conus purpurascens kappa-PVIIA analogue peptide, F9M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
AAE38345 standard; peptide; 27 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 7; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE38337 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JAN-2003; 2003WO-US002384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JAN-2002; 2002US-0352219P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) COGNETIX INC.
) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                    /label= Hyp
                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pemberton-Goodman KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-679464/64.
                                                                                                                                                                                                                                                                                        purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                      WO2003063782-A2
                                                                                                                                                                                                                                                                                                                            Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 27 AA;
                                                                                20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                               07-AUG-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Olivera BM;
                                          AAE38345;
```

(COGN-)

Conus

Ä,

Mcintosh

Temple DL,

```
ö
sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
                                                                                                                                              Gaps
                                                                                                                                            ·.
                                                                                                  96.3%; Score 155; DB 6; Length 27; 92.6%; Pred. No. 4.7e-10;
                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Conus purpurascens kappa-PVIIA analogue peptide, R2A.
                                                                                                                                      1; Mismatches
                                                                                                                                                                            27
                                                                                                                                                                                                              27
                                                                                                                                                                                            CRIPNOKCFQHLDDCCSRKCNAFNKCV
                                                                                                                                                                        1 CRIXNOKCFQHLDDCCSRKCNRFNKCV
                                                                                                                                                                                                                                                                                                            ¥.
                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                              20-NOV-2003
```

Æ

AAE38337;

AAE38337 ID AAE3 XX AC AAE3

RESULT 32

ઠે g

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute hear failure, peripheral circulation disturbances, hypertension, angina, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, escheral ischaemia, coronary artery bypass graft (GABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The present sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart diseaes; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
 ischaemic heart disease, cerebral ischaemia, anxiety disorder; diabetes, organ protectant, arrhythmia, repeffusion injury, hypertension, angina, retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive,heart failure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96.3%; Score 155; DB 6; Length 27; 92.6%; Pred. No. 4.7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                   Mcintosh JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conus purpurascens kappa-PVIIA analogue peptide, Q10A.
                                                                                                                                                                                                                                                                                                                                                                                                 Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAIPNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 7; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE38356 standard; peptide; 27 AA
                                                                                                                                                                                                                                                                                                                                                                                                 Pemberton-Goodman KE, Jones RM,
                                                                                                                                                                                                                                                                         28-JAN-2003; 2003WO-US002384.
                                                                                                                                                                                                                                                                                                          29-JAN-2002; 2002US-0352219P
                                                                                                                                                                                                                                                                                                                                           (COGN-) COGNETIX INC.
(UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                             /label= Hyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-NOV-2003 (first entry)
ischaemic heart disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 92.6
es 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-679464/64.
                                                                                            Conus purpurascens
                                                                                                                                                                                                    WO2003063782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 27 AA;
                                                                                                                                            Modified-site
                                                                                                                                                                                                                                    07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE38356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                    Olivera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE38356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
```

```
present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                           a mammal comprises
                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to kappa-PVIIA-related conotoxins and their use as
                                                                                                                                                                                                                                                                                                                                                                                                                                  organ protectants. The invertion also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart fallure, peripheral circulation disturbances, hypertension, angina, cerebral eschanals, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The presensequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                               Mcintosh JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                           Protection and preservation of an organ e.g. heart of
use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conus purpurascens kappa-PVIIA analogue peptide, Q6A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 155; DB 6;
Pred. No. 4.7e-10;
                                                                                                                                                                                                                                                             Jones RM, Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRIPNOKCFAHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Page 8; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE38350 standard; peptide; 27 AA.
                                                                                                                                                      28-JAN-2003; 2003WO-US002384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96.3%;
                                                                                                                                                                                   29-JAN-2002; 2002US-0352219P
                                                           /label= Hyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Hyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 92.6
les 25; Conservative
                                                                                                                                                                                                                  (COGN-) COGNETIX INC. (UTAH ) UNIV UTAH RES
                                                                                                                                                                                                                                                                 Pemberton-Goodman KE,
                                                                                                                                                                                                                                                                                                            WPI; 2003-679464/64
 Conus purpurascens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conus purpurascens.
                                                                                          WO2003063782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
Modified-site
                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-NOV-2003
                                                                                                                                                                                                                                                                               Olivera BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE38350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE38350
ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
```

29-MAR-2001.

```
The invention relates to kappa-PVIIA-related conotoxins and their use as protectants. The invention also relates to a method of arresting, related conotoxins and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the diabetes, retinopathy, neuropathy, incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, cerebral ischaemia, coronary artery bypass graft (CABG) surgery, schaemic heart disease, asthma and congestive heart failure. The present exercises of the cone surphresses of the present sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                        Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
cerebral ischaemia; ocular ischaemia; asthma; N24A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=,"The C-terminus is either a carboxyl group or an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
0
                                                                                                                                                                         Mcintosh JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 155; DB 6; Length 27;
Pred. No. 4.7e-10;
1; Mismatches 1; Indels
                                                                                                                                                                         Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Snail Kappa-conotoxin PVIIA analogue N24A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                Disclosure, Page 7; 32pp; English.
                                                                                                                                                                        Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU10213 standard; peptide; 27 AA
                                                                    28-JAN-2003; 2003WO-US002384
                                                                                               29-JAN-2002; 2002US-0352219P
                                                                                                                          (COGN-) COGNETIX INC.
(UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25; Conservative
                                                                                                                                                                   Pemberton-Goodman KE,
                                                                                                                                                                                                             WPI; 2003-679464/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conus purpurascens.
Synthetic.
              WO2003063782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200121648-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                         07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-JAN-2002
                                                                                                                                                                                    Olivera BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU10213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
```

```
ô
                                                                                                                                                                            Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-conotoxin PVIIA peptide.
                                                                                                                                                                                                                                                                  The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conctoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular analogue of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; D14A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "The C-terminus is either a carboxyl group or an
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                       Mccabe RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 153; DB 4; Length 27;
Pred. No. 7.7e-10;
0; Mismatches 1; Indels
                                                                                                                      Layer RT,
                                                                                                                    Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Snail Kappa-conotoxin PVIIA analogue D14A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CRIXNQKCFQHLDDCCSRKCNRFAKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CRIXNOKCFQHLDDCCSRKCNRFNKCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU10209 standard; peptide; 27 AA
                                                                                                                                                                                                                                              Claim 1; Page 28; 46pp; English.
                         21-SEP-2000; 2000WO-US025827.
                                                22-SEP-1999; 99US-0155135P.
20-JUL-2000; 2000US-0219438P.
                                                                                                                                                                                                                                                                                                                                                                                                                              95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-SEP-2000; 2000WO-US025827.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0155135P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                     WPI; 2001-648090/74.
                                                                                        (COGN-) COGNETIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conus purpurascens.
Synthetic.
                                                                                                                Cornell-Bell AH,
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200121648-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                     26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-MAR-2001
                                                                                                                               Jones RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU10209;
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

Jones RR;

```
The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac isochaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
                                                                                                                        Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; F9A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating disorders associated with radical depolarization of excitable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "The C-terminus is either a carboxyl group or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mccabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Layer RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 153; DB 4;
Pred. No. 7.7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Snail Kappa-conotoxin PVIIA analogue F9A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CRIXAQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ź
                                                                                                                                                                                                                                                                      Claim 1; Page 28; 46pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-SEP-1999; 99US-0155135P.
20-JUL-2000; 2000US-0219438P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.0%;
96.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-SEP-2000; 2000WO-US025827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU10201 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amide group'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        analogue of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26; Conservative
                                                                                                                                                                                                           conotoxin PVIIA peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (COGN-) COGNETIX INC.
                                                                WPI; 2001-648090/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-648090/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cornell-Bell AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200121648-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
         Jones RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU10201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jones RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 39
      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TX BX X BX X BX X BX X B X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to treating disorders associated with radical comprisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia, and asthma. The present sequence is a kappa-conotoxin PVIIA
                                                                                                                                                                                                                                                                Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappaconotoxin PVIIA peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; NSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "The C-terminus is either a carboxyl group or
                                                                                                                        Mccabe RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Layer RT, Mccabe RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                        Layer RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.0%; Score 153; DB 4;
96.3%; Pred. No. 7.7e-10;
iive 0; Mismatches 1;
                                                                                                                     Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cornell-Bell AH, Pemberton KE, Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Snail Kappa-conotoxin PVIIA analogue N5A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRIXNQKCFQHLDACCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         æ
                                                                                                                     Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 28; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU10219 standard; peptide; 27
20-JUL-2000; 2000US-0219438P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-SEP-2000; 2000WO-US025827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0155135P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JUL-2000; 2000US-0219438P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                analogue of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amide
                                                          (COGN-) COGNETIX INC
                                                                                                                                                                                                     WPI; 2001-648090/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (COGN-) COGNETIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  purpurascens
                                                                                                               Cornell-Bell AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200121648-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-SEP-1999;
```

16-JAN-2002

AAU10219;

RESULT 38

g δ

Query Match

Best Loc Matches

Synthetic.

Conus

29-MAR-2001

an

RT;

ô

Gaps

ô

```
The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with channel, especially cardiac for treating disorders associated with channel, especially cardiac ischaemia, cerebral ischaemia, ocular analogue of the invention
membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-conotoxin PVIIA peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; D13A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C-terminus is either a carboxyl group or an
                                                                                                                                                                                                                   Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Layer RT,
                                                                                                                                                                                                                                                       Pred. No. 7.76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Snail Kappa-conotoxin PVIIA analogue D13A.
                                                                                                                                                                                                                                                                                          1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                           1 CRIXNQKCAQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                         Ş
                                                  Claim 1; Page 27; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                 AAU10215 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cornell-Bell AH, Pemberton KE,
                                                                                                                                                                                                                                          95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-SEP-1999; 99US-0155135P.
20-JUL-2000; 2000US-0219438P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-SEP-2000; 2000WO-US025827.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "The
                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                              26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (COGN-) COGNETIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-648090/.74.
                                                                                                                                                                                                                                                    Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conus purpurascens.
Synthetic.
                                                                                                                                                                                                             Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200121648-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-MAR-2001
                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                             AAU10215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jones RR;
                                                                                                                                                                                                                                                                                                                                                         RESULT 40
g
                                                                                                                                                                                                                                                                                                                                                                                            ò
```

```
depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-pVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with channel, especially cardiac lacohaemia, cerebral ischaemia, coular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
cerebral ischaemia; ocular ischaemia; asthma; N21A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappaconotoxin PVIIA peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or an
                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "The C-terminus is either a carboxyl group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Layer RT, Mccabe RT
                                                                                                                                                                                                                             ö
                                                                                                                                                                                                Length 27;
                                                                                                                                                                                      95.0%; Score 153; DB 4; Length 27 larity 96.3%; Pred. No. 7.7e-10; Conservative 0; Mismatches 1; Indels
               invention relates to treating disorders associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Snail Kappa-conotoxin PVIIA analogue N21A.
                                                                                                                                                                                                                                                 1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                      1 CRIXNQKCFQHLADCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                        Ź
                                                                                                                                                                                                                                                                                                                                              AAU10211 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 28; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-SEP-2000; 2000WO-US025827.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-SEP-1999; 99US-0155135P.
20-JUL-2000; 2000US-0219438P.
                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (COGN-) COGNETIX INC.
                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-648090/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conus purpurascens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cornell-Bell AH,
                                                                                                                                                           Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200121648-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                   26,
                                                                                                                                                                                                                                                                                                                                                                                                          16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                               AAU10211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                        Query Match
                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jones RR;
                                                                                                                                                                                                      Best Loc
Matches
ò
                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                       Gaps
```

Mccabe RT;

Claim 1; Page 28; 46pp; English

conotoxin PVIIA peptide.

21

```
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003063782-A2
                  Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                               Key
Modified-site
                                                                                                                                                                                                                              20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Olivera BM;
                                                                                                                                                                                                      AAE38351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                      RESULT 43
                                                                                                                                                                  AAE38351
ID AAE
                                                                                                                셤
                                                                                                                                                                                          ò
                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present
                                                                                                                                                                                                                                                                                                                                                      ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reporfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a mammal comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to kappa-PVIIA-related conotoxins and their use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, cerebral ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The presen sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting,
                                                                                                                                                                                                                                                                                                                                           Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
salt. The conotoxing are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
                                                                                                                              Gaps
                                                                                                                               ö
                                                                                                   Score 153; DB 4; Length 27; Pred, No. 7.7e-10; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mcintosh JM;
                                                                                                                                                                                                                                                                                                                   Conus purpurascens kappa-PVIIA analogue peptide, N24A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protection and preservation of an organ e.g. heart of
use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Temple DL,
                                                                                                                                                                   1 CRIXNQKCFQHLDDCCSRKCARFNKCV 27
                                                                                                                                                     1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 7; 32pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pemberton-Goodman KE, Jones RM,
                                                                                                                                                                                                                                         AAE38353 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JAN-2003; 2003WO-US002384.
                                                                                                     95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JAN-2002; 2002US-0352219P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (COGN-) COGNETIX INC.
(UTAH ) UNIV UTAH RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Hyp
                                                                                                                                                                                                                                                                                          (first entry)
                                                    analogue of the invention
                                                                                                                              26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-679464/64.
                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                   Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003063782-A2
                                                                              Sequence 27 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                          20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Olivera BM;
                                                                                                                                                                                                                                                                  AAE38353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide
                                                                                                                               Matches
                                                                                                                                                                                                                   RESULT 42
                                                                                                                                                                                                                             AAE38353
     88888888
                                                                                                                                                      ò
                                                                                                                                                                        a
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a mammal comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to kappa-PVIIA-related conotoxins and their use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           related conctoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, cerebral ischaemia, cornary artery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The presensequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-
                                                                   Gaps
                                                                   ö
   Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mcintosh JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 27;
                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conus purpurascens kappa-PVIIA analogue peptide, N21A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protection and preservation of an organ e.g. heart of use of a compound binding to kappa-PVIIA-binding site.
Score 153; DB 6; Lo
Pred. No. 7.7e-10;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 153; DB 6;
Pred. No. 7.7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jones RM, Temple DL,
                                                                                                                                                                        1 CRIPNOKCFQHLDDCCSRKCNRFAKCV 27
                                                                                                                                   1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                         Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 7; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                  AAE38351 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JAN-2002; 2002US-0352219P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JAN-2003; 2003WO-US002384
   Query Match
Best Local Similarity 92.6%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Hyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (COGN-) COGNETIX INC. (UTAH ) UNIV UTAH RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pemberton-Goodman KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-679464/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conus purpurascens
```

Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure;

Location/Qualifiers

Conus purpurascens

/label= Hyp

Modified-site

WO2003063782-A2

07-AUG-2003

28-JAN-2003; 2003WO-US002384. 29-JAN-2002, 2002US-0352219P

(COGN-) COGNETIX INC. (UTAH) UNIV UTAH RES

Conus purpurascens kappa-PVIIA analogue peptide, D13A.

(first entry)

20-NOV-2003

AAE38355;

AAE38355 standard; peptide; 27 AA.

RESULT 45

.; 0

AAE38355

```
Purple come snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to kappa-PVIIA-related conotoxins and their use as protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the ireatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral cerebral scheemia, coronary artery bypass graft (CABG) surgery, ischaemic, each and congestive heart failure. The present sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a mammal comprises
            Gaps
          ö
         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mcintosh JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protection and preservation of an organ e.g. heart of use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                       purpurascens kappa-PVIIA analogue peptide, F9A.
         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 153; DB 6;
Pred. No. 7.7e-10;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Temple DL,
      1; Mismatches
                             CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                1 CRIPNOKCFQHLDDCCSRKCARFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Page 7; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jones RM,
                                                                                                                              AAE38341 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JAN-2003; 2003WO-US002384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JAN-2002; 2002US-0352219P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (COGN-) COGNETIX INC.
(UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                  /label= Hyp
                                                                                                                                                                                           (first entry)
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pemberton-Goodman KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-679464/64.
                                                                                                                                                                                                                                                                                                                                          Conus purpurascens.
                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003063782-A2.
                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 27 AA;
                                                                                                                                                                                          20-NOV-2003
 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Olivera BM;
                                                                                                                                                            AAE38341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Matches
                                                                                                                                g
                             à
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hyperension, angina, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, cerebral ischaemia, coronary artery bypass graft (GABG) surgery, sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                               Protection and preservation of an organ \mathbf{e}.\mathbf{g}. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                           Mcintosh JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 153; DB 6; Length 27;
Pred. No. 7.7e-10;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                           Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Page 8; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE38349 standard; peptide; 27 AA.
                                                                                                                                                                                                                                                                                                                                                          Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25; Conservative
                                                                                                                                                                                                                                                                                                                                                        Pemberton-Goodman KE,
                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-679464/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                   Olivera BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE38349
ID AAE3
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
```

ö

.; 0

1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27

ò 셤

۲,

Best Local Similarity 92.6 Matches 25; Conservative

Length 27; 1; Indels

AAE38349;

```
ischaemic heart diseame; cerebral ischaemia; anxiety disorder; diabetes; organ protectant, arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to kappa-PVIIA-related conotoxins and their use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organ protectants. The invertion also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral escapana, coronary artery bypass graft (cAsG) surgery, ischemmia, coronary artery bypass graft (cAsG) surgery, ischemmic heart disease, asthma and congestive heart failure. The presensequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; H11A.
                                              snail, kappa-PVIIA-related conotoxin; urinary incontinence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Temple DL, Mcintosh JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
Conus purpurascens kappa-PVIIA analogue peptide, NSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 153; DB 6;
Pred. No. 7.7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Snail Kappa-conotoxin PVIIA analogue H11A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CRIXAQKCFQHLDDCCSRKCNRFNKCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CRIXNOKCFOHLDDCCSRKCNRFNKCV
                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 8; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27
                                                                                                                                                                                                                                                                                                                                                                                                   28-JAN-2003; 2003WO-US002384
                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JAN-2002; 2002US-0352219P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COGNETIX INC.
UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU10208 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pemberton-Goodman KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-679464/64.
                                                                                                                                                                              Conus purpurascens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                              WO2003063782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 27 AA;
                                                                                                                                                                                                                        Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                          07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Olivera BM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU10208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (COGN-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU10208
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, cerebral ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The present sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                             Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischemic heart diseaes; cerebral ischemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.0%; Score 153; DB 6; Length 27; 92.6%; Pred. No. 7.7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mcintosh JM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                        Conus purpurascens kappa-PVIIA analogue peptide, D14A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 7.76
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRIPNOKCFQHLDACCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 7; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE38359 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JAN-2002; 2002US-0352219P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JAN-2003; 2003WO-US002384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (COGN-) COGNETIX INC. (UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                            /label= Hyp
                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pemberton-Goodman KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-679464/64.
                                                                                                                                                                                                                                                                                    Conus purpurascens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003063782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                          20-NOV-2003
```

07-AUG-2003

Olivera BM;

ö

Gaps

.. 0

25;

Matches

8 g

AAE38359; RESULT 47
AAE38359
ID AAE38
XX
AC AAE38
DT 20-NO
XX

Query Match

present

/label= Hyp

```
The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, treatment of arrhythmia, utinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, vasospassa accompanying subarachnoid haemorrhage, anxiety disorder, oerebral ischaemia, coronary artery bypass graft (GABG) surgery, sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                               Protection and preservation of an organ e.g. heart of use of a compound binding to kappa-PVIIA-binding site.
    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 7; 32pp; English.
                                                                                                                                                                 28-JAN-2003; 2003WO-US002384.
                                                                                                                                                                                                        29-JAN-2002; 2002US-0352219P
                                                                                                                                                                                                                                             (COGN-) COGNETIX INC.
(UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                           Pemberton-Goodman KE,
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-679464/64.
                                                                                WO2003063782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 27 AA;
  Key
Modified-site
                                                                                                                        07-AUG-2003
                                                                                                                                                                                                                                                                                                                                   Olivera BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB96846
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active radical depolarisation of excitable membrane by activations are used for treating disorders associated with channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia, and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-conotoxin PVIIA peptide.
                                                                                                                                           /note= "The C-terminus is either a carboxyl group or an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Purple cone snail, kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              Mccabe RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.8%; Score 151; DB 4; Length 27; 96.3%; Pred. No. 1.3e-09; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       Temple DL, Layer RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conus purpurascens kappa-PVIIA analogue peptide, H11A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                      'note= "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                       Pemberton KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 28; 46pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE38348 standard; peptide; 27
                                                                                                                                                                                                                                                                                       21-SEP-2000; 2000WO-US025827.
                                                                                                                                                                                                                                                                                                                                22-SEP-1999; 99US-0155135P.
20-JUL-2000; 2000US-0219438P.
                                                                                                                                                                     amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 96.3
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           (COGN-) COGNETIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-648090/74.
  Conus purpurascens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                Cornell-Bell AH,
                                                                                                                                                                                                        WO200121648-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 27 AA;
                                                                              Modified-site
                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-NOV-2003
                                                                                                                                                                                                                                                  29-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jones RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE38348;
```

SS XX S X X S X X B X B X

a mammal comprises

Mcintosh JM;

Jones RM, Temple DL,

```
ö
                                                                                                                                                                                                                                                                                                                                                                                        neuroprotective; cerebroprotective; cardiovascular; antiinflammatory; antipagraine; antidabetic; tranquiliser; vulnerary; antipsychotic; anxiolytic; neuroleptic; tranquiliser; vulnerary; antipsychotic; neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia; stroke; cerebrovascular accident; brain trauma; spinal chord trauma; atchwing; suffocation; perinatal asphyxia; hypoglycaemic event; pain; migraine; inflammation; cardiovascular disorder; psychiatric disorder; psychosis; anxiety; schizophrenia.
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                      Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant;
                                                     .;
0
Query Match 93.8%; Score 151; DB 6; Length 27; Best Local Similarity 92.6%; Pred. No. 1.3e-09; Matches 25; Conservative 1; Mismatches 1; Indels
                                                                              1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                  Omega-conopeptide E6.2 toxin sequence.
                                                                                                                                                                                                             ABB96846 standard; peptide; 27 AA.
                                                                                                                                                                                                                                                                                           12-JUL-2002. (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40200207675-A2.
```

Conus purpurascens

AAE38348
XX
AC AAE3
XX
AC AAE3
DE CONV
XX
XX
XX
XW
FULF
KW
iscl
KW
refi
XW
refi
XX

RESULT 49

ઠે 셤

```
The invention relates to isolated omega-conopeptides, nucleic acid sequences encoding them, and propeptide sequences. The activity of the peptides of the invention may be described as, analgesic, anticonvulsant, vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular, antiniflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary, antipicity antimigraine, antidiabetic, tranquiliser, vulnerary, antipicity of voltage gated ion channels. They may be used for treating or preventing disorders associated with voltage gated ion channels such as neurological disorders, e.g. seizure (associated vith epilepsy), neurotoxic injury associated with conditions of hypoxia, anoxia ischaemia, stroke, cerebrovascular accident, brain or spinal chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic events; pain e.g. migraine; inflammation or cardiovascular disorders. They may also be used for treating psychiatric disorders e.g. psychosis, anxiety or schizophrenia. The analgesic agents of the invention show diminished side effects and toxicity, and are non-addictive. The sequences given in records ABB96807-ABB96905 represent omega-conopeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant; neuroprotective; cerebroprotective; cardiovascular; antinflammatory; antingaraine; antidabelic; tranquillaer; vulnerary; antipsychotic; anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy; neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia; stroke; cerebrovascular accident; brain trauma; spinal chord trauma; drowning; sulfocation; perinatal asphyxia; hypoglycaemic event; pain; migraine; inflammation; cardiovascular disorder; psychiatric disorder; psychosis; anxiety; schizophrenia.
                                                                                                                                                                                                                                                                                                            New omega-conopeptides useful for treating disorders associated with voltage gated ion channels e.g. pain, inflammation, neurologic or cardiovascular disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.8%; Score 78.5; DB 5; Length 27; 46.2%; Pred. No. 0.098; ive 6; Mismatches 7; Indels
                                                                                                                                                                                                                   Garrett JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M, Watkins M,
Cartier GE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CRIXNOKCFQHLDDCCSRKCNRFNKC
                                                                                                                                                                                                                                                                                                                                                                                                Claim 1(a); Page 71; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Omega-conopeptide E6.2 propeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB96638 standard; peptide; 72 AA
                                                                                            21-JUL-2000; 2000US-0219616P.
05-FEB-2001; 2001US-0265888P.
                                                         23-JUL-2001; 2001WO-US023041
                                                                                                                                                        UNIV UTAH RES FOUND.
COGNETIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 46.2
Warches 12; Conservative
                                                                                                                                                                                                                   Mcintosh JM,
                                                                                                                                                                                                                                        Jones RM,
                                                                                                                                                                                                                                                                             WPI; 2002-257318/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 toxin sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 27 AA;
                                                                                                                                                        (UTAH ) UNIV
(COGN-) COGNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-JUL-2002
                                                                                                                                                                                                                   Olivera BM,
                                                                                                                                                                                                                                        Jacobsen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB96638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 51
ABB96638
ò
```

Conus ermineus

```
The invention relates to isolated omega-conopeptides, nucleic acid sequences encoding them, and propeptide sequences. The activity of the peptides of the invention may be described as, analgesic, anticonvulsant, vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular, antinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary, antinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary, antinflammatory activity of voltage gated ion channels. They may be used for treating or preventing disorders, e.g. seizure (associated ion channels such as neurological disorders, e.g. seizure (associated with epilepsy), neurotoxic injury associated with conditions of hypoxia, anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal chord trauma, drowning, suffecation, perinatal asphyxia or hypoglycaemic events; pain e.g. migraine; inflammation or cardiovascular disorders. They may also be used for treating psychiatric disorders e.g. psychosis, amxiety or schizophrenia. The analgesic agents of the invention show diminished side effects and toxicity, and are non-addictive. The sequences given in records ABB96595-ABB96697 represent omega-conopeptide
                                                                                                                                                                                                                                                                                                                      New omega-conopeptides useful for treating disorders associated with voltage gated ion channels e.g. pain, inflammation, neurologic or cardiovascular disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Omega conopeptide; OCT; analgesia; inhibition; voltage-gated; calcium channel; neurone; contraction; guinea pig; ileum; WVIA; binding site; toxin; marine; snail; Conus; opiod; chronic pain; narcotics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7
                                                                                                                                                                                                                           Shon K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 5; Length 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Indels
                                                                                                                                                                                                                             Garrett JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48.8%; Score 78.5; DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46.2%; Pred. No. 0.22
ive 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |: ::||| | |||:: | :||
47 CKPKGRKCFPHQKDCCNKTCTR-SKC 71
                                                                                                                                                                                                                           Mcintosh JM, Watkins M,
Jones RM, Cartier GE;
                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1(c); Page 42; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR39628 standard; peptide; 26 AA.
                                                                                                                   21-JUL-2000; 2000US-0219616P. 05-FEB-2001; 2001US-0265888P.
                                                                                13-JUL-2001; 2001WO-US023041
                                                                                                                                                                      UTAH ) UNIV UTAH RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 46.2
Matches 12; Conservative
                                                                                                                                                                                          COGN-) COGNETIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             propeptide sequences
                                                                                                                                                                                                                                                                              WPI; 2002-257318/30.
                                                                                                                                                                                                                                                                                                 N-PSDB; ABL98897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 72 AA;
                                                                                                                                                                                                                           Olivera BM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-2003
20-DEC-1993
                                                 31-JAN-2002
                                                                                                                                                                                                                                             Jacobsen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR39628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNX-202.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR39628
ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
```

ï

us-10-627-685a-26.rag

WO9310145-A1

```
The sequences given in AAR19608-30 are omega conopeptides (OCTS) and derivatives of these, which may be used to produce analgesia in a mammal. These OCTS inhibit voltage-gated calcium channels selectively in neuronal tissue. This is shown by the peptides ability to stimulate contraction in guinea pig ileum and to bind to OCT WNIA binding sites present in neuronal tissue. OCTS are components of peptide toxins derived from marine snails of the genus Conus, and act as calcium channel blockers. These OCTS may be used to replace opiods in the treatment of chronic pain or to reduce the opiod dosage required. This helps to reduce dependence on and tolerance to opiod narcotics. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                  Use of omega-cono-peptide(s) which selectively inhibit voltage-gated calcium channels - to induce analgesia, enhance opiate analgesics, treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ischaemia; neuronal; omega-conotoxin; OCT; MVIIA; MVIIC; MVIID; MVIIB; GVIA; GVIIA; RVIA; SVIA; TVIA; SVX-207; siroke; delayed treatment; antihistamine; blood pressure; N-type voltage-gated Ca currents; N-channel mediated neurotransmitter release.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                   Valentino KL, Miljanich GP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.6%; Score 75; DB 2; Length 26; 42.3%; Pred. No. 0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Indels
                                                                    /note= "Amidated C-terminal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CKLKGQSCSRLMYDCCSGSCGRSGKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR37774 standard; peptide; 26 AA.
                                                                                                                                                                                                                                   Gohil K,
                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 2; 90pp; English.
                                                                                                                                                    92WO-US011349
                                                                                                                                                                            91US-00814759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 42.3'
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
(first entry)
                  .1. .16
8. .20
                                                                                                                                                                                                                              Justice A, Singh T,
                                                                                                                                                                                                     (NEUR-) NEUREX CORP.
                                                                                                                                                                                                                                                          WPI; 1993-227270/28
            Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 26 AA;
                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                                                          30-DEC-1991;
                                                                                                                                                30-DEC-1992;
                                                                                            WO9313128-A1
                                                                                                                      08-JUL-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2003
08-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      on and tole
PN field.)
                                                                                                                                                                                                                                                                                                                pain etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR37774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNX-202.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 53
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ď
```

```
The C-terminal is amidated. Ischaemia-related neuronal damage in mammals is reduced by admin., 4-24 hr after onset of ischaemia, of a cpd. (I) which binds selectively to an omega-conotoxin (OCT) WVIA site in neuronal tissue. (I) has selectivity at least 100 expressed as ratio of binding affinity for the MVIA site to that for the MVIC site. (I) is come of the OCTS MVIA. MVIB. (VIA, GVIA) or RVIA or it is the cpd. SNX-C 207. (I) is esp. used to reduce neuronal damage caused by stroke. By within 1 hr of the onset of ischaemia) a greater redn. in neuronal damage is achieved. (I) is admin. e.g. by intracerebroventricular (ICV) in achieved. (I) is admin. e.g. by intracerebroventricular (ICV) in achieved in action at 0.1-20 microg/kg, but can also be given iv. (opt. after treatment with antihistanines to minimise redn. in blood pressure caused by (I)). (I) is also at least as effective as the specified conotoxins control tissue and (2) selective inhibition of N-type voltage-gated ca currents in neuronal tissue and (2) selective inhibition of N-channel mediated controxins concorning the concorning to reverse and the specified conocoxins concopeptides are given in AAR37752-62. Several analog omega-conopeptides
                                                                                                                                                                                                                                                                   Redn. of neuronal damage caused by ischaemia - by admin. of cpds. that bind specifically to omega-conotoxin MVIIA binding sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                            Bitner RS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conopeptide; cone snail; pain; analgesic; neuropathy; epidural;
N-type voltage-sensitive calcium channel; block; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNX-202, omega conopeptide derivative used for pain relief.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 46.6%; Score 75; DB 2; Length 26; l Similarity 42.3%; Pred. No. 0.23; 11; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                          Fox JA, Valentino KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CKLKGQSCSRLMYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 2; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW19570 standard; peptide; 26 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "amidated"
                                                                     92WO-US009766
                                                                                                     91US-00789913
92US-00916478
                                                                                                                                                                                      Bowersox SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                    WPI; 1993-182487/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 11; Conserva
                                                                                                                                                   (NEUR-) NEUREX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 26 AA;
                                                                                                                                                                                 Miljanich GP,
Yamashiro DH;
                                                                   12-NOV-1992;
                                                                                                   12-NOV-1991;
                                 27-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9701351-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-JAN-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW19570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW19570
q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

ó

Singh T;

Justice A,

```
Valentino KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-00742774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Valentino KL,
                                                                                                                                                                                                                                                                  46.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
(first entry)
 Miljanich GP,
                                                                                                                                                                                                                                                                                                11; Conservative
                                                         cono:peptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-582596/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NEUR-) NEUREX CORP.
                             WPI; 1997-064830/06
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                       neuropathic pain
                                                                                                                                                                                                                                      Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Miljanich GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-DEC-1991;
15-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-AUG-2003
06-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US5824645-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-0CT-1998
                                                                                                                                                                                                         PF field.)
Gohil KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW72625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 release.
                                                          Omega
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conus.
                                                                                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 56
                                                                                                                                                                                                                                                                                                                                                                                                                     AAW72625
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                             AAW19555-W19572 are omega conopeptides (OCB) derived from natural peptides from Conus sp. (cone snails). The peptides and their analogues are used as analgesides acting by blocking N+Type voltage-sensitive calcium channels. The OCB can be used to treat neuropathic pain as a result of e.g. insult to the spinal cord or peripheral nerves, cancer, bone degenerative diseases, AIDS, reflex sympathetic dystrophy, herpes coster neuropathy, diabetic neuropathy, hyperesthesia, allodynia or hyperalgesia. The OCB are preferably administered in a medicament via an epidural route in a continuous infusion or sustained release formulation. The OCB can provide pain relief when administered epidurally in the absence of a permeation enhancer, at doses that are comparable to effective analgesic doses using intrachecal administration. OC cormulations comprising an OC and a carboxylic acid buffer anti-oxidant. They also confer stability to solutions containing them for prolonged treatment methods and long-term storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                         Stable omega conopeptide compositions - for producing analgesia and for inhibiting progression of neuropathic pain disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         conopeptide; analgesic; treatment; neuropathic pain; inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                  Kristipati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neuronal damage; schizophrenia; tardive dyskinesia; analgesia;
acute dystonic reactions; inflammation; epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'Match 46.6%; Score 75; DB 2; Length 26; Local Similarity 42.3%; Pred. No. 0.23; es 11; Conservative 5; Mismatches 10; Indels
                                                                                                         , Gohil K, Adriaenssens PI,
Luther RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CRIXNQKCFQHLDDCCSRKCNRFNKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW12985 standard; peptide; 26 AA.
                                                                                                                                                                                                                                      Disclosure; Fig 4; 47pp; English.
             96WO-US011041.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91US-00814759.
                                         95US-00496847
96US-00613400
                                                                                                                  Bowersox SS,
Pettus MR, Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Omega conopeptide SNX-202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
                                                                                     (NEUR-) NEUREX CORP.
                                                                                                                                                            WPI; 1997-100012/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NEUR-) NEUREX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 26 AA;
                                           27-JUN-1995;
                                                         08-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-DEC-1991;
30-DEC-1992;
                                                                                                                 Amstutz GA,
Gadbois T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
22-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US5587454-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW12985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Omega
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 55
AAW12985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
```

ઠે

```
Conus genus; marine snail; cone snail; omega-conopeptide; analgesia; nociceptive pain; neuropathic pain; neuronal tissue; conocoxin; inflammation; schizophrenia; tardive dyskinesia; acute dystonic reaction; rheumatoid arthritis; epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A method has been developed for the treatment of inflammation in a subject. The method comprises administration of an omega-conopeptide effective to: (i) block voltage-gated calcium channels; (ii) bind with high affanity to an omega-conopeptide binding site; and (iii) inhibit neurotransmitter release from nervous tissue. The method is used to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treatment of inflammation, comprises administration of omega-conopeptide - effective to block voltage-gated calcium channels, bind with high affinity to omega-conopeptide binding site, and inhibit neuro-transmitter
                                                                                                                                                                        The present peptide is an omega conopeptide, useful as an analgesic, especially for treating neuropathic pain. The peptide, which can be prepared by solid phase synthesis, can also be used to inhibit neuronal damage and treat schizophrenia, tardive dyskinesia, acute dystonic reactions, inflammation and epilepsy. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
- useful as analgesics, esp. for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Singh T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Justice A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conus genus analogue omega-conopeptide SNX-202.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gohil KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 75;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Col 51-52; 58pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW72625 standard; peptide; 26 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 2; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91US-00814759.
93US-00049794.
96US-00675354.
```

ö

us-10-627-685a-26.rag

```
produce analgesia (especially in subjects experiencing neuropathic pain); produce analgesia (especially in subjects experiencing neuropathic pain); reactions, rheumatoid arthritis, and epilepsy. The present sequence components of peptide toxins produced by marine snails of the genus context, and which act as calcium channel blockers. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                    Omega-conopeptide; peptide toxin; snail; calcium channel blocker; analgesia; guinea pig ileum; omega-conotoxin; pain; neuropathic.
                                                                                                       Score 75; DB 2; Length 26;
Pred. Nc. 0.23;
5; Mismatches 10; Indels
                                                                                                                            10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Justice A,
                                                                                                                                                                                                                                                                                                                                                               /note= "C-terminal amide"
                                                                                                                                          1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                     Valentino KL,
inflammation and associated pain. The
                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                Ą.
                                                                                                                                                                                                                                                                  Analog omega-conopeptide SNX-202.
                                                                                                                                                                                                           AAW95584 standard; protein; 26
                                                                                                     46.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                       96US-00675354
                                                                                                                                                                                                                                                                                                                                                                                                                                        91US-00814759
93US-00049794
                                                                                                                                                                                                                                                 (first entry)
                                                                                                                       11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gohil KC,
                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NEUR-) NEUREX CORP
                                                                                     Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Miljanich GP,
                                                                                                                                                                                                                                                                                                                                                                                                                     03-JUL-1996;
                                                                                                                                                                                                                                               29-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                       30-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                  US5859186-A
                                                                                                                                                                                                                                                                                                                                                                                                  12-JAN-1999
                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                      Query Match
                                                                                                                                                                                                                              AAW95584;
                                                                                                                                                                                                                                                                                                                          Conus sp.
                                                                                                                       Matches
                                                                                                                                                                                         RESULT 57
88888888888888
                                                                                                                                           à
                                                                                                                                                            g
```

Sequences AAM95574-589 represent sequences of analog omega-conopeptides. Omega-conopeptides are components of peptide toxins produced by marine snails of the genus Conus, and which act as calcium channel blockers. The invention relates to a method of producing analgesia in a mammal that comprises administering an omega conopeptide having activities in (a) inhibiting electivally stimulated contraction of guinea pig ileum and (b) selectively binding to omega conopeptide WNIAA binding sites in neuronal tissue, where these activities are within the ranges of those of omega-conocoxing MVIAA and TVIA. The method is used for treating chronic pain, especially neuropathic pain Production of analgesia in mammal - by administration of omega cono-Disclosure; Fig 2A-B; 59pp; English. peptide(s)

WPI; 1999-120002/10

Seguence 26 AA;

```
ò
                           Gaps
                           ö
                          10; Indels
      DB 2;
                        5; Mismatches
   46.6%; Score 75; ilarity 42.3%; Pred. No. (Conservative 5; Mismatch
                                       1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                    Similarity
Query Match
Best Local Simi
Matches 11;
                                       à
                                                        g
```

ż AAY56496 standard; peptide; (first entry) 16-FEB-2000

ö

Gaps

·,

RESULT

Omega conopeptide, analgesic, nociceptive, neuropathic, pain, conotoxin, marine snail, peptide toxin, inflammation, binding, voltage-gated calcium channel, inhibition, norepinephrine, noradrenaline, Analogue omega conopeptide SNX-202. anti-inflammatory.

Conus sp.

Location/Qualifiers /note= "amidated" 1. .16 8. .20 Disulfide-bond Disulfide-bond Disulfide-bond Modified-site US5994305-A. 30-NOV-1999

91US-00814759. 93US-00049794. 96US-00675354. 96US-00742774. 98US-00138439. 21-AUG-1998; 30-DEC-1991; L5-APR-1993; 03-JUL-1996

(ELAN-) ELAN PHARM INC

01-NOV-1996;

Gohil KC; Miljanich GP, Valentino KL, Justice A, Singh T, WPI; 2000-038270/03 Measuring the activity of test compounds in blocking voltage-gated calcium channels, binding to the omega conopeptide binding site and inhibiting norephrene (noradrenaline) release for treating inflammation.

Disclosure; Fig 2; 47pp; English.

A method has been developed of selecting a test compound for treating inflammation. The method comprises measuring the activity of the test compound in blocking voltage-gated calcium channels, binding to the omega compound in blocking voltage-gated calcium channels, binding to the omega release from nervous tissue. The method is useful for selecting compounds for treating inflammation. The selected compounds are capable of producing analgesia an amemalian subject with chronic or intractable opiold analgesia genes of the prior art which cause dependency and tolerance, requiring potentially dangerous increases in opioid doses to achieve the analgesic effect. The present sequence represents an omega conopeptide given in the present invention

Sequence 26 AA;

DB 3; Length 26; 46.6%; Score 75;

```
Synthetic.
                                                                                                                                                                                      epilepsy.
                                                                                                 AAB19462;
                                                                                                                                                                                                                    Conus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Singh T,
                                                          RESULT 60
                                                                     AAB19462
                           셤
                                                                                                 ठ
           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is an omega-conopeptide analogue. Omega-conopeptides are components of peptide toxins produced marine snails of the genus conus. Omega-conopeptides and their derivatives act as calcium channel blockers and may be useful for producing analgesia in nociceptive and neuropathic pain. The peptides bind to omega-conopeptide binding sites, which are present mainly in neuronal tissue, and inhibit norepinephrine release from nervous tissue. Conopeptides such as WVIAA are effective as therapeutic agents for treating neurogenic conditions such as echizophrenia, tardive dyskinesia and acute dystonic reactions,
                                                                                                                                                                          Marine snail; omega-conopeptide; calcium channel blocker; SNX-202; toxin; matalgesic; antiinflammactory; anticonvulsant; neuroleptic; norepinephrine release inhibitor; schizophrenia; tardive dyskinesia; acute dystonic reaction; inflammation; epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Selecting a compound for producing analgesia involves measuring activity of test compound in blocking voltage-gated calcium channels, binding to omega conopeptide binding site and inhibiting norepinephrine release.
            Gaps
           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Justice A;
           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Valentino KL, Miljanich GP,
           10;
Pred. No. 0.23
5; Mismatches
                                                                                                                                                                                                                                                                                                        /note= "C-terminal amide"
                             26
                                         CKLKGQSCSRLMYDCCSGSCGRSGKC
                             1 CRIXNQKCFQHLDDCCSRKCNRFNKC
                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                 Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Fig 2; 58pp; English.
                                                                                                AAB14370 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                 91US-00814759.
93US-00049794.
96US-00675354.
96US-00742774.
                                                                                                                                                                                                                                                                                                                                                                 99US-00298017
 42.3%;
                                                                                                                                     (first entry)
                                                                                                                                                        Omega-conopeptide SNX-202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inflammation and epilepsy
          11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             (ELAN-) ELAN PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Singh T, Gohil KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-490177/43
Local Similarity
                                                                                                                                                                                                                                                                           Disulfide-bond
Disulfide-bond
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 26 AA;
                                                                                                                                                                                                                                                                  Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                 23-APR-1999;
                                                                                                                                      06-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                    10-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                         21-AUG-1998;
                                                                                                                                                                                                                                                                                                                           US6087091-A
                                                                                                                                                                                                                                                                                                                                             11-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                             15-APR-1993
03-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                 31-NOV-1996
                                                                                                                                                                                                                            Conus sp.
Synthetic.
                                                                                                                  AAB14370;
Best Loc
Matches
                                                                            RESULT 59
AAB14370
                                                                                                        셤
                              ઠે
```

Gaps

ö

46.6%; Score 75; DB 3; Length 26; 42.3%; Pred. No. 0.23; ive 5; Mismatches 10; Indels

Query Match
Best Local Similarity 42.3
Matches 11; Conservative

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents an omega-conopeptide analogue. Omega-conopeptides are components of peptide toxins which act as voltage-gated calcium channel inhibitors. The peptides are used to enhance the enalgesic effect produced by an opiate in a mammalian subject. The method comprises administering to the subject an omega-conopeptide which is able to inhibit electrically stimulated contraction of the guinea pig lleum and bind to omega-conopeptide MVIIA binding sites present in neuronal tissue. Omega-conopeptides are useful for enhancing the analgesic effect produced by an opiate. Omega-conopeptides may also be used in the treatment of pain, in reducing neuronal damage related to an ischemic condition in mammals, and in treating schizophrenia, tardive dyskinesia and acute dystonic reactions, inflammation and epilepsy
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Omega-conopeptide; voltage-gated calcium channel inhibitor; analgesic; peptide toxin; opiate; pain; neurónal damage; ischemic condition; schizophrenia; tardive dyskinesia; acute dystonic reaction; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enhancing analgesia produced by opiates by administering an omega-
conopeptide that inhibits electrically stimulated contraction of guinea
pig ilium and binds to omega-conopeptide MVIIA binding sites in neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                             Sequence of an omega-conopeptide analogue designated SNX-202.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Justice A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 46.6%; Score 75; DB 4; Length 26; 1. Similarity 42.3%; Pred. No. 0.23; 11; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Miljanich GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "amidated residue"
56
                                  1 CKLKGQSCSRLMYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Col 51-52; 58pp; English.
CRIXNOKCFQHLDDCCSRKCNRFNKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ą
                                                                                                                                                                                                               AAB19462 standard; peptide; 26 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Valentino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93US-00049794.
93US-00081863.
96US-00675354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-00392979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91US-00814759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-00742774
98US-00138439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-00298017
                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ELAN-) ELAN PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-030946/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gohil KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-APR-1999;
                                                                                                                                                                                                                                                                                                                                 06-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US6136786-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
```

```
Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant; neuroprotective; cerebroprotective; cardiovascular; antiinflammatory; antidiabetic; tranquiliser; vulnerary; antipsychotic; anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy; setroke; cerebrovascular accident; hypoxia; noxia; ischaemia; stroke; cerebrovascular accident; brain trauma; spinal chord trauma; drowning; suffocation; perinatel apphyxia; hypoglycaemic event; pain; psychosis; anxiety; schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New omega-conopeptides useful for treating disorders associated voltage gated ion channels e.g. pain, inflammation, neurologic o cardiovascular disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                        Shon K;
                                                                                                                                                                                                                                                                                                                                                                                                                       Garrett JE,
   56
                      56
                                                                                                                                     Omega-conopeptide S6.2 toxin sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                     I, Watkins M,
Cartier GE;
 CRIXNOKCFOHLDDCCSRKCNRFNKC
            1 CKLKGOSCSRLMYDCCSGSCGRSGKC
                                                                     ABB96887 standard; peptide; 26 AA.
                                                                                                                                                                                                                                                                                                                                                   21-JUL-2000; 2000US-0219616P.
05-FEB-2001; 2001US-0265888P.
                                                                                                                                                                                                                                                                                                                                23-JUL-2001, 2001WO-US023041
                                                                                                                                                                                                                                                                                                                                                                                   (UTAH ) UNIV UTAH RES FOUND. (COGN-) COGNETIX INC.
                                                                                                                12-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                    Mcintosh JM,
Jones RM, Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-257318/30.
                                                                                                                                                                                                                                                                  Conus striatus
                                                                                                                                                                                                                                                                                     WO200207675-A2
                                                                                                                                                                                                                                                                                                            31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                   Olivera BM,
                                                                                                                                                                                                                                                                                                                                                                                                                               Jacobsen R,
                                                                                            ABB96887;
                                                    RESULT
                                                                                  ò
                  g
```

Sequences encoding them, and propertide sequences. The activity of the peptides of the invention may be described as, analgesic, anticonvulsant vasotropic, cardiant, neuroprotective, cerebroprotective, cardiant, neuroprotective, cerebroprotective, vulnerary, antinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary, of vodulating the activity of voltage gated ion channels. They may be used for treating or preventing disorders associated with voltage gated ion channels such as neurological disorders, e.g. seizure (associated noxia, ischaemia, stroke, cerebrovascular accident, brain or spinal, chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic they may also be used for treating psychiatric disorders.

They may also be used for treating psychiatric disorders.

They may also be used for treating psychiatric disorders e.g. psychosis, anxiety or schizophrenia. The analgesic agents of the invention show ammander also and the activity, and are non-addictive. The may also be used for treating psychiatric disorders e.g. psychosis, alminished side effects and toxicity, and are non-addictive. The varmantaned side effects and toxicity, and are non-addictive. The sequences given in records ABB96807-ABB96905 represent omega-conopeptide toxin sequences invention relates to isolated omega-conopeptides, nucleic acid Claim 1(a); Page 72; 195pp; English.

Sequence 26 AA;

Length 26; 46.0%; Score 74; DB 5;

```
ô
           Gaps
           ö
           Indels
         10;
  Pred. No. 0.29;
5; Mismatches
                    1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                   56
                             42.3%;
       Conservative
Similarity
       11;
Best Local S
Matches 11
                    ò
                                셤
```

RESULT 62

Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant; neuroprotective; carebroprotective; cardiovascular; antiinflammatory; antimigraine; antidiabelic; tranquiliser; vulnerary; antipsychotic; anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy; stroke; cerebrovascular accident; hypoxia; anoxia; ischaemia; stroke; cerebrovascular accident; brain trauma; spinal chord trauma; drowning; suffecation; perinatal asphyxia; hypoglycaemic event; pain; migraine; inflammation; cardiovascular disorder; psychiatric disorder; psychosis; anxiety; schizophrenia. ABB96679 standard; peptide; 30 AA. Omega-conopeptide S6.2 propeptide. (first entry) 12-JUL-2002 ABB96679;

Conus striatus WO200207675-A2

31-JAN-2002.

23-JUL-2001; 2001WO-US023041.

21-JUL-2000; 2000US-0219616P. 05-FEB-2001; 2001US-0265888P.

(UTAH) UNIV UTAH RES FOUND. (COGN-) COGNETIX INC

Shon K; Garrett JE, Matkins M, Cartier GE; Mcintosh JM, Jones RM, Olivera BM, Jacobsen R,

WPI; 2002-257318/30. N-PSDB; ABL98938. New omega-conopeptides useful for treating disorders associated with voltege gated ion channels e.g. pain, inflammation, neurologic or cardiovascular disorders.

Claim 1(c); Page 62; 195pp; English.

The invention relates to isolated omega-conopeptides, nucleic acid
sequences encoding them, and propeptide sequences. The activity of the
peptides of the invention may be described as, analgesic, anticonvulsant,
vasotropic, cardiant, neuroprotective, creebroprotective, cardiovascular,
antinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary,
antipythotic, anxiolytic and neuroleptic. Peptides of the invention act
by modulating the activity of voltage gated in channels. They may be
used for treating or preventing disorders, e.g. seizure (associated
not papiepsy), neurotoxic injury associated with conditions of hypoxia,
on channels such as neurological disorders, e.g. seizure (associated
nota, ischaemia, stroke, cerebrovascular accident, brain or spinal
chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic
chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic
They may also be used for treating psychiatric disorders e.g. psychosis,
anxiety or schizophremia. The analgesic agents of the invention show
diminished side effects and toxicity, and are non-addictive. The
robentide semishres

```
sednences
                                                                                                                                                                                                         64
                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                     AAR3961
                                                                                                                                                           유
ន្តដ្ត
                                                                                                                                 ò
                                                                                                                                                                                                                                      The invention relates to isolated omega-conopeptides, nucleic acid sequences encoding them, and propeptide sequences. The activity of the sequences encoding them, and propeptide sequences. The activity of the peptides of the invention may be described as analogesic, anticonvulsant, vasorropic, cardiant, neuroprotective, creatoropic cardiovascular, antinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary, antipsychotic, anxiolytic and neuroleptic. Peptides of the invention act by modulating the activity of voltage gated ion channels. They may be used for treating or preventing disorders e.g. seizure (associated ion channels such as neurological disorders, e.g. seizure (associated ion channels such as neurological disorders, e.g. seizure (associated ion channels such as neurological disorders, e.g. seizure (associated ion channels arokai, ischaemia, stroke, cerebrovascular accident, brain or spinal chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic events; pain e.g. migraine; inflammation or cardiovascular disorders.

They may also be used for treating psychiatric disorders e.g. psychosis, anxiety or schizophrenia. The analgesic agents of the invention show anxiety or schizophrenia. The analgesic agents of the invention show diminished side effects and toxicity, and are non-addictive. The
                                                          ö
                                                                                                                                                                                                                                                                                                          Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant; neuroprotective; cerebroprotective; cardiovascular; antiinflammatory; antimigraine; antidiabetic; tranquiliser; vulnerary; antipsychotic; anxiolytic; neuroleptic; voltage gated ion channel; seizure; epileps; neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia; stroke; cerebrovascular accident; brain trauma; spinal chord trauma; attoxe; cerebrovascular accident; spin trauma; spinal chord trauma; drowning; suffocation; cardiovascular disorder; psychiatric disorder; migraine; inflammation; cardiovascular disorder; psychiatric disorder;
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           omega-conopeptides useful for treating disorders associated with age gated ion channels e.g. pain, inflammation, neurologic or
                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shon K;
                           46.0%; Score 74; DB 5; Length 30; 42.3%; Pred. No. 0.33;
                                                          10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Garrett JE,
                                                        5; Mismatches
                                                                                                      1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26

 Watkins M,
Cartier GE;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1(c); Page 55; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                psychosis; anxiety; schizophrenia.
                                                                                                                                                                                                                                                                                 Omega-conopeptide P6.1 propeptide.
                                                                                                                                                                                         ABB96666 standard; peptide; 72 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUL-2001; 2001WO-US023041.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-2000; 2000US-0219616P. 05-FEB-2001; 2001US-0265888P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UTAH ) UNIV UTAH RES FOUND.
(COGN-) COGNETIX INC.
                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Olivera BM, Mcintosh JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cardiovascular disorders.
                                                        11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-257318/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conus purpurascens.
                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ABL98925
Sequence 30 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200207675-A2
                                                                                                                                                                                                                                                    12-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jacobsen R,
                                                                                                                                                                                                                       ABB96666;
                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            voltage
                                                          Matches
                                                                                                                                                            RESULT 63
                                                                                                                                                                          ABB96666
g
                                                                                                                g
                                                                                                                                                                                         δ
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequences given in AAR39608-30 are omega conopeptides (OCTs) and derivatives of these, which may be used to produce analgesia in a mammal. These OCTs inhibit voltage-gated calcium channels selectively in neuronal tissue. This is shown by the peptides ability to stimulate contraction in guinea pig ileum and to bind to OCT MVIIA binding sites present in neuronal tissue. OCTs are components of peptide toxins derived from marine snalls of the genus Conus, and act as calcium channel blockers. These OCTs may be used to replace opiods in the treatment of chronic pain or to reduce the opiod dosage required. This helps to reduce dependence on and tolerance to opiod narcotics. (Updated on 25-MAR-2003 to correct
given in records ABB96595-ABB96697 represent omega-conopeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of omega-cono-peptide(s) which selectively inhibit voltage-gated calcium channels - to induce analgesia, enhance opiate analgesics, treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Omega conopeptide; OCT; analgesia; inhibition; voltage-gated; calcium channel; neurone; contraction; guinea pig; ileum; MVIIA; binding site; toxin; marine; snail; Conus; opiod; chronic pain;
                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gohil K, Valentino KL, Miljanich GP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 71; DB 2; Length 26; Pred. No. 0.62;
                                                                                                                        Length 72;
                                                                                                                                                                              7; Indels
                                                                                                                           DB 5;
                                                                                                                                                      0.86;
                                                                                                                                                                              3; Mismatches
                                                                                                                           45.3%; Score 73;
50.0%; Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                               AAR39615 standard; peptide; 26 AA.
                                                                                                                                                                                                                                 1 CRIXNQKCFQHLDDCCSRKC 20
                                                                                                                                                                                                                                                               Claim 1; Fig 1; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92WO-US011349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91US-00814759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                              10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Justice A, Singh T,
                          propeptide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NEUR-) NEUREX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1993-227270/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                   Local Similarity
                                                                           Sequence 72 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-2003
20-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9313128-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVIB/SNX183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 narcotice.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR39615;
                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                         Best Loc
Matches
```

Gaps

; 0

Indels

11;

42.3%; Pred. No. 0.62; ive 4; Mismatches

11; Conservative

Best Local Similarity Matches 11; Conserv

1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26 CKLKGQSCRKTSYDCCSGSCGRSGKC 26

g

à

```
Ischaemia-related neuronal damage in mammals is reduced by admin., 4-24

hr after onset of ischaemia, of a cpd. (I) which binds selectively to an comega-conotoxin (OCT) MVIIA site in neuronal tissue. (I) has selectivity at least 100 expressed as ratio of binding affinity for the MVIIA site to comega-conotoxin; (OCT) MVIIA site in neuronal affinity for the MVIIA, GVIIA (COT) MVIIA or it is the cpd. SNX-207. (I) is esp. used to reduce neuronal damage caused by stroke. By delaying admin. for some time (compare compare compare redn. in neuronal damage is achieved. (I) is admin. e.g. by creater redn. in neuronal damage is achieved. (I) is admin. e.g. by contracerebroventricular (ICV) injection at 0.1-20 microg/kg, but can also intracerebroventricular (ICV) injection at 0.1-20 microg/kg, but can also compare specified conotoxins for (I). (I) is also at least as effective as the specified conotoxins for (I) selective inhibition of N-type volteage. Compared neuronal tissue and (2) selective inhibition of N-type volteage. Comman mediated neuroral tissue and (2) selective inhibition of N-type volteage. Compared neuronal tissue and (2) selective inhibition of N-type volteage. Compared neuronal tissue and (2) selective inhibition of N-type volteage. Compared neuronal tissue and (2) selective inhibition of N-type volteage. Compared conopeptides are given in AAR37752-62. Several analog correct PN field.)
             ö
                                                                                                                                                                                                                                                                                                                     Ischaemia; neuronal; omega-conotoxin; OCT; MVIIA; MVIIC; MVIID; MVIIB; GVIA; GVIIA; RVIA; SVIA; TVIA; SVIB; SNX-207; stroke; delayed treatment; antihistamine; blood pressure; N-type voltage-gated Ca currents; N-channel mediated neurotransmitter release.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Redn. of neuronal damage caused by ischaemia - by admin. of cpds. that bind specifically to omega-conotoxin MVIIA binding sites.
           Gaps
           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bitner RS;
         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Valentino KL,
         11;
     4; Mismatches
                                CRIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fox JA,
                                                                     1 CKLKGOSCRKTSYDCCSGSCGRSGKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                       AAR37760 standard; peptide; 26 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Fig 1, 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92WO-US009766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91US-00789913.
92US-00916478.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bowersox SS,
                                                                                                                                                                                                                                  (revised)
(first entry)
11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1993-182487/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NEUR-) NEUREX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Miljanich GP,
Yamashiro DH;
                                                                                                                                                                                                                                                                                     SVIB/SNX-183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9310145-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-NOV-1991;
17-JUL-1992;
                                                                                                                                                                                                                                25-MAR-2003
08-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-MAY-1993.
                                                                                                                                                                                            AAR37760;
                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
Matches
                                                                                                                          RESULT 65
                                                                                                                                                                                            ò
                                                                    셤
```

```
AAW19544-W19553 are naturally occurring omega conopeptides (OCS) isolated from Conus sp. (cone snails). The peptides and their analogues are used as analgesics acting by blocking N-type voltage-sensitive calcium channels. The OCS can be used to treat neuropathic pain as a result of e.g. insult to the spinal cord or peripheral nerves, cancer, bone e.g. insult to the spinal cord or peripheral nerves, cancer, bone charped diseases, AIDS, reflex sympathetic dystrophy, herpes zoster neuropathy, diabetic neuropathy, hyperesthesia, allodynia or or peripheral reversity and an edicament via an optimious infusion or sustained release formulation. The OCS can provide pain relief when administered epidurally in the absence of a permeation enhancer, at doses that are comparable to comparable doses using intrathecal administration. OC formulations comprising an OC and a carboxylic acid buffer anti-oxidant. They also confer stability to solutions containing them for prolonged converse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stable omega conopeptide compositions - for producing analgesia and inhibiting progression of neuropathic pain disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kristipati
                                                                                                                                                                            Conopeptide, cone snail; pain; analgesic; neuropathy; epidural;
N-type voltage-sensitive calcium channel; block; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                            Natural omega-conopeptide SVIB/SNX-183 used for pain relief.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 44.1%; Score 71; DB 2; Length 26; Best Local Similarity 42.3%; Pred. No. 0.62; Matches 11; Conservative 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adriaenssens PI,
                                                                                                                                                                                                                                                                                            /note= "optionally amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 2, Fig 3; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3, Gohil K,
Luther RR;
                                                                                                                                                                                                                                                             Location/Qualifiers
                             AAW19551 standard; peptide; 26 AA.
                                                                                                                                                                                                                                                                                                                                                                                        96WO-US011041.
                                                                                                                                                                                                                                                                                                                                                                                                                       95US-00496847.
96US-00613400.
                                                                                                 (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bowersox SS,
Pettus MR, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NEUR-) NEUREX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-100012/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 26 AA;
                                                                                                                                                                                                                                                                         Modified-site
                                                                                              27-AUG-2003
13-OCT-1997
                                                                                                                                                                                                                                                                                                                         WO9701351-A1
                                                                                                                                                                                                                                                                                                                                                                                     26-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                    27-JUN-1995;
08-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                        16-JAN-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amstutz GA,
Gadbois T,
                                                               AAW19551;
                                                                                                                                                                                                                            Conus.
RESULT 66
                  AAW19551
                                ò
```

Length 26;

DB 2;

Score 71;

44.18;

Query Match

26 AA;

```
rheumatoid arthritis; epilepsy.
                                                                                                                             CORP.
                                                                                                                                                               WPI; 1998-582596/49.
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                         Sequence 26 AA;
                                                                                                                             (NEUR-) NEUREX
                                                                                                                                               Miljanich GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
Modified-site
                                                                        01-NOV-1996;
                                                                                                  15-APR-1993;
03-JUL-1996;
                                                                                         30-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-MAR-1999
                                      US5824645-A
                                                        20-0CT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US5859186-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW95571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conus sp.
                                                                                                                                                                                                             release
                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW9557
   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conus genus, marine snail; cone snail; omega-conopeptide; analgesia; nociceptive pain; neuropathic pain; neuronal tissue; conotoxin; inflammation; schizophrenia; tardive dyskinesia; acute dystonic reaction;
                                                                                                                                                                                                                                                                                                                                                                      The present peptide is an omega conopeptide, useful as an analgesic, especially for treating neuropathic pain. The peptide, which can be prepared by solid phase synthesis, can also be used to inhibit neuronal damage and treat schizophrenia, tardive dyskinesia, acute dystonic reactions, inflammation and epilepsy. (Updated on 25-MAR-2003 to correct
                                                                                                                                   Omega conopeptide; analgesic; treatment; neuropathic pain; inhibition; neuronal damage; schizophrenia; tardive dyskinesia; analgesia; acute dystonic reactions; inflammation; epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                            cono:peptide(s) - useful as analgesics, esp. for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                           Singh
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Indels
                                                                                                                                                                                                                                                                                           Justice A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conus genus natural omega-conopeptide SVIB/SNX-183.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 71; DB 2,
Pred. No. 0.62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                                                                                                                                                          Valentino KL,
CKLKGQSCRKTSYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CKLKGQSCRKTSYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                       Disclosure; Col 45-46; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CRIXNOKCFOHLDDCCSRKCNRFNKC
                                                      AAW12974 standard; peptide; 26 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW72612 standard; peptide; 26 AA.
                                                                                                                                                                                                                                              91US-00814759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.18;
                                                                                                                                                                                                                            93US-00049794
                                                                                                                                                                                                                                                      92WO-US011349
                                                                                         (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
(first entry)
                                                                                                                   Omega conopeptide SNX-183
                                                                                                                                                                                                                                                                                          Miljanich GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Conservative
                                                                                                                                                                                                                                                                        (NEUR-) NEUREX CORP.
                                                                                                                                                                                                                                                                                                            WPI; 1997-064830/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                       neuropathic pain.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 26 AA;
                                                                                                                                                                                                                            15-APR-1993;
                                                                                                                                                                                                                                              30-DEC-1991;
                                                                                                                                                                                                                                                       30-DEC-1992;
                                                                                       25-MAR-2003
22-APR-1997
                                                                                                                                                                                                           24-DEC-1996.
                                                                                                                                                                                          US5587454-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-AUG-2003
06-JAN-1999
                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                          Gohil KC,
                                                                                                                                                                                                                                                                                                                                                                                                                      field.)
                                                                       AAW12974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW72612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                             Omega
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 68
AAW72612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                           RESULT
          음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        요
```

```
subject. The method comprises administration of an omega-conopeptide effective to: (i) block voltage-gated calcium channels; (ii) bind with high affinity to an omega-conopeptide binding site, and (iii) inhibit neurotransmitter release from nervous tissue. The method is used to treat forther analgesia especially in subjects experienting neuropathic pain; and to treat schizophrenia, tardive dyskinesia and acute dystonic reactions, rheumatoid arthritis, and epilepsy. The present sequence represents a natural omega-conopeptide. Omega-conopeptides are components of peptide toxins produced by marine snails of the genus Conus, and which act as calcium channel blockers. (Updated on 27-AUG-2003 to correct OS
                                                                                                                                                                                                                                                                                                                                                                                          Treatment of inflammation, comprises administration of omega-conopeptide - effective to block voltage-gated calcium channels, bind with high affinity to omega-conopeptide binding site, and inhibit neuro-transmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A method has been developed for the treatment of inflammation in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Omega-conopeptide, peptide toxin; snail; calcium channel blocker; analgesia; guinea pig ileum; omega-conotoxin; pain; neuropathic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                               Singh T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 71; DB 2; Length 26;
Pred. No. 0.62;
4; Mismatches 11; Indels
                                                                                                                                                                                                                                                               Justice A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "C-terminal amide"
                                                                                                                                                                                                                                                               Gohil KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CKLKGQSCRKTSYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CRIXNOKCFQHLDDCCSRKCNRFNKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Fig 1, 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Omega-conopeptide SVIB/SNX-183.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW95571 standard; protein; 26
                                                             91US-00814759.
93US-00049794.
96US-00675354.
96US-00742774.
                                                                                                                                                                                                                                                               Valentino KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Conservative
```

Gaps

XGX#X##X#X#X#X#X###X

us-10-627-685a-26.rag

```
A method has been developed of selecting a test compound for treating inflammation. The method comprises measuring the activity of the test compound in blocking voltage-gated calcium channels, binding to the omega conopeptide binding site and inhibiting norepinephrine (noradrenaline) for treating inflammation. The method is useful for selecting compounds for treating inflammation. The selected compounds are capable of producing analgesia in a mammalian subject with chronic or intractable pain. Analgesia caused by selected compounds may reduce the reliance on opioid analgesic agents of the prior art which cause dependency and tolerance, requiring potentially dangerous increases in opioid doses to achieve the analgesic effect. The present sequence represents an omega conopeptide given in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Marine snail; omega-conopeptide; calcium channel blocker; SVIB; SNX-183; toxin; analgesic; antiinflammatory; anticonvulsant; neuroleptic; norepinephrine release inhibitor; schizophrenia; tardive dyskinesia; acute dystonic reaction; inflammation; epilepsy.
                                   Measuring the activity of test compounds in blocking voltage-gated calcium channels, binding to the omega conopeptide binding site and inhibiting norepinephrine (noradrenaline) release for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Justice A;
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 71; DB 3; Length 26;
Pred. No. 0.62;
4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gohil KC, Valentino KL, Miljanich GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note≈ "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                        Disclosure; Fig 1; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB14359 standard; peptide; 26 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Omega-conopeptide SVIB/SNX-183.
                                                                                                                                                                                                                                                                                                                                                                                                                                 44.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91US-00814759.
93US-00049794.
96US-00675354.
96US-00742774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-00298017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-DEC-2000' (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ELAN-) ELAN PHARM INC.
   WPI; 2000-038270/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disulfide-bond
Disulfide-bond
Disulfide-bond
Modified-site
                                                                                        inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-APR-1993;
03-JUL-1996;
01-NOV-1996;
21-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US6087091-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB14359:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Singh T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB14359
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                              Sequences AAM95564-573 represent primary sequences of natural omegaconopeptides. Omega-conopeptides are components of peptide toxins produced by marine snalls of the genus Conus, and which act as calcium channel blockers. The invention relates to a method of producing analgesia in a mammal that comprises administering an omega conopeptide of guinea pig ileum and (b) selectively binding to omega conopeptide of guinea pig ileum and (b) selectively binding to omega conopeptide will binding sites in neuronal tissus, where these activities are within the ranges of those of omega-conotoxins MVIA and TVIA. The method is used for treating chronic pain, especially neuropathic pain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Omega conopeptide; analgesic; nociceptive; neuropathic; pain; conotoxin; matine snail; peptide toxin; inflammation; binding; voltage-gated calcium channel; inhibition; norepinephrine; noradrenaline; anti-inflammatory.
                                                                                                                                                                                                                            Production of analgesia in mammal - by administration of omega cono-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                     Singh T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gohil KC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.1%; Score 71; DB 2; Length 26; 42.3%; Pred. No. 0.62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Indels
                                                                                                                                                                   Justice A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Valentino KL, Miljanich GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
                                                                                                                                                             Valentino KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Natural omega conopeptide SVIB/SNX-183.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CKLKGQSCRKTSYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                              Disclosure; Fig 1B; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY56480 standard; peptide; 26
                                       96US-00675354.
                                                                       91US-00814759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91US-00814759.
93US-00049794.
96US-00675354.
96US-00742774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-00138439.
                                                                                                                                                            Gohil KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ELAN-) ELAN PHARM INC.
                                                                                                                                                                                            WPI; 1999-120002/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Singh T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 11; Conserv
                                                                                                                        (NEUR-) NEUREX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 26 AA;
                                                                                                                                                          Miljanich GP,
                                 03-JUL-1996;
                                                                     30-DEC-1991;
15-APR-1993;
 12-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-APR-1993;
03-JUL-1996;
01-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US5994305-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-NOV-1999
                                                                                                                                                                                                                                                  peptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Justice A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loca
Matches
```

ઠે d ö

Gaps

· 0

us-10-627-685a-26.rag

```
RESULT 73
                                                                                                                                                                                                                                                                                                             AAB19449
  886666666666888
                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                   ö
                                                                                             The present sequence is an omega-conopeptide from marine snails of the genus Conus. Omega-conopeptides are components of peptide toxins produced by the cone snails, and which act as calcium channel blockers. Natural omega-conopeptides and their derivatives may be useful for producing analgesia in nociceptive and neuropathic pain. The peptides bind to omega-conopeptide binding sites, which are present mainly in neuronal tissue, and inhibit norepinephrine release from nervous tissue. Conopeptides such as MVIIA and TVIA are effective as therapeutic agents for treating neurogenic conditions such as schizophrenia, tardive dyskinesia and acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a teactive group (III) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a
                        Selecting a compound for producing analgesia involves measuring activity of test compound in blocking voltage-gated calcium channels, binding to omega conopeptide binding site and inhibiting norepinephrine release.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity.
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thibaudeau K;
                                                                                                                                                                                                                                                         Match 44.1%; Score 71; DB 3; Length 26; Local Similarity 42.3%; Pred. No. 0.62; les 11; Conservative 4; Mismatches 11; Indels
                                                                                                                                                                                                            dystonic reactions, inflammation and epilepsy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Holmes DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Page 653-654; 733pp; English.
                                                                                                                                                                                                                                                                                                            1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                          1 CKLKGQSCRKTSYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Milner PG,
                                                                        Example 4; Fig 1; 58pp; English
                                                                                                                                                                                                                                                                                                                                                                                                AAB92221 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0134406P.
99US-0153406P.
99US-0159783P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-MAY-2000; 2000WO-US013576.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Toxin peptide SEQ ID NO:1397
                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ezrin AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CONJ-) CONJUCHEM INC.
WPI; 2000-49017/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-112059/12.
                                                                                                                                                                                                                                   Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200069900-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-MAY-1999;
10-SEP-1999;
15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                              22-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bridon DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                        AAB92221;
                                                                                                                                                                                                                                                                         Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                  셤
```

```
ö
peptidase stabilised therapeutic peptide composed of 3-50 amino acids.

(I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in peptides are not reatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Omega-conopeptide, voltage-gated calcium channel inhibitor, analgesic, peptide toxin; opiate; pain; neuronal damage; ischemic condition; schizophrenia; tardive dyskinesia; acute dystonic reaction; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enhancing analgesia produced by opiates by administering an omega-
conopeptide that inhibits electrically stimulated contraction of guinea
pig illum and binds to omega-conopeptide MVIIA binding sites in neuronal
tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primary sequence of a natural omega-conopeptide SVIB/SNX-183.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Justice
                                                                                                                                                                                                                                                                                                                                                                                            Score 71; DB 4; Length 26; Pred. No. 0.62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Miljanich GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "amidated C-terminal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Valentino KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB19449 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93US-00049794.
93US-00081863.
96US-00675354.
96US-00138439.
99US-00138439.
                                                                                                                                                                                                                                                                                                                                                                                               44.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-00392979
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 42.3
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-030946/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gohil KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                 Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELAN-) ELAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US6136786-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB19449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Singh T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conus sp.
```

1 CKLKGQSCRKTSYDCCSGSCGRSGKC

d

Ź 27

ABB96876 standard; peptide;

```
The present sequence represents an omega-conopeptide. Omega-conopeptides channel inhibitors. The peptides are used to enhance the analgesic effect broduced by an opiate in a mammalian subject. The method comprises administering to the subject an omega-conopeptide which is abbe to bind to omega-conopeptide MITA binding sites present in neuronal tissue. Omega-conopeptides are useful for enhancing the analgesic effect by an opiate. Omega-conopeptides may also be used in the treatment of pain, in reducing neuronal damage related to an ischemic condition in dammals, and in treating schizophrenia, tardive dyskinesia and acute dystonic reactions, inflammation and epilepsy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention comprises peptides having calcium channel blocking activities which are derived from the venomous saliva of assassin bugs. The calcium channel blocking peptides of the invention are useful for treating stenocardia, hypertension, myocarditis, arrhythmia and cerebral ischaemia. The present amino acid sequence represents a cone snail wcondtoxin peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cone snail; venomous saliva; calcium channel blocking activity;
stenocardia; hypertension; myocarditis; arrhythmia; cerebral ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A new peptide derived from venomous saliva of assassin bug, has calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.1%; Score 71; DB 4; Length 26;
42.3%; Pred. No. 0.62;
Live 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CRIXNOKCFQHLDDCCSRKCNRFNKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cone snail w-conotoxin peptide SVIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 4; 26pp; Japanese.
   Disclosure; Fig 1; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA015126 standard; peptide; 26 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-SEP-2000; 2000JP-00266187.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-SEP-2000; 2000JP-00266187.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          channel blocking activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 11; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SUNR ) SUNTORY LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-421068/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JP2002080499-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-MAR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            w-conotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA015126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA015126
\frac{1}{2} \frac{1}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
```

Omega-conopeptide, analgesic; anticonvulsant; vasotropic; cardiant; neuroprotective; cerebroprotective; cardiovascular; antinflammatory; antimigraine; antidabetic; tranquilisesr; vulnerary; antipsychotic; anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy; stroke; cerebrovascular accident; brain trauma; spinal chord trauma; stroke; cerebrovascular accident; brain trauma; spinal chord trauma; drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain; migraine; inflammation; cardiovascular disorder; psychiatric disorder; psychosis; anxiety; schizophrenia.

ö

Gaps

ò

Conus purpurascens.

WO200207675-A2.

31-JAN-2002

Omega-conopeptide P6.3 toxin sequence.

(first entry)

12-JUL-2002

ABB96876;

```
The invention relates to isolated omega-conopeptides, nucleic acid sequences encoding them, and propebtide sequences. The activity of the periods of the invention may be described as, analgesic, anticonvulsant, vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular, antipleychotic, anxiolytic and neuroleptic. Peptides of the invention act of modulating the activity of voltage gated in channels. They may be used for treating or preventing disorders associated with voltage gated in channels and as neurological disorders, e.g. seizure (associated with epilepsy), neurotoxic injury associated with conditions of hypoxia, anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal events; pain e.g. migraine; inflammation or acrdiovascular disorders.

They may also be used for treating psychiatric disorders e.g. psychosis, anxiety or schizophrenia. The analgesic agents of the invention show and element and events in the analgesic agents of the invention show and element and events and exects and encodictive. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diminished side effects and toxicity, and are non-addictive. The sequences given in records ABB96807-ABB96905 represent omega-conopeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New omega-conopeptides useful for treating disorders associated with voltage gated ion channels e.g. pain, inflammation, neurologic or cardiovascular disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shon K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Garrett JE,

    Watkins M,
Cartier GE;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1(a); Page 72; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-2000; 2000US-0219616P.
05-FEB-2001; 2001US-0265888P.
                                                                                                                                                                                                                                                                                                                                                                                                     23-JUL-2001; 2001WO-US023041.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UTAH ) UNIV UTAH RES FOUND.
(COGN-) COGNETIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mcintosh JM,
Jones RM, Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-257318/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  toxin sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Olivera BM,
Jacobsen R,
```

ö

Gaps

; 0

Indels

Score 71; DB 5; Length 26; Pred. No. 0.62; 4; Mismatches 11; Indels

44.18;

11; Conservative

Matches

Local Similarity

Query Match

Sequence 26 AA;

ö

1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26

```
Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant; neuroprotective; carebroprotective; cardiovascular; antidilammatory; antimizate; antidabetic; tranquiliser; vulnerary; antipsychotic; anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy; neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia; stroke; cerebrovascular accident; brain trauma; spinal chord trauma; drowning; sulfocation; perinatal asphyxia; hypoglycaemic event; pain; migraine; inflammation; cardiovascular disorder; psychlatric disorder; psychosis; anxiety; schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New omega-conopeptides useful for treating disorders associated with voltage gated ion channels e.g. pain, inflammation, neurologic or cardiovascular disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shon K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Garrett JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mcintosh JM, Watkins M,
Jones RM, Cartier GE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1(c); Page 56; 195pp; English.
                                                                                                                                                         Omega-conopeptide P6.3 propeptide.
                                                                                  ABB96668 standard; peptide; 72 AA
 20
            2 CKKTGRKCFPHQKDCCGRAC 21
CRIXNOKCFOHLDDCCSRKC
                                                                                                                                                                                                                                                                                                                                                                                23-JUL-2001; 2001WO-US023041.
                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-2000; 2000US-0219616P.
05-FEB-2001; 2001US-0265888P.
                                                                                                                                                                                                                                                                                                                                                                                                                                           (UTAH ) UNIV UTAH RES FOUND.
(COGN-) COGNETIX INC.
                                                                                                                                  12-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-257318/30.
N-PSDB; ABL98927.
                                                                                                                                                                                                                                                                                                            Conus purpurascens.
                                                                                                                                                                                                                                                                                                                                 WO200207675-A2.
                                                                                                                                                                                                                                                                                                                                                         31-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Olivera BM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jacobsen R,
                                                                                                          ABB96668;
                                                           RESULT 76
ABB96668
                                                                                               ሯ
                     8
```

The invention relates to isolated omega-conopeptides, nucleic acid sequences encoding them, and propeptide sequences. The activity of the sequences encoding them, and propeptide sequences. The activity of the peptides of the invention may be described as, analgesic, anticonvulsant, vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular, antinifisammatory, antimigraine, antidiabetic, tranquiliser, vulnerary, antipaychotic, anxiolytic and neurolegic. peptides of the invention act by modulating the activity of voltage gated ion channels. They may be used for treating or preventing disorders associated with voltage gated ion channels such as neurological disorders, e.g. seizure (associated vith epilepsy), neurotoxic injury associated with conditions of hypoxia, anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal anoxia, drowning, suffocation, perinatal asphyxia or hypoglycaemic events; pain e.g. migraine; inflammation or cardiovascular disorders. They may also be used for treating psychiatric disorders e.g. psychosis, anxiety or schlzophrenia. The analgesic agents of the invention show diminished side effects and toxicity, and are non-addictive. The sequences given in records ABB96595-ABB96697 represent omega-conopeptide

Sequence 72 AA;

propeptide sequences

sequences encoding them, and propeptide sequences. The activity of the peptides of the invention may be described as, analgasic, anticonvulsant, vasotropic, cardiant, neuroprotective, creebroprotective, cardialsant, antiinflammatory, antimigraine, antidabetic, tranquiliser, vulnerary, antipsychotic, anxiolytic and neuroleptic. Peptides of the invention act by modulating the activity of voltage gated ion channels. They may be used for treating or preventing disorders associated with voltage gated ion channels such as neurological disorders, e.g. seizure (associated with epilepsy), neurotoxic injury associated with conditions of hypoxia, anxia, ischaemia, stroke, cerebrovascular accident, brain or spinal chord trauma, drowning, suffocation, perinatal asphyxia or hyposlycaemic events; pain e.g. migraine; inflammation or cardiovascular disorders.

The invention relates to isolated omega-conopeptides, nucleic acid

Example 2; Page 62; 195pp; English.

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                          /label= OTHER
/note= "OTHER is Tyr, 1251-Tyr, mono-iodo-Tyr or di-iodo-
Tyr or O-sulpho-Tyr or O-Phospho-Tyr"
                                                                                                                                                                                                                                           Omega-conopptide; analgesic; anticonvulsant; vasotropic; cardiant; neuroprotective; cerebroprotective; cardiovascular; antiinflammatory; antimparaine; antidiabetic; tranquiliser; vulnerary; antipsychotic; anxiolytic; neuroleptic; tranquiliser; vulnerary; seizure; epileps; neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia; stroke; cerebrovascular accident; brain trauma; spinal chord trauma; drowning; sulfocation; perinatal asphyxia; hypoglycaemic event; pain; migraine; inflammation; cardiovascular disorder; psychiatric disorder; psychosis; anxiety; schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New omega-conopeptides useful for treating disorders associated with voltage gated ion channels e.g. pain, inflammation, neurologic or
                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Garrett JE, Shon K;
Length 72;
                         7; Indels
  DB 5;
                                                                                                                                                                                                                     Omega-conopeptide S6.2 generic toxin sequence.
44.1%; Score 71; DB 50.0%; Pred. No. 1.4; ive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mcintosh JM, Watkins M,
Jones RM, Cartier GE;
                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                         ABB96786 standard; peptide; 26 AA
                                                  1 CRIXNQKCFQHLDDCCSRKC 20
                                                                 CKKTGRKCFPHQKDCCGRAC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-2000; 2000US-0219616P.
05-FEB-2001; 2001US-0265888P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-JUL-2001; 2001WO-US023041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                             (first entry)
                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cardiovascular disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COGNETIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-257318/30.
             Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference 13
                                                                                                                                                                                                                                                                                                                                                                             Conus striatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200207675-A2
                                                                                                                                                                                            12-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Olivera BM,
Jacobsen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-JAN-2002
                                                                                                                                                                    ABB96786;
  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (COGN-)
                                                                                                                RESULT 77
                                                                                                                               ABB96786
                                                                                                                                           g
                                                    ठे
```

antipsychotic, anxiolytic and neuroleptic. Peptides of the invention act used wouldating the activity of voltage gated ion channels. They may be used for treating or preventing disorders associated with voltage gated ion channels such as neurological disorders, e.g. seizure (associated anoxia, ischeemia, stroke, cerebrovascular accident, brain or spinal events; pain e.g. migraine; inflammation perinatal asphyxia or hypoglycaemic rhey may also be used for treating psychiatric disorders e.g. psychosis, anxiety or schizophrenia. The analgesic agents of the invention show diminished side effects and toxicity, and are non-addictive. The sequences given in records ABB96698-ABB96806 represent omega-conopeptide generic toxin sequences

ö

ö

Gaps

; 0

11; Indels

Score 64; DB 5; Length 26; Pred. No. 3.6; 4; Mismatches 11; Indels

39.8%;

Query Match
Best Local Similarity 42.35,
Local Similarity 42.35,
Local Similarity 42.35,

ð

Sequence 26 AA;

```
They may also be used for treating psychiatric disorders e.g. psychosis, anxiety or schizophrenia. The analgesic agents of the invention show diminished side effects and toxicity, and are non-addictive. The sequences given in records ABB96698-ABB96806 represent omega-conopeptide generic toxin sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "OTHER is Tyr, 1251-Tyr, mono-iodo-Tyr or di-iodo-
Tyr or O-sulpho-Tyr or O-Phospho-Tyr"
                                                                                                                                                                                                                                                                                                                                                            neuroprotective; cerebroprotective; cardiovascular; antinflammatory; antinglammatory; antinglammatory; antinglame; antinflammatory; antinglarine; antidabetic; tranquiliser; vulnerary; antingsychotic; anxiolytic; neuroleptic; voltage gated ion channal; seizure; epilepsy; neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia; stroke; cerebrovascular accident; brain trauma; spinal chord trauma; drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain; migraine; inflammation; cardiovascular disorder; psychiatric disorder; psychosis; anxiety; schizophrenia.
                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                 Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant;
                                                                                                                                        .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Garrett JE, Shon K;
                                                                                                             5; Length 26;
                                                                                                                                      10; Indels
                                                                                                                                                                                                                                                                                                                       Omega-conopeptide w-SVIB generic toxin sequence.
                                                                                                             DB
                                                                                                                                   5; Mismatches
                                                                                                         41.6%; Score 67;
42.3%; Pred. No.
                                                                                                                                                       1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26

    Watkins M,
Cartier GE;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                              ABB96790 standard; peptide; 26 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JUL-2001; 2001WO-US023041.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0219616P.
2001US-0265888P.
                                                                                      UTAH RES FOUND.
                                                                                                                                                                                                                                                                                               12-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mcintosh JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jones RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UTAH ) UNIV UTAH RES
(COGN-) COGNETIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-257318/30.
                                                                              Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conus striatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200207675-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Olivera BM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jacobsen
                                                                                                                                                                                                                      RESULT 78
                                                                                                                                                                                                                               ABB96790
    88888888
                                                                                                                                                                                                                                                          ò
                                                                                                                                                                              a
```

```
Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant; neuroprotective; cerebroprotective; cardiovascular; antiinflammatory; antimigraine; antidiabetic; tranquiliser; vulnerary; antipsychotic; anxiolytic; neuroleptic; voltage gated ion channel; sarizure; peliepsy; neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia; stroke, cerebrovascular accident; brain trauma; spinal chord trauma; drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain; migraine; inflammation; cardiovascular disorder; psychiatric disorder; psychosis; anxiety; schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                       label= OTHER
note= "OTHER is Pro or Hydroxy Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= OTHER
/note= "OTHER is Pro or Hydroxy Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                             label≃ OTHER
note= "OTHER is Pro or Hydroxy Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= OTHER
/note= "OTHER is Pro or Hydroxy Pro"
                                                                                                                                                                       Omega-conopeptide P6.1 generic toxin sequence.
1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
               Location/Qualifiers
                                                                                               ġ.
                                                                                         ABB96772 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-2000; 2000US-0219616P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-FEB-2001; 2001US-0265888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUL-2001; 2001WO-US023041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UTAH ) UNIV UTAH RES FOUND. (COGN-) COGNETIX INC.
                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                    Conus purpurascens.
                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200207675-A2
                                                                                                                                               12-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-JAN-2002.
                                                                                                                   ABB96772;
                                                                                                    요
```

The invention relates to isolated omega-conopeptides, nucleic acid sequences encoding them, and propeptide sequences. The activity of the peptides of the invention may be described as, analgesic, anticonvulsant, vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular, antiinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary,

opeptides useful for treating disorders associated with ion channels e.g. pain, inflammation, neurologic or

New omega-conopeptides useful for

cardiovascular disorders.

voltage gated

Example 2; Page 63; 195pp; English.

```
The invention relates to isolated omega-conopeptides, nucleic acid
sequences encoding them, and propeptide sequences. The activity of the
peptides of the invention may be described as, analgesic, anticonvulsant,
vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular,
antiinflammatory, antimigatahe, antidiabetic, tranquiliser, vulnerary,
antiphychotic, anxiolytic and neuroleptic. Peptides of the invention act
by modulating the activity of voltage gated ion channels: They may be
used for treating or preventing disorders associated with voltage gated
ion channels such as neurological disorders, e.g. seizure (associated
with epilepsy), neurocoxic injury associated with conditions of hypoxia,
anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal
chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic
cevents; pain e.g. migraine; inflammation or cardiovascular disorders.
They may also be used for treating psychiatric disorders e.g. psychosis,
anxiety or schizophrenia. The analgesic agents of the invention show
diminished side effects and toxicity, and are non-addictive. The
sequences given in records ABB96698-ABB96806 represent omega-conopeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuroprotective; cerebroprotective; cardiovascular; antiinflammatory; antimpraine; antidabetic; tranquiliser; vulnerary; antipsychotic; antiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy; neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia; stroke; cerebrovascular accident; brain trauma; spinal chord trauma; drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain; migralne; inflammation; cardiovascular disorder; psychiatric disorder; psychosis; anxiety; schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                omega-conopeptides useful for treating disorders associated with age gated ion channels e.g. pain, inflammation, neurologic or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
      Garrett JE, Shon K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.8%; Score 64; DB 5; Length 27; 55.0%; Pred. No. 3.7; 11ve 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Omega-conopeptide P6.1 toxin sequence.
  Watkins M,
                      Cartier GE;
                                                                                                                                                                              Example 2; Page 56; 195pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB96874 standard; peptide; 27 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CRIXNOKCFOHLDDCCSRKC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CKTXGRKCFXHQKDCCGRAC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0219616P
2001US-0265888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-JUL-2001; 2001WO-US023041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                       cardiovascular disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-JUL-2002 (first entry)
Mcintosh'JM,
Jones RM, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 55.0
les 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               generic toxin sequences
                                                             WPI; 2002-257318/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200207675-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-2000;
05-FEB-2001;
    Olivera BM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-JAN-2002
                      Jacobsen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB96874;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                       voltage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

```
equences encoding them, and properties equences. The activity of the peptides of the invention may be described as, analgesic, anticonvulsant, vasotropic, cardiant, neuroprotective, cerebroprotective, cardiavascular, antinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary, antimigraine, antidiabetic, tranquiliser, vulnerary, antipsychotic, anxiolytic and neuroleptic. Peptides of the invention act by modulating the activity of voltage gated ion channels. They may be used for treating or preventing disorders seasociated with voltage gated ion channels such as neurological disorders, e.g. seizure (associated with epilepsy), neurotoxic injury associated with conditions of hypoxia, anoxia, ischemaia, erroke, cerebrovascular accident, brain or spinal chord trauma, drowning, sulffocation, perinatal asphyxia or hypoglycamic events; pain e.g. migraine; inflammation or cardiovascular disorders. They may also be used for treating psychiatric disorders e.g. psychosis, anxiety or schizophrenia. The analgesic agents of the invention show diminished side effects and toxicity, and are non-addictive. The sequences given in records ABB96807-ABB96905 represent omega-conopeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant; neuroprotective; cerebroprotective; cardiovascular; antiinflammatory; antimigraine; antidiabetic; tranquiliser; vulnerary; antipsychotic; anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy; neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia; stroke; cerebrovascular accident; brain trauma; spinal chord trauma; drowning; sulfocation; perinatal asphyxia; hypoglycaemic event; pain; migraine; inflammation; cardiovascular disorder; psychiatric disorder;
                                                                                                                                      New omega-conopeptides useful for treating disorders associated with voltage gated ion channels e.g. pain, inflammation, neurologic or cardiovascular disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                     nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                         Shon K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39.8%; Score 64; DB 5; Length 27; 55.0%; Pred. No. 3.7; ive 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                          The invention relates to isolated omega-conopeptides,
                                       Garrett JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Omega-conopeptide Cr6.3 toxin sequence.
                                 M, Watkins M,
Cartier GE;
                                                                                                                                                                                                                              Claim 1(a); Page 72; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB96842 standard; peptide; 27 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    psychosis; anxiety; schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CRIXNQKCFQHLDDCCSRKC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 CKTXGRKCFXHQKDCCGRAC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-JUL-2002 (first entry)
                                         Mcintosh JM,
Jones RM, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 55.0
Matches 11; Conservative
(COGN-) COGNETIX INC.
                                                                                                     WPI; 2002-257318/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conus circumcisus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coxin sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 27 AA;
                                       Olivera BM,
Jacobsen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB96842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 81
ABB96842
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
```

23-JUL-2001; 2001WO-US023041. 21-JUL-2000; 2000US-0219616P. 05-FEB-2001; 2001US-0265888P.

WO200207675-A2. 31-JAN-2002.

Olivera BM, Mcintosh JM, Watkins M, Garrett JE, Shon K; Jacobsen R, Jones RM, Cartier GE;

21-JUL-2000; 2000US-0219616P. 05-FEB-2001; 2001US-0265888P. (UTAH) UNIV UTAH RES FOUND.

(COGN-) COGNETIX INC.

Shon K;

1, Watkins M, Garrett JE, Cartier GE;

```
The invention relates to isolated omega-conopeptides, nucleic acid sequences encoding them, and propeptide sequences. The activity of the peptides of the invention may be described as, analgesic, anticonvulsant, vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular, antinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary, antinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary, by modulating the activity of voltage gated in channels. They may be used for treating or preventing disorders, e.g. seizure (associated with epilepsy), neurotoxic injury associated with conditions of hypoxia, anoxia, isolaemia, stroke, cerebrovascular accident, brain or spinal chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic they may also be used for treating psychiatric disorders e.g. psychosis, anxiety or schizophrenia. The analgesic agents of the invention show sequences given in records ABB96807-ABB96905 represent omega-conopeptide
                                                                                                                           New omega-conopeptides useful for treating disorders associated with voltage gated ion channels e.g. pain, inflammation, neurologic or cardiovascular disorders.
                                                                                                                                                                                 Claim 1(a); Page 71; 195pp; English.
               (UTAH ) UNIV UTAH RES FOUND. (COGN-) COGNETIX INC.
                                                       Olivera BM, Mcintosh JM,
                                                                      Jones RM,
                                                                                                 WPI; 2002-257318/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 27 AA;
                                                                     Jacobsen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB96626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB96626
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
```

Gaps 1; Ouery Match 39.4%; Score 63.5; DB 5; Length 27; Best Local Similarity 37.0%; Pred. No. 4.2; Matches 10; Conservative 8; Mismatches 8; Indels 1 CRIXNOKCFOHLDDCCSRKCNRFN-KC 26

Omega-conopeptide, analgesic, anticonvilsant, vasotropic, cardiant; neuroprotective, cerebroprotective, cardiovascular, antiinflammatory, antimigraine, antidabetic, tranquiliser; vulnerary; antipsychotic; antiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy; neurological disorder; neurocoxic injury; hypoxia; anoxia; ischaemia; stroke, cerebrovascular accident; brain trauma; spinal chord trauma; stroke, cerebrovascular accident; brain trauma; spinal chord trauma; migraine; inflammation; perinetal asphyxia; hypoglycaemic event; pain; psychosis; anxiety; schizophrenia. Omega-conopeptide Cr6.3 propeptide. ABB96626 standard; peptide; 73 AA. (first entry)

Conus circumcisus. WO200207675-A2.

23-JUL-2001; 2001WO-US023041.

```
The invention relates to isolated owega-conopeptides, nucleic acid
sequences encoding them, and propeptide sequences. The activity of the
peptides of the invention may be described as, analgesic, anticonvulsant,
vasotropic, cardiant, neuroprotective, cerebroprotective, cardiavascular,
antinflammatory, antimigrathe, antidiabelic, tranquiliser, vulnerary,
antiphyshotic, anxiolytic and neuroleptic. Peptides of the invention act
conting the activity of voltage gated ion channels. They may be
used for treating or preventing disorders associated with voltage gated
to no hannels such as neurological disorders, e.g. seizure (associated
of the pilepsy, neurocoxic injury associated with conditions of hypoxia,
anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal
chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic
chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic
chord trauma, drowning, inflammation or cardiovascular disorders.
They may also be used for treating psychiatric disorders enviety or schizophrenia. The analgesic agents of the invention show
sequences given in records ABB96697 represent omega-conopeptide
nrowshirias amminines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
                                                                                                                                                                                                                                   New omega-conopeptides useful for treating disorders associated with voltage gated ion channels e.g. pain, inflammation, neurologic or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CRIXNOKCFQHLDDCCSRKCNRFN-KC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1(c); Page 36; 195pp; English.
                                                                                                                                                                                                                                                                        cardiovascular disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 37.0
Les 10; Conservative
                                                                                                                                                                          WPI; 2002-257318/30.
                                                                                                                                                                                            N-PSDB; ABL98885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 73 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 83
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
```

Tyrosinase inhibitor; pupae; house fly; melanin; dermal medicine; cosmetic; food preservative; insecticide. /label= Tyr, OTHER /note= "OTHER = 3,4-dihydroxyphenylalanine" Location/Qualifiers AAW06589 standard; peptide; 38 AA Tyrosinase inhibitor peptide. 95JP-00038405 14-FEB-1997 (first entry) Misc-difference 32 27-FEB-1995; JP08231592-A. 10-SEP-1996. Synthetic. AAW06589; AAW06589

```
Conus betulinus
                                                                                                                                                                                                                                                                                                             Sequence 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200202590-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-2000; 2
27-OCT-2000; 2
08-NOV-2000; 2
14-NOV-2000; 2
29-JAN-2001; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB88659;
                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 85
                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB88659
 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                               7
                                                                                                                     This sequence represents a tyrosinase inhibitor peptide which was isolated from the pupae of house flies. The peptide has a high inhibitory activity on tyrosinase, which catalyses biological production of melanin pigment, and is stable at ambient pH. The peptide can be used for dermal medicines, cosmetics, food preservatives and insecticides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pure I-conotoxin peptides isolated from venom of cone snails, useful for
the regulation of the flow of potassium through potassium channels in the
treatment of e.g. multiple sclerosis.
                                                                      tyrosinase - useful for dermal medicines, cosmetics,
                                                                                                                                                                                                                                                                                                                                                                                                     Conotoxin; Conus; I-conotoxin; I-superfamily conotoxin; venom; antidote; cone snail; marine gastropod; neuroprotective; antinflammatory; ophthalmological; antibacterial; anticonvulsant; muscular; antidiabetic; cardiout; immunosuppressive; notropic; antiaddictive; cytostatic; cardiant; immunosuppressive; nootropic; analgesic; antimigraine; relaxant; antirheumatic; antiarthritic; dermatological; tranquilliser; neuroleptic; H-ATPase stimulator;
                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                    Conus betulinus I-superfamily conotoxin type I peptide SEQ:369.
                                                                                                                                                                                                                             7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Olivera BM;
                                                                                                                                                                                                        39.1%; Score 63; DB 2; Length 38; 39.3%; Pred. No. 6.3;
                                                                                                                                                                                                                             9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mcintosh JM,
                                                                                                                                                                                                                             6; Mismatches
                                                                                                                                                                                                                                                  1 CRIXNQKCFQHLDDCCSRKCNR-FNKCV 27
                                                                                                                                                                                                                                                              CLANGSKCYSH-DVCCTKRCHNXAKKCV 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               potassium agonist; curare antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jiminez Shen GS;
                                                                                                    Claim 1; Page 2; 9pp; Japanese.
                                                                                                                                                                                                                                                                                                                         ABB88797 standard; peptide; 36
         95JP-00038405.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-0CT-2000; 2000US-0243410P.
08-NOV-2000; 2000US-024581P.
14-NOV-2000; 2000US-024714P.
29-JAN-2001; 2001US-0264256P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JUN-2001; 2001WO-US020796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUN-2000; 2000US-0304166P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                               (first entry)
                              (SIYA ) SANSEI SEIYAKU KK
                                                                                                                                                                                                                             11; Conservative
                                                                                 food preservatives, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shetty R,
Jones RM,
                                                                    Peptide inhibitor of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COGNETIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-171634/22.
                                                  WPI; 1996-461344/46
                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conus betulinus
                                                                                                                                                                                      Sequence 38 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200202590-A2
         27-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                              22-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Walker CS,
Watkins M,
                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                            ABB88797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (COGN-)
                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                   ઠે
```

```
The present invention describes substantially pure 1-conocorn perpetute invention describes substantially pure 1-conocorn perpetute invention describes substant, antidabetic, antiaddictive, cardatar, antidabetic, antidabetic, antidaddictive, cardatar, antidabetic, antidaddictive, cardatar, antidabetic, antidaddictive, independent controlation, represented the cardation of antidarthritic, dermaclogical, trangulaliser and neuroleptic activities. Controlater in the treatment of multiple sclerosis, acute antegonist. (I) can be used as an H-ATPase stimulator, potasium agonist and curare antidional leukoencephalomyelitis, optic neuromyelitis, progressive antidional leukoencephalomyelitis, optic neuromyelitis, progressive multifocal leukoencephalomyelitis, adrenoleukodystrophy, acute transverse myelitis, subacute sclerosing panencephalomyelitis, metachromic leukodystrophy, Pelizaeus Merzbacher disease, spinal cord injury, leukodystrophy, Pelizaeus Merzbacher disease, spinal cord injury, cotulinum toxin poisoning, Huntington's chorea, compression and entrapment neuropathies, cardiovascular disease, reactive gliosis, hyperglycaemia, immunosuppression, cocaine addiction, cancer, cognitive chyperglycaemia, immunosuppression, cocaine addiction, cancer, cognitive chyperglycaemia, immunosuppression, cocaine addiction, cancer, cognitive chyperglycaemia, immunosuppression, cocaine addiction, cancer, cognitive chical depolarisation of excitable membranes, and disorders associated with voltage gated ion channels, pain and a neuromuscular disorder. (I) are also useful for the treatment of autoimmune disease, and cancing arthritis, systemic lupus eryhrematosus, Alzheimer's, anxiety and schizophrenia. Abisbas62 to Abisbas78 and Ablahemer's anxiety and schizophrenia. Abisbas62 to Abisbas8746 to Abisbaser invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cone snail; marine gastropod; neuroprotective; antiinflammatory; ophthalmological; antibacterial; anticonvulsant; muscular; antidiabetic; cardicvascular; antiarrhythmic; cardiant; immunosuppressive; nootropic; antiaddictive; cytostatic; cerebroprotective; antiasthmatic; vasotropic; analgesic; antimigraine; relaxant; antirheumatic; antiarthriic; dermatcological; tranquilliser; neuroleptic; H-ATPase stimulator; potassium agonist; curare antagonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conotoxin; Conus; I-conotoxin; I-superfamily conotoxin; venom; antidote;
                                                                                    The present invention describes substantially pure I-conotoxin peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conus betulinus I-superfamily conotoxin peptide sequence SEQ:167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Length 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 62.5;
Pred. No. 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLSLGQRCERH-SDCCGYLCCFYDKCV 27
3; Page 81; 260pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB88659 standard; peptide; 73 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0243410P.
2000US-0246581P.
2000US-0247714P.
2001US-0264256P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JUN-2001; 2001WO-US020796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 40...
Best Local 11; Conservative
```

```
The present invention describes substantially pure I-conotoxin peptides of 30 -50 residues (I). (I) have neuroprotective, antiinflammatory, cardiovascular, antidate, antidabetic, antiadiative, muscular, cardiovascular, antidate, antidabetic, antiadiative, relaxant, antiarthritic, dermatological, tranquilliser and neuroleptic, antiarthritic, dermatological, tranquilliser and neuroleptic activities.

(I) can be used as an H-Arpaes stimulator, potassium agonist and curare disseminated encephalomyelitis, optic neuromyelitis, progressive, antificoal leukoencephalopathy, adrenolatedystrophy, acute transverse complication to the standard disseminated encephalopathy, adrenolatedystrophy, acute transverse complication, betulinum toxin poisoning, Huntington's chorea, compression and hyperglycaemia, immunosuppression, cocaine addiction, cancer, cognitive contrapment neuropathies, cardiovascular disease, reactive gliosis, dysfunction, disorders resulting from the defects of neurotranmitter colocking drugs. (I) can also be used to treat disorders associated with woltage gated ion channels, pain and a neuromuscular disorders associated with voltage gated ion channels, pain and a neuromuscular disorders. Contoxin. They are also useful for the treatment of autoimmune diseases, are also useful for the treatment of autoimmune diseases. Contoxin. They are also useful for the treatment of autoimmune diseases, and schizophrenia. Abusba662 to Abla8778 and Abbs8546 to Abbs8934

represent sequences used in the exemplification of the present invention
                                                                                                                                                                                            Pure I-conotoxin peptides isolated from venom of cone snails, useful for the regulation of the flow of potassium through potassium channels in the treatment of e.g. multiple sclerosis.
                                                                                          Jiminez EC, Mcintosh JM,
Shen GS;
                                                                                                                                                                                                                                                                                Claim 2; Page 54; 260pp; English.
                    (UTAH ) UNIV UTAH RES FOUND.
(COGN-) COGNETIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 40.73
Best Local 11; Conservative
                                                                                        Shetty R,
Jones RM,
                                                                                                                                                  WPI; 2002-171634/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 73 AA;
                                                                                 Walker CS,
Watkins M,
```

10; Indels 1; 38.8%; Score 62.5; DB 5; Length 73; 40.7%; Pred. No. 12; iive 5; Mismatches 10; Indels 1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27 39 CLSLGQRCERH-SDCCGYLCCFYDKCV 64 ò 셤

Gaps

ABB96774 standard; peptide; 27 AA. 12-JUL-2002 (first entry)

Omega-conopeptide P6.3 generic toxin sequence.

neuroprotective, cerebroprotective; cardiovascular; antiinflammatory; antimigraine; antidiabetic; tranquiliser; vulnerary; antiinflammatory; anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy; neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia; stroke; cerebrovascular accident; brain trauma; spinal chord trauma; drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain; migraine; inflammation; cardiovascular disorder; psychiatric disorder; psychosis; anxiety; schizophrenia. Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant;

/label= OTHER /note= "OTHER is Pro or Hydroxy Pro" /label≃ OTHER /note≃ "OTHER is Pro or Hydroxy Pro" /label= OTHER /note= "OTHER is Pro or Hydroxy Pro" Location/Qualifiers Conus purpurascens. Misc-difference 27 Misc-difference 13 Misc-difference 1 SX CCCCCCCCCCCCCCXX SX LLX X B X X B

Olivera BM;

WO200207675-A2.

31-JAN-2002.

23-JUL-2001; 2001WO-US023041.

21-JUL-2000; 2000US-0219616P. 05-FEB-2001; 2001US-0265888P.

(UTAH) UNIV UTAH RES FOUND. (COGN-) COGNETIX INC.

Mcintosh JM, Watkins M, Garrett JE, Jones RM, Cartier GE; Olivera BM, Jacobsen R,

WPI; 2002-257318/30.

New omega-conopeptides useful for treating disorders associated with voltage gated ion channels e.g. pain, inflammation, neurologic or cardiovascular disorders.

Example 2; Page 56; 195pp; English.

The invention relates to isolated omega-conopeptides, nucleic acid sequences encoding them, and propeptide sequences. The activity of the peptides of the invention may be described as, analgesic, anticonvulsant, vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular, antiphylammacory, antimigrathe, antidiabetic, tranquiliser, vulnerary, antiphylammacory, antimigrathe, antidiabetic, tranquiliser, vulnerary, antiphylaming the activity of voltage gated ion channels. They may be used for treating or preventing disorders associated with voltage gated in channels such as neurological disorders, e.g. seizure (associated ino channels such as neurological disorders, e.g. seizure (associated anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic events; pain e.g. migraine; inflammacion or cardiovascular disorders.

They may also be used for treating psychiatric disorders e.g. psychosis, anxiety or schizophrenia. The analgesic agents of the invention show contains and toxicity, and are non-addictive. The

Sequence 27 AA;

Gaps ٥, Score 62; DB 5; Length 27; Pred. No. 6.1; 7; Indels 3; Mismatches 38.5%; Local Similarity 50.0 es 10; Conservative Query Match Matches

1 CRIXNQKCFQHLDDCCSRKC 20

à

. 0

AAU05927 standard; peptide; 76 AA. RESULT 87
AAU05927
ID AAU05:
XX
AC AAU05
XX
DT 24-OC

AAU05927;

24-OCT-2001 (first entry)

```
Cone snail; O-superfamily conotoxin; sodium channel; demyelinating disease; multiple scleroslis; Huntingdon's disease; neuropathy; carpal tunnel syndrome; cardiovascular disorder; congestive heart failure; cancer; immunosuppression; epilepsy; asthma;
                                                                                                                                                                                                                                                                               New O-superfamily polypeptides useful for treating voltage gated ion channel disorders, including demyellnating diseases i.e. multiple
                                                                                                                                                                                                                           Watkins M, Hillyard DR, Mcintosh JM;
        Cone snail O-superfamily conotoxin propeptide, Di6.5.
                                                                                                                                                                                                                                                                                                                   Claim 15; Page 60; 277pp; English.
                                                                                                                                                   30-DEC-1999; 99US-0173754P.
26-UUJ-2000; 2000US-0214253P.
20-UUJ-2000; 2000US-0219440P.
27-OCT-2000; 2000US-0243412P.
                                                                                                                                  28-DEC-2000; 2000WO-US035431
                                                                                                                                                                                                UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                           Cartier GE,
                                                             ischaemia; stroke; pain.
                                                                                                                                                                                                                        BM, Call
                                                                                                                                                                                                        (COGN-) COGNETIX INC
                                                                                                                                                                                                                                                    WPI; 2001-418352/44.
N-PSDB; AAS10951.
                                                                                              WO200149312-A2
                                                                             Conus distans
                                                                                                                 12-JUL-2001.
                                                                                                                                                                                                                          Olivera BM,
Layer RT,
```

The sequence is a cone snail O-superfamily conotoxin propeptide. The sequence is a cone snail O-superfamily conotoxin propeptide. The sequence is a cone snail o-superfamily conotoxin propeptides are useful for regulating the flow of sodium through sodium channels in an individual and the treatment or prevention of disorders cassociated with voltage gated ion channel disorders, including associated with voltage gated ion channel disorders, including demyelinating diseases i.e. multiple sclerosis, optic neuromyelitis, defence phalomyelitis adrenoleukodystrophy, acute transverse myelitis, progressive multifocal leukoencephalomyelitis (SSPE), metachromatic leukodystrophy, colsoning huntington's, compression, entrapment neuropathies i.e. ulnar polsoning Huntington's, compression, entrapment neuropathies i.e. ulnar cardiac arrhythmias and congestive heart failure, reactive gliosis, cardiac arrhythmias and congestive heart failure, reactive gliosis, hyperglycemena, immunosuppression, cocaine addiction, cancer, cognitive dysfunction, neurotransmitter disorders (i.e. Eaton-Lambert syndrome) and creversal of curare and other neuromuscular blocking drugs. The neurological disorder is a seizure, preferably one associated with ceptiengy. The neurological disorder is a neurotoxic injury is associated with hypoxia, anoxia or ischaemia. The neurotoxic injury is associated with expoxia or hypoglycaemic events. The disorder is pain i.e. migraine, apphyxia or hypoglycaemic events. The disorder is pain i.e. migraine, daorder is a infilammation or a cardiovascular disorder is pain in pain or about to splice subjected to a pain causing event, and to treat disorders associated with subjected to a pain causing event, and to treat disorders associated with radical depolarisation of excitable membranes by activating a KATP channel, the disorders include cardiac, ocular and cerebral ischaemia and

```
Sequence 76 AA;
```

```
The invention relates to isolated omega-conopeptides, nucleic acid sequences encoding them, and propeptide sequences. The activity of the peptides of the invention may be described as, analgesic, anticonvulsant, vasocropic, cardiant, neuroprotective, cerebroprotective, cardiant, antimigraine, antidiabetic, tranquiliser, vulnerary, antipsychotic, anxiolytic and neuroleptic. Peptides of the invention act by modulating the activity of voltage gated ion channels. They may be used for treating or preventing disorders associated with voltage gated ion channels such as neurological disorders, e.g. seizure (associated with epilepsy), neurotoxic injury associated with conditions of hypoxia,
                                                                                                                                                                                                                               Omega-conopeptide, analgesic, anticonvulsant, vasotropic, cardiant, neuroprotective; cerebroprotective; cardiovascular; antiinflammatory; antimigraine; antidiabetic; tranquiliser; vulnerary; antipsychotic; anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy; neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia; stroke, cerebrovascular accident; brain trauma; spinal chord trauma; stroke, suffocation; perinatal asphyxia; hypoglycaemic event; pain; migraine; inflammation; cardiovascular disorder; psychiatric disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .... wmega-conopeptides useful for treating disorders associated with voltage gated ion channels e.g. pain, inflammation, neurologic or cardiovascular disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shon K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "OTHER is Pro or Hydroxy Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "OTHER is Pro or Hydroxy Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= OTHER
/note= "OTHER is Pro or Hydroxy Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "OTHER is Pro or Hydroxy Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Garrett JE,
                                                                                                                                                                                                   Omega-conopeptide E6.2 generic toxin sequence
48 CNEAQEHCTQN-PDCCSESCNKFVGRCL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mcintosh JM, Watkins M,
Jones RM, Cartier GE;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Page 42; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                   psychosis; anxiety; schizophrenia.
                                                                                                   Ź
                                                                                                   ABB96741 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-2000; 2000US-0219616P.
05-FEB-2001; 2001US-026588BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JUL-2001; 2001WO-US023041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UTAH ) UNIV UTAH RES FOUND
                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             label_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (COGN-) COGNETIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-257318/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                         Conus ermineus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200207675-A2
                                                                                                                                                                12-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Olivera BM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jacobsen R,
                 ద
```

5

Gaps

5

Score 62; DB 4; Length 76; Pred. No. 14; 6; Mismatches 9; Indels

Query Match ' 38.5%; Best Local Similarity 39.3%; Matches 11; Conservative

ï

us-10-627-685a-26.rag

```
anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal blord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic events; pain e.g. migraine; inflammation or cardiovascular disorders. They may also be used for treating psychiatric disorders e.g. psychosis, anxiety or schizophrenia. The analgesic agents of the invention show sequences given in records ABB96698-ABB96806 represent omega-conopeptide generic toxin sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequences given in AAR19608-30 are omega conopeptides (OCTs) and derivatives of these, which may be used to produce analgesia in a mammal. These OCTs inhibit voltage-gated calcium channels selectively in neuronal tissue. This is shown by the peptides ability to stimulate contraction in pauronal tissue. This is shown by the peptides ability to stimulate contraction in quantonal tissue. OCTs are components of peptide toxins derived from marine snails of the genus Comus, and act as calcium channel blockers. These OCTs may be used to replace opiceds in the treatment of chronic pain or to reduce the opiced dosage required. This helps to reduce dependence on and tolerance to opiced narcotics. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of omega-cono-peptide(s) which selectively inhibit voltage-gated calcium channels - to induce analgesia, enhance opiate analgesics, treat
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Omega conopeptide, OCT, analgesia, inhibition, voltage-gated, calcium channel, neurone; contraction, guinea pig; ileum; MVIIA, binding site; toxin; marine, snail; Conus; opiod; chronic pain;
                                                                                                                                                                                                              1,
                                                                                                                                                                             Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Miljanich GP;
                                                                                                                                                                                                           Indels
                                                                                                                                                                                                           9
                                                                                                                                                                             DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Valentino KL,
                                                                                                                                                                            Score 61.5; D
Pred. No. 6.9;
                                                                                                                                                                                                        5; Mismatches
                                                                                                                                                                                                                                                    4 XNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                  Ą
                                                                                                                                                                                                                                                                                                                                           AAR39616 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gohil K,
                                                                                                                                                                         38.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 1; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92WO-US011349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91US-00814759
                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
(first entry)
                                                                                                                                                                    Query Match
Best Local Similarity 47.8
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Singh T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1993-227270/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NEUR-) NEUREX CORP
                                                                                                                                         Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MVIIC/SNX230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9313128-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-2003
20-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-JUL-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 narcotics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Justice A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                          AAR39616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pain etc.
                                                                                                                                                                                                                                                                                                               RESULT 89
                                                                                                                                                                                                                                                                                                                              AAR39616
88866666666888
                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                              g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequences given in AAR39608-30 are omega conopeptides (OCTS) and derivatives of these, which may be used to produce analgesia in a mammal. These OCTS inhibit voltage-gated calcium channels selectively in neuronal tissue. This is shown by the peptides ability to stimulate contraction in guinea pig ileum and to bind to OCT MVIIA binding sites present in marine snails of the genus Conus, and act as calcium channel blockers. These OCTS may be used to replace opiods in the treatment of chronic pain or to reduce the opiod dosage required. This helps to reduce dependence on and tolerance to opiod narcotics. (Updated on 25-MAR-2003 to correct by field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of omega-cono-peptide(s) which selectively inhibit voltage-gated calcium channels - to induce analgesia, enhance opiate analgesics, treat
                                                                                 Gaps
                                                                                                                                                                                                                                                                                                 Omega conopeptide; OCT; analgesia; inhibition; voltage-gated; calcium channel; neurone; contraction; guinea pig; ileum; MVIIA; binding site; toxin; marine; snall; Conus; opiod; chronic pain;
                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Miljanich GP;
                                                                             12; Indels
                                                  Score 61; DB 2;
Pred. No. 7.6;
4; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Valentino KL,
                                                                                                 1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                Location/Qualifiers
1. .16
                                                                                                                                                                                          Ą.
                                                                                                                                                                                   AAR39617 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gohil K,
                                                 37.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 1, 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92WO-US011349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91US-00814759
                                                                                                                                                                                                                                       (revised)
(first entry)
                                                           Similarity 38.5
0; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Justice A, Singh T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NEUR-) NEUREX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1993-227270/28
                       Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                 Disulfide-bond
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                      Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-DEC-1992;
                                                                      10;
                                                                                                                                                                                                                                    25-MAR-2003
20-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9313128-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-JUL-1993.
PN field.)
                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                              AAR39617;
                                               Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pain etc.
                                                                                                                                                                                                                                                                           SNX231.
                                                                       Matches
                                                                                                                                                            RESULT 90
                                                                                                                                                                          AAR39617
                                                                                                                                                                                   ð
                                                                                                                       g
```

Length

DB 2;

37.9%; Score 61;

Query Match

ઠે

```
Sequence 26 AA;
                                                                                                                                                                                                                                                                                                   RESULT 92
        g
                                                                                                                                                                  ò
                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ischaemia-related neuronal damage in mammals is reduced by admin.; 4-24

The after onset of ischaemia, of a cpd. (I) which binds selectively to an omega-conotoxin (OCT) MVITA site in neuronal tissue. (I) has selectivity

at least 100 expressed as ratio of binding affinity for the MVITA site to that for the MVIIC site. (I) is one of the OCTS MVIIA, MVIIB, GVIAA, GVIIA

CC or RVIAA or it is the Cpd. SNX-207. (I) is esp. used to reduce neuronal damage caused by stroke. By delaying admin. for some time (compare 10.5051403 where cpds. are given within 1 hr of the onset of ischaemia) a greater redn. in neuronal damage is achieved. (I) is admin. e.g. by intracerebroventricular (ICV) injection at 0.1-20 microg/kg, but can also in blood pressure caused by (I). (I) is also at least as effective as the specified conotoxins for (I) selective inhibition of N-type voltage.

C dannel mediated neurotransmitter release in neuronal tissue. Primary channel mediated neurotransmitter release in neuronal tissue. Primary comega-conopeptides are given in AAR37752-62. Several analog correct PN field.)
                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          delayed treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Redn. of neuronal damage caused by ischaemia - by admin: of cpds. that bind specifically to omega-conotoxin MVIIA binding sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ischaemia, neuronal, omega-conotoxin, OCT; MVIIA, MVIIC, MVIID, MVIIB, GVIA, GVIIA, RVIA, SVIA, TVIA, SVIB, SNX-207; stroke, delayed treatmen antihistamine; blood pressure; N-type voltage-gated Ca currents;
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Valentino KL, Bitner RS;
                                   ö
                                   Indels
                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-channel mediated neurotransmitter release
                                   4; Mismatches
     Pred. No.
                                                                                  56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "hydroxyproline"
                                                                                                                      1 CKGKGAPCRKTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fox JA,
                                                                                  1 CRIXNOKCFQHLDDCCSRKCNRFNKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Fig 1, 103pp; English.
                                                                                                                                                                                                                                                                     AAR37762 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92WO-US009766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91US-00789913.
ilarity 3'8.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bowersox SS,
                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .16
                                                                                                                                                                                                                                                                                                                                                                              (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NEUR-) NEUREX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1993-182487/22
     Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Miljanich GP,
Yamashiro DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9310145-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                              25-MAR-2003
08-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                            AAR37762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNX-231.
                                                                                                                                                                                                                 RESULT 9
                                                                                                                              원
```

```
Ischaemia-related neuronal damage in mammals is reduced by admin., 4-24

Traffer onset of ischaemia, of a cpd. (I) which binds selectively to an omega-conotoxin (oCT) WVIA site in neuronal tissue. (I) has selectivity of at least 100 expressed as ratio of binding affinity for the MVIIA site to that for the MVIIC site. (I) is one of the OCTS MVIIA, MVIIB, GVIA, GVIIA or RNA or it is the cpd. SNX-207. (I) is esp. used to reduce neuronal damage caused by stroke. By delaying admin. for some time (compare to USSO1403 where cpds. are given within 1 hr of the onset of ischaemia) a greater redn. in neuronal damage is achieved. (I) is admin. e.g. by intracerebroventricular (ICV) injection at 0.1-20 microg/kg, but can also compare to be given i.v. (opt. after treamment with antihistamines to minimise redn. in blood pressure caused by (I)). (I) is also at least as effective as the specified conotoxins for (I) selective inhibition of N-type voltage. C gated Ca currents in neuronal tissue and (2) selective inhibition of N-type voltage. C channel mediated neurotransmitter release in neuronal tissue. Primary comega-conopeptides are given in AAR37752-62. Several analog correct PN field.)
                                                  ö
                                                                                                                                                                                                                                                                                                                                                    Ischaemia, neuronal; omega-conotoxin, OCT; MVIIA, MVIIC; MVIID; MVIIB; QVIA; GVIIA; RVIA; SVIA; VVIB; SNX-207; stroke; delayed treatment; antihistamine; blood pressure; N-type voltage-gated Ca currents; N-channel mediated neurotransmitter release.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Redn. of neuronal damage caused by ischaemia – by admin. of cpds. that
bind specifically to omega-conotoxin MVIIA binding sites.
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bitner RS;
                                                  ö
               Score 61; DB 2; Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bowersox SS, Fox JA, Valentino KL,
                             Pred. No. 7.6;
4; Mismatches
                                                                                                     1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Fig 1; 103pp; English.
                                                                                                                                                                                                   AAR37761 standard; peptide; 26 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91US-00789913.
                 37.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92WO-US009766
                                                                                                                                                                                                                                                                                     (first entry)
Query Match
Best Local Similarity 38.5.
Best Local 10, Conservative
                                                                                                                                                                                                                                                                     (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1993-182487/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NEUR-) NEUREX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Miljanich GP,
Yamashiro DH;
                                                                                                                                                                                                                                                                                                                      MVIIC/SNX-230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9310145-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-NOV-1991;
17-JUL-1992;
                                                                                                                                                                                                                                                                  25-MAR-2003
08-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                    AAR37761;
```

us-10-627-685a-26.rag

```
AAM19544-W19553 are naturally occurring omega conopeptides (OCs) isolated from Conus sp. (cone snails). The peptides and their analogues are used as analgesics acting by blocking N-type voltage-sensitive calcium channels. The OCs can be used to treat neuropathic pain as a result of e.g. insult to the spinal cord or peripheral nerves, cancer, bone curopathy, diabetic neuropathy, hyperesthesia, allodynia or neuropathy, diabetic neuropathy, hyperesthesia, allodynia or chycalgesia. The OCs are preferably administered in a medicament via an optimuous infusion or sustained release formulation. The OCs can provide pain relief when administered epidurally in the absence of a permeation enhancer, at doses that are comparable to fective analgesic doses using intrathecal administration. OC formulations comprising an OC and acroboxylic acid buffer anti-oxidant. They also confer stability to solutions containing them for prolonged corrections in the statement methods and long-term storage. (Updated on 27-AUG-2003 to
                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stable omega conopeptide compositions - for producing analgesia and for inhibiting progression of neuropathic pain disorders.
                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kristipati R;
                                                                                                                                                                                                                                                                                                                                                       Conopeptide; cone snail; pain; analgesic; neuropathy; epidural;
N-type voltage-sensitive calcium channel; block; Conus.
                                                                                     ,
0
                                                                                                                                                                                                                                                                                                                        Natural omega-conopeptide MVIIC/SNX-230 used for pain relief.
                                              37.9%; Score 61; DB 2; Length 26; 38.5%; Pred. No. 7.6; ive 4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bowersox SS, Gohil K, Adriaenssens PI,
Pettus MR, Luther RR;
                                                                                                       1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                           Disclosure, Fig 2, 47pp, English.
                                                                                                                                                                                                               AAW19552 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96WO-US011041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95US-00496847,
96US-00613400
                                                                                                                                                                                                                                                                               (revised)
(first entry)
                                                                              Conservative
                             Query Match
Best Local Similarity
Thes 10; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NEUR-) NEUREX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-100012/09.
                Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9701351-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-JUN-1995;
08-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ą,
                                                                                                                                                                                                                                                                             27-AUG-2003
13-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-JAN-1997.
                                                                                                                                                                                                                                                AAW19552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amstutz (Gadbois
                                                                                                                                                                                 RESULT 93
                                                                                                                                                                                                     AAW19552
X S
                                                                                                         ઠે
                                                                                                                                   셤
```

```
Conus genus, marine snail; cone snail; omega-conopeptide; analgesia; cocieptivo pain; neuropathic pain; neuronal tissue; conotoxin; inflammation; schizophrenia; tardive dyskinesia; acute dystonic reaction; rheumatoid arthritis; epilepsy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subject. The method comprises administration of an ownega-conopeptide high affective to: (i) block voltage-gated calcium channels; (ii) bind with high affinity to an omega-conopeptide binding site; and (iii) inhibit neurotransmitter release from nervous tissue. The method is used to treat produce analgesia (especially in subjects experiencing neuropathic pain); produce analgesia (especially in subjects experiencing neuropathic pain); and to treat schizophrenia, tardive dyskinesia and acute dystonic represents a natural omega-conopeptide. Omega-conopeptides are components of peptide toxins produced by marine snails of the genus Conus, and which exit as calcium channel blockers. (Updated on 27-AUG-2003 to correct OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treatment of inflammation, comprises administration of omega-conopeptide - effective to block voltage-gated calcium channels, bind with high affinity to omega-conopeptide binding site, and inhibit neuro-transmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A method has been developed for the treatment of inflammation in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 61; DB 2; Length 26;
Pred. No. 7.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Indels
                                                                                                                                                                                           Conus genus natural omega-conopeptide MVIIC/SNX-230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Justice A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gohil KC,
1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Fig 1; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW72613 standard; peptide; 26 AA.
                                                                                                                                                                                                                                                                                                                                                                                         96US-00742774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Valentino KL,
                                                                                                                                                                                                                                                                                                                                                                                                                     91US-00814759.
                                                                                                                                                                                                                                                                                                                                                                                                                                  93US-00049794.
                                                                                      AAW72614 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37.9%;
                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 38.5 tes 10; Conservative
                                                                                                                                                  (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NEUR-) NEUREX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-582596/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Miljanich GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26 AA;
                                                                                                                                                 27-AUG-2003
06-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                03-JUL-1996;
                                                                                                                                                                                                                                                                                                                             US5824645-A.
                                                                                                                                                                                                                                                                                                                                                        20-0CT-1998
                                                                                                                   AAW72614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 release.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW72613
ID AAW7
                                                                                                                 g
```

1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26

ö

Gaps

ö

Score 61; DB 2; Length 26; Pred. No. 7.6; 4; Mismatches 12; Indels

37.9%;

Query Match Best Local Similarity 38.5 Matches 10; Conservative

Query Match

°

AAW72613;

Conub.

```
conopeptides. Omega-conopeptides are components of peptide toxins produced by marine snails of the genus Conus, and which act as calcium channel blockers. The invention relates to a method of producing analgesia in a mammal that comprises administering an omega conopeptide having activities in (a) inhibiting electrically stimulated contraction of guinea pig ileum and (b) selectively binding to omega conopeptide MVIA binding sites in neuronal tissue, where these activities are within the ranges of those of omega-conotoxins MVIA and TVIA. The method is used for treating chronic pain, especially neuropathic pain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequences AAW95564-573 represent primary sequences of natural omega-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Production of analgesia in mammal - by administration of omega cono-
                                                                                                                                          toxin; snail; calcium channel blocker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Omega-conopeptide, peptide toxin; snail; calcium channel blocker; analgesia; guinea pig ileum; omega-conotoxin; pain; neuropathic.
                                                                                                                                          Omega-conopeptide; peptide toxin; snail; calcium channel blocker
analgesia; guinea pig ileum; omega-conotoxin; pain; neuropathic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 61; DB 2; Length 26;
Pred. No. 7.6;
4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                  /label= 4Hyp
/note= "4-Hydroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Valentino KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CKGKGAPCRKTMYDCCSGSCGRRGKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CRIXNQKCFQHLDDCCSRKCNRFNKC
                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 1B; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW95573 standard; protein; 26 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96US-00675354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91US-00814759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.9%;
                                                                                   Omega-conopeptide SNX-231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Omega-conopeptide SNX-230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gohil KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-120002/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NEUR-) NEUREX
                                                                                                                                                                                                                                                                                                                       Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Miljanich GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-JUL-1996;
                           29-MAR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US5859186-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-JAN-1999
                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide (s)
                                                                                                                                                                                                                                                                Conus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW95573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 X C C C C C C C C X S X L L X L X L X L X L X L X L X L L L L L L L L L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A method has been developed for the treatment of inflammation in a subject. The method comprises administration of an omega-conopeptide effective to: (i) block voltage-gated calcium channels; (ii) bind with high affinity to an omega-conopeptide binding site; and (iii) inhibit neurotransmitter release from nervous tissue. The method is used to treatmention and associated pain. The treatment can also be used to produce analgesia (especially in subjects experiencing neuropathic pain); and to treat schizophrenia, tardive dyskinesia and acute dystonic reactions, rheumatoid arthritis, and epilepsy. The present sequence represents a natural omega-conopeptide. Omega-conopeptides are components of peptide toxins produced by marine snails of the genus Conus, and which act, as calcium channel blockers. (Updated on 27-AUG-2003 to correct OS
                                                                                                                                                                                                                              Conus genus; marine snail; cone snail; omega-conopeptide; analgesia; oxodiceptivo pain; neuropathic pain; neuronal tissue; conotoxin; inflammation; schizophrenia; tardive dyskinesia; acute dystonic reaction; rheumatoid arthritis; epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treatment of inflammation, comprises administration of omega-conopeptide - effective to block voltage-gated calcium channels, bind with high affinity to omega-conopeptide binding site, and inhibit neuro-transmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Justice A, Singh T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 61; DB 2; Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12, Indels
                                                                                                                                                                         Conus genus natural omega-conopeptide SVX-231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gohil KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Hyp
/note= "hydroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CRIXNQKCFQHLDDCCSRKCNRFNKC
                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 1; 58pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Miljanich GP, Valentino KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96US-00742774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93US-00049794
96US-00675354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91US-00814759
                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 38.5
les 10; Conservative
                                                                                   (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NEUR-) NEUREX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-582596/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
Modified-site
                                                                          27-AUG-2003
06-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-APR-1993;
03-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US5824645-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-OCT-1998
```

release

Singh T;

Justice A,

ö

Gaps

ö

AAW95572 standard; protein; 26 AA

RESULT 96 AAW95572 ID AAW95 XX AC AAW95:

AAW95572

Query Match

Matches

셤 ઢ

field.)

Key

```
A method has been developed of selecting a test compound for treating inflammation. The method comprises measuring the activity of the test compound in blocking voltage-gated calcium channels, binding to the omega conopeptide binding site and inhibiting norepinephrine (noradrenaline) release from nervous tissue. The method is useful for selecting compounds for treating inflammation. The selected compounds are capable of producing analgesia in a mammalian subject with chronic or intractable pain. Analgesia caused by selected compounds may reduce the reliance on popioid analgesic agents of the prior art which cause dependency and tolerance, requiring potentially dangerous increases in opioid doses to achieve the analgesic effect. The present sequence represents an omega conopeptide given in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Omega-conotoxin, venom, predatory marine snail, N-type calcium channel, neuronal damage reduction, ischemia, analgesia, opiate analgesia, schizophrenia, stimulant induced psychosis, hypertension, inflammation,
                                                                                                                                                                                              Measuring the activity of test compounds in blocking voltage-gated calcium channels, binding to the omega conopeptide binding site and inhibiting norepinephrine (noradrenaline) release for treating inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bronchotension; neuropathic pain; voltage sensitive calcium channel
                                                                                                                             Miljanich GP, Gohil KC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.9%; 'Score 61; DB 3; Length 26; 38.5%; Pred. No. 7.6; Live 4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nielsen KJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of an omega-conotoxin MVIIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CKGKGAPCRKTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alewood PF,
                                                                                                                         Valentino KL,
                                                                                                                                                                                                                                                                                     Disclosure, Fig 1; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY43715 standard; peptide; 26 AA.
               93US-00049794.
96US-00675354.
96US-00742774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98AU-00002989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-AU000288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lewis RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Conservative
                                                                                    (ELAN-) ELAN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYQU ) UNIV QUEENSLAND
                                                                                                                         Singh T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                            WPI; 2000-038270/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-013226/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 26 AA;
             15-APR-1993;
03-JUL-1996;
01-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drinkwater RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09954350-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6-APR-1999;
                                                                                                                         Justice A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conus magus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY43715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY43715
           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequences AAM95564-573 represent primary sequences of natural omegaconopeptides. Omega-conopeptides are components of peptide toxins produced by marine snalls of the genus Conus, and which act as calcium analgesia in a mammal that comprises to a method of producing analgesia in a mammal that comprises administering an omega conopeptide of guinea pig ileum and (b) selectrically stimulated contraction of guinea pig ileum and (b) selectrically shiding to omega conopeptide WIIA binding sites in neuronal tissue, where these activities are within used for treating chronic pain, especially neuropathic pain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Omega conopeptide; analgesic; nociceptive; neuropathic; pain; conotoxin; marine snail; peptide toxin; inflammation; binding; voltage-gated calcium channel; inhibition; norepinephrine; noradrenaline; anti-inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 Production of analgesia in mammal - by administration of omega cono-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                       Singh T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.9%; Score 61; DB 2; Length 26; 38.5%; Pred. No. 7.6; iive 4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                               Valentino KL, Justice A,
                                                                                        /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Natural omega conopeptide MVIIC/SNX-235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |: : | : : | | | CKGKGAPCRKTMYDCCSGSCGRRGKC 26
                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CRIXNOKCFQHLDDCCSRKCNRFNKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Fig 1B; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY56481 standard; peptide; 26 AA
                                                                                                                                                                                                  96US-00675354
                                                                                                                                                                                                                                       91US-00814759
93US-00049794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-00138439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91US-00814759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                             Gohil KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 38.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                     (NEUR-) NEUREX CORP.
                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-120002/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 26 AA;
                                                                                                                                                                                                                                                                                                                         Miljanich GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ñ
                                                                   Modified-site
                                                                                                                                                                                                03-JUL-1996;
                                                                                                                                                                                                                                   30-DEC-1991;
                                                                                                                                                                                                                                                      15-APR-1993;
                                                                                                                           US5859186-A
                                                                                                                                                             12-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                        peptide(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-NOV-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-DEC-1991;
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US5994305-A.
                   Conus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY56481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conus sp.
```

ð 셤 ö

Gaps

```
calcium channels
```

The present sequence represents an omega-conotoxin. Omega-conotoxins are isolated from women of predatory marine snails, and have a selectivity for N-type calcium channels over P/Q type channels, and so block N-type calcium channels. The omega-conotoxins of the invention can be used in any disease or disorder where blockage of N-type calcium channels is required, e.g. in the reduction of neuronal damage following ischemia, production of analgesia, or enhancement of opiate analgesia, in the treatment of schizophrenia, stimulant induced psychoses, hypertension, inflammation, and diseases which cause bronchotension, and also in the inhibition of progression of neuropathic pain. They can also be used in screen to identify compounds with activity at N-type voltage sensitive peptides used for the treatment of disorders and diseases where Novel peptides used for the treatment of the Neguired. Disclosure; Page 12; 81pp; English.

Sequence 26 AA;

Gaps ·, 37.9%; Score 61; DB 3; Length 26; 38.5%; Pred. No. 7.6; 12; Indels 4; Mismatches 1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26 10; Conservative Best Local Similarity Matches 10; Conserv Query Match ò

AAB14377 standard; peptide; 26 AA

AAB14377;

(first entry)

Omega-conopeptide MVIIC/SNX-230.

Marine snail; omega-conopeptide; calcium channel blocker; MVIIC; SNX-230; toxin; analgesic; antiinflammatory; anticonvulsant; neuroleptic; norepinephrine release inhibitor; schizophrenia; tardive dyskinesia; acute dystonic reaction; inflammation; epilepsy.

gb. Conus

/note= "C-terminal amide" Location/Qualifiers Disulfide-bond Disulfide-bond Disulfide-bond Modified-site

US6087091-A

11-JUL-2000

23-APR-1999;

99US-00298017.

91US-00814759 93US-00049794 96US-00675354 96US-00742774 98US-00138439 30-DEC-1991; 01-NOV-1996 21-AUG-1998 15-APR-1993 03-JUL-1996

(ELAN-) ELAN PHARM INC.

Miljanich GP, Valentino KL, Gohil KC, WPI; 2000-490177/43 Singh T,

Selecting a compound for producing analgesia involves measuring activity of test compound in blocking voltage-gated calcium channels, binding to

```
ö
                                                                                  The present sequence is an omega-conopeptide from marine snails of the genus Conus. Omega-conopeptides are components of peptide toxins produced by the cone snails, and which act as calcium channel blockers. Natural omega-conopeptides and their derivatives may be useful for producing analgesia in nociceptive and neuropathic pain. The peptides bind to omega-conopeptide binding sites, which are present mainly in neuronal tissue, and inhibit norepinephrine release from nervous tissue. Conopeptides such as MVIIA and TVIA are effective as therapeutic agents for treating neurogenic conditions such as schizophrania, tardive dyskinesia and acute
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
omega conopeptide binding site and inhibiting norepinephrine release.
                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                 Score 61; DB 3; Length 26;
Pred. No. 7.6;
4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                              dystonic reactions, inflammation and epilepsy
                                            Disclosure, Fig 1; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                        37.9%;
                                                                                                                                                                                                                                                                                                                                                                                   37.9
Best Local Similarity 38.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                           Sequence 26 AA;
```

1 CKGKGAPCRKTMYDCCSGSCGRRGKC 26 completed: April 18, 2005, 20:33:44 he : 126.5 secs Search

Job time

1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26

ò

this page Blank luspiol

ë

Run Š

```
App.
2, Appl.
2, Appli
1, Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Applisequence 1, Applisequence 3, Applisequen
  Appl
Appl
Appl
Appl
Appl
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                   Appli
Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                         Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                   Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                              Sequence
Sequence
Sequence
Sequence
  Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                     Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                               Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                             Sequence
Sequence
Sequence
                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
Sequence
Sequence
                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
US-08-675-354-29
US-08-655-918-29
US-09-138-439-29
US-08-6113-400A-29
US-09-298-017-29
US-09-392-979A-29
US-09-191-647-9
US-09-540-245A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S-09-298-017-21
S-09-392-979A-21
S-09-949-016-9481
S-09-641-612-2
                                                                                                                                                   US-09-894-882-372
US-09-894-882-155
US-09-894-882-164
US-09-894-882-173
US-09-894-882-176
US-08-185-432-18
                                                                                                                                                                                                                                US-09-121-457-3
US-08-937-236-6
US-08-569-214-6
US-08-937-236-5
US-08-937-236-5
US-09-641-612-5
US-09-121-457-4
US-09-121-457-4
US-09-121-457-4
US-07-689-693B-2
US-08-049-794-2
US-08-049-794-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-937-236-3
US-08-569-214-3
US-08-569-214-2
US-08-569-214-2
US-08-496-421-2
US-08-496-421-21
US-08-742-774-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -09-138-439-21
-08-613-400A-21
                                                                                                                                                                                                                                                                                                                                                                                               US-08-675-354-2
US-08-965-918-2
US-09-039-168-2
US-09-138-439-2
                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-613-400A-2
US-09-298-017-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-392-979A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -07-689-693B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -08-675-354-21
-08-965-918-21
                                                                                                                                                                                                                       US-08-899-232-3
US-09-121-457-3
                                                                                                                                                                                                                                                                                                                                                                         -08-496-847-2
-08-742-774-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-675-354-1
US-08-675-354-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -08-742-774-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -07-789-913-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -08-049-794-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5424218-2
                                                                                                                                                                                                            25523
25523
25523
12572
11292
11292
1292
1292
2703
2703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1276
1291
1291
1295
26
                                                                                                                                                                                                                                                                                           Appli
                                                                           April 18, 2005, 20:24:17 ; Search time 30.5 Seconds (without alignments) 66.083 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19, Assequence 8, App
Sequence 167, 2
Sequence 207, 2
Sequence 207, 2
Sequence 29, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1
                                                                                                                                                                                                                                                                                                                                      GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - 09-894-882-369
- 09-894-882-167
- 09-749-637A-207
- 08-049-794-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-619-936-1
US-07-789-913-19
US-08-049-19
US-08-08-75-354-19
US-08-675-318-19
US-08-675-318-19
US-09-138-439-19
US-09-298-017-19
US-09-298-017-19
US-09-392-979A-19
US-09-392-979A-19
US-08-049-847-8
US-08-08-913-8
US-08-08-913-8
US-08-08-913-8
US-08-95-918-8
US-08-95-918-8
US-08-95-918-8
US-08-95-918-8
US-08-95-918-8
US-09-138-439-8
US-09-298-017-8
US-09-392-979A-8
US-09-392-979A-8
US-09-392-979A-8
US-09-392-979A-8
US-09-392-979A-8
US-09-392-979A-8
US-09-392-979A-8
US-09-984-882-167
                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-742-774-29
                                                                                                                          US-10-627-685A-26
161
1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                           513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                        Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries
                                                          protein search, using sw model
                                                                                                                                                                         BLOSUM62DX
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                       length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                        Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ........
                                                                                                                                                                                                                                                                                          Post-processing:
                                                                                                                                                                                                                                                       Minimum DB seq
Maximum DB seq
                                                                                                                                         Perfect score:
                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62.5
62.5
62
61
61
61
                                                         protein -
                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                         Database
```

Result No.

```
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /product= "4Hyp"
OTHER INFORMATION: /note= "Amino acid 4 may be 4-trans-hydroxyproline."
                                                                                                                                                                               APPLICANT: Tetrau, Heinrich
APPLICANT: Shon, Ki-Joon
APPLICANT: Grilley, Michelle
TITLE OF INVENTION: Conotoxin Peptide PVIIA
NUMBER OF SEQUENCES:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Mashington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                COUPER: U.S.A.

ZOUPTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 161; DB 1;
Best Local Similarity 100.0%; Pred. No. 3.9e-12;
Matches 27; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24260-107674-04
ALIGNMENTS
                                                                                                          Sequence 1, Application US/08619936
Patent No. 5672682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SARA, STEPHEN A.
REGISTRATION NUMBER: 39,609
REFRENCE/DOCKET NUMBER: 24260
TELEFAX: 202-962-8300
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYRE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disulfide-bond
8..20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disulfide-bond
15..26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disulfide-bond
1..16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY:
; LOCATION:
US-08-619-936-1
```

```
RESULT 2
US-07-789-913-19
i Sequence 19; Application US/07789913
i Patent No. 555905
i GENERAL INFORMATION:
APPLICANT: Miljanich, George P.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Walentino, Karen L.
APPLICANT: Yamashiro, Donald H.
ITILE OF INVENTION: Ischemia-Related Neuronal Damage
NUMBER OF SEQUENCES: 28
CORRESPONDENCES: 28
CORRESPONDENCES: 28
ADDRESSEE: Law Offices of Peter Dehlinger
STREDT: 350 Cambridge Avenue, Suite 300
COTTY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 46.6%; Score 75; DB 1; Length 26; Best Local Similarity 42.3%; Pred. No. 0.023; Matches 11; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TIBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
CURSTRICATION NUMBER: US/07/789,913
FILING DATE: 19911112
CLASSIFICATION NUMBER: US 07/789,913
FILING DATE: 02-MO-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/440,094
FILING DATE: 22-NOV-1989
ATONNEY/AGENT INPORMATION:
REGISTRATION NUMBER: 34,444
RESTERNICE/POCKET UNMBER: 34,444
RESTERNICE/POCKET UNMBER: 34,444
RESTERNICE/POCKET UNMBER: 34,444
RESTERNICE/POCKET UNMBER: 34,444
RELERRATION NUMBER: 34,444
RELERRATION FOR SEO ID NO: 19:
SEQUENCE CHARACTERISTICS:
TURPOTHER: ARMANO ACTION ACTION ACTION
TWO THE COMPUTER SEO ID NO: 19:
SEQUENCE CHARACTERISTICS:
TWO THE COMPUTER ALL ACTION ACTION
TWO THE COMPUTER ALL ACTION
THE COMPUTER ACTION
THE COMPUTER ALL ACTION
THE COMPUTER ALL ACTION
THE COMPUTER ACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-049-794-19
; Sequence 19, Application US/08049794
; Patent No. 5697454
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: GOHIL, KISHOR C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE: SNX-202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ర
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-07-789-913-19
```

Gaps . 0

Indels

1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT JUSTICE, ALAN
APPLICANT SINCH, TEJINDER
APPLICANT SINCH, TEJINDER
APPLICANT GOHLL, KISHOR C
APPLICANT VALENTINO, KAREN L
APPLICANT MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS: ADDRESSE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
STREET: ADD ALCOURTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 46.6%; Score 75; DB 1; Length 26; Best Local Similarity 42.3%; Pred. No. 0.023; Matches 11; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,774
                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,847
FILING DATE: 27-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.31
TELEPRAK: 650-324-0980
TELEPRAK: 650-324-0980
TELEPRAK: 650-324-0960
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TURE amino acids
TURE AMINO ACID ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
US-08-496-847-19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: 08/675,354
FILING DATE: 03-011-1996.
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-APR-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CKLKGQSCSRLMYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19, Application US/08742774
Patent No. 5824645
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94106
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 34,444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stratford, Carol A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-742-774-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19, Application US/08496847

Patent No. 5795864

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bowersox, Stephen S.
APPLICANT: Adrianssens, Peter I.
APPLICANT: Adrianssens, Peter I.
APPLICANT: Adrianssens, Peter I.
APPLICANT: Kristipati, Ramssharma
TITLE OF INVENTION: FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES:
ADDRESSER: Dehlinger & Absociates
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 46.6%; Score 75; DB 1; Length 26; Best Local Similarity 42.3%; Pred. No. 0.023; Matches 11; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/049,794

FILING DATE: 19930415

CLASSITCATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/814,759

FILING DATE: 30-DEC-1991

ATTORNEY/AGENT INFORMATION:

NAME: Strafford, Carol A.

REGISTRATION NUMBER: 34,44

REFERENCE/DOCKET NUMBER: 5865-0009.30

TELLEPHONE: (415) 324-0860

INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Dehlinger & Associates
350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CKLKGQSCSRLMYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Palo Alto
                                                                                                                                                                                                                                                                                                    COUNTRY: US
ZIP: 94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
US-08-496-847-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-049-794-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
```

·.

```
APPLICANT: Amsturz, Gary A.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Gohil, Kishorchandra
APPLICANT: Adriaenseens, Peter I.
APPLICANT: Adriaenseens, Peter I.
APPLICANT: Aristipati, Ramasharma
TITLE OF INVENTION: METHODS AND FORMULATIONS FOR PREVENTING
TITLE OF INVENTION: PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 36
ADDRESSE: Dehlinger & Associates
                                                                                   Length 26;
                                                                                                                          10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,918
FILING DATE: 07-NOV-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Mohr. Judy M.
REGISTRATION NUMBER: 38,563
REFERENCE/DOCKET NUMBER: 5865-0009.34
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                        Query Match

46.6%; Score 75; DB 2;
Best Local Similarity 42.3%; Pred. No. 0.023;
Matches 11; Conservative 5; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 75; DB 2;
Pred. No. 0.023;
5; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
           INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
                                                                                                                                                                1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                       1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CKLKGQSCSRLMYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                 Sequence 19, Application US/08965918
Patent No. 5891849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 19, Application US/09138439
; Patent No. 5994305
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 42.3
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: ' amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S
                    US-08-675-354-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-965-918-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-138-439-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
                                                                                                                                                                  ð
                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR
APPLICANT: GALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: BNHANCING OPIATE ANALGESIA AND
TITLE OF INVENTION: BNHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                          ch 46.6%; Score 75; DB 2; Length 26; 
l Similarity 42.3%; Pred. No. 0.023; 
11; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPER READABLE FORM:
MEDIUM TYPER: Floppy disk
COMPUTER IBM PC compatible
COMPUTER FREADABLE FORM:
MEDIUM TYPER: Flow PC-DOS/MS-DOS
SOFTWARE: PREFERING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PREFERING DATA:
APPLICATION NUMBER: US/08/675,354
FILING DATE: 03-UUL-1996
CLASSIFTCATION: 530
PRIOR APPLICATION: DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 30-DEC-1991
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY AGENT INFORMATION:
NAME: Stratford Carol A.
REGISTRATION NUMBER: 346-CANAGA 3A
                                                                                                                                                                                                                                                          ; INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
US-08-742-774-19
                                                                                                                                                                                                                                                                                                                                                                                                                1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CKLKGQSCSRLMYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-675-354-19
; Sequence 19, Application US/08675354
; Patent No. 5859186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 586.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                      TELECOMMUNICATION INFORMATION TELEPHONE: (415) 324-0880
                                 TELEPHONE: (415) 324-0860
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 aming acids
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 26 amino acids
                                                                                                                                                                                             MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 11; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: JUSTIC
                                                                                                                                                                                                                                           ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE
                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Pal
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

ô

Gaps

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gequence 19, Application US/09298017

Patent No. 6087091

GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: JUSTICE, ALAN
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA
NUMBER OF SEQUENCES:
ADDRESSED: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

46.6%; Score 75; DB 3; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.023;
Matches 11; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patentin Release #1.0, Version #1.25
                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTEXEN FOR Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/613,400A
FILING DATE: 08-MAR-1996
CLASSIFICATION 514
PRICA APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
US-08-613-400A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CKLKGÓSCSRLMYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/09/298,017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MBDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,794
                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 51
TELECOMMUNICATION INFORMATION
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                   ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Pal
STATE: CA
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-298-017-19
  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 46.6%; Score 75; DB 2; Length 26; Best Local Similarity 42.3%; Pred. No. 0.023; Matches 11; Conservative 5; Mismatches 10; Indels
                                       APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: VALENTINO, KAREN L
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA AND
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19, Application US/08613400A
Fatent No. 6054429
GENERAL INFORMATION:
APPLICANT: Bowersox, S. Scott
APPLICANT: Cadbois, Theresa
APPLICANT: Luther, Mark, R.
APPLICANT: Luther, Robert, R.
TITLE OF INVENTION: IMPROVED EPIDURAL
TITLE OF INVENTION: METHOD OF PRODUCING ANALGESIA
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/138,439
                                                                                                                                                                                                          ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-04-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTERNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,44
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CKLKGQSCSRLMYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INPORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
                        SINGH, TEJINDER
GOHIL, KISHOR C
JUSTICE, ALAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                        Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-613-400A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-138-439-19
```

g

```
APPLICANT: Milanich, George P.
APPLICANT: Milanich, George P.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Pox, James A.
APPLICANT: Pox, James A.
APPLICANT: Bitner, Robert S.
APPLICANT: Wanentino, Donald H.
TITLE OF INVENTION: Delayed Treatment Method of Reducing TITLE OF INVENTION: Ischemia-Related Neuronal Damage NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
                                                                                                                                                                  Ouery Match
Best Local Similarity 42.3%; Pred. No. 0.023;
Matches 11; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

44.1%; Score 71; DB 1; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.065;
Matches 11; Conservative 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19911112
CLASSIFICATION NUMBER: US/07/789,913
FILING DATE: 19911112
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/561,766
FILING DATE: 02-04G-1990
FILING DATE: 22-000-1989
ATORNEY/AGENT INFORMATION:
NAME: Strafford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0005.30
TELECOMMUNICATION INFORMATION:
TELEPHOME: (415) 324-0960
INFORMATION PROPRATION:
TELEPHOME: (415) 324-0960
INFORMATION PROR SEQ ID NO: 8:
SEQUENCE CHRRACTERISTICS:
TENDOME: CHRRACTERISTICS:
                                             HYPOTHETICAL: NŌ

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: SNX-202, FIGURE 2

US-09-392-979A-19
                                                                                                                                                                                                                                                                  1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                     | CKLKGQSCSRLMYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/07789913
Patent No. 5559095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 26 amino acids
TYPE: AMINO ACID
TOPOLOGY: both
                      MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-07-789-913-8
                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
46.6%; Score 75; DB 3; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.023;
Matches 11; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/392,979A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSEE: Law Offices of Peter Dehlinger
?: 350 Cambridge Avenue, Suite 300
Palo Alto
ATTORNEY/AGENT INFORMATION:

NAME: Stratford, Carol A.

REGISTRATION NUMBER: 34444

REFERENCE/DOCKET NUMBER: 5865-0009.30

TELEPHONE: (415) 324-0880

TELEPHONE: (415) 324-0960

INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acid
TYPE: amino acid
TOPOLOGY: Linear

MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLIANS LICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-04-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTOMBEY SCRAFTON:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                           ) ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
US-09-298-017-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CRIXNOKCFQHLDDCCSRKCNRFNKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CKLKGÓSCSRLMYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19, Application US/09392979A
Patent No. 6136786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : TELEFAX: (415) 324-0880

INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS: LENGTH: 26 amino acids TYPE: amino acid TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offic
STREET: 350 Cambridg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
US-09-392-979A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
```

Gaps

원 ò

```
APPLICANT: Adriaenssens, Peter I.
APPLICANT: Kristipati, Ramasharma
TITLE OF INVENTION: METHODS AND
TITLE OF INVENTION: FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

44.1%; Score 71; DB 1; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.065;
Matches 11; Conservative 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHII, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: VALENTINO, GORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
                                                                                                                                                                                                 STATE:

CONDTRY:

21P: 94106-1546

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM COMPATIBLE

COMPUTER: IBM COMPATIBLE

COMPUTER: IBM COMPATIBLE

COMPUTER: DS

SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATE:

PILING DATE: 27-JUN-1995

CLASSIFICATION NUMBER: US/08/496,847

PILING DATE: 27-JUN-1995

CLASSIFICATION S14

ATTORNEY/AGENT INFORMATION:

NAME: Stratford, Carol A

REGISTRATION NUMBER: 34,444

REGISTRATION NUMBER: 5865-0009.31

TELECHONE: 650-324-0880

TELEPHONE: 650-324-0880

TELEPHONE: GS0-324-0880

TELEPHONE: GS0-324-0880

TELEPHONE: GS0-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1 US-08-496-847-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
ATREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
                                                                                        NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 cklikejschktsydccsescensekc 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/08742774
Patent No. 5824645
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: Patentin Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: 1; near
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-742-774-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.1%; Score 71; DB 1; Length 26; 42.3%; Pred. No. 0.065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Indels
                                                                                                                                                                                                                                          APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHLL, KISHOR C
APPLICANT: GOHLL, KISHOR C
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA AND
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTE: 743.0

COMPUTE: 743.0

MEDIUM TYPE: Floppy disk

COMPUTE: TBM PC compatible

COMPUTE: TBM PC compatible

COMPUTE: TBM PC compatible

COMPUTE: TBM PC compatible

COMPUTE: TBM PC COMPUTE: 10508/049,794

APPLICATION NUMBE: US/08/049,794

FILING DATE: 19330415

CLASSIFICATION: S14

PRIOR APPLICATION: DATA: APPLICATION: NUMBER: US 07/814,759

FILING DATE: 30-DEC-1991

APPLICATION NUMBER: US 07/814,759

FILING DATE: 30-DEC-1991

APPLICATION NUMBER: 34,444

REGISTRATION NUMBER: 34,444

REGISTRATION NUMBER: 34,444

REFERENCE/DOCKET NUMBER: 5665-0009.30

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Mismatches
                                                    CKLKGQSCRKTSYDCCSGSCGRSGKC 26
                     CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/08049794
Patent No. 5587454
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amstutz, Gary A.
Bowersox, Stephen S.
Gohil, Kishorchandra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/08496847
Patent No. 5795864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 26 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Amstutz
APPLICANT: Bowerso:
APPLICANT: Gohil, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94306
                                                                                                                                     RESULT 13
US-08-049-794-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-08-496-847-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-049-794-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
```

a

· 0

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ameticz, Gary A.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Gohil, Kishorchandra
APPLICANT: Adriaenseens, Peter I.
APPLICANT: Kristipati, Ramasharma
TITLE OF INVENTION: METHODS AND FORMULATIONS FOR PREVENTING
TITLE OF INVENTION: PROGRESSION OF NEUROPATHIC PAIN
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

44.1%; Score 71; DB 2; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.065;
Matches 11; Conservative 4; Mismatches 11; Indels
                                                                                                                                                                                                                                             TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
US-08-675-354-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER. READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 07-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
                                    REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
TELEPAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5865-0009.34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/08965918
Patent No. 5891849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 07-NOV-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Mohr, Judy M.
REGISTRATION NUMBER: 38,563
REFRENCE/DOCKET NUMBER: 5866
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                       Carol A
                                                                                                                                                                                                              26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 26 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         650-324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
ZIP: 94306-1546
                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JS-08-965-918-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-965-918-8
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/08675354
Patent No. 585186
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: GOHIL, KISHOR C
APPLICANT: GOHIL, KISHOR C
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND TITLE OF INVENTION: BNANCING OPLATE ANALGESIA AND TITLE OF SEQUENCES: 34
CORRESPONDENCE ADDRESS: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match

44.1%; Score 71; DB 2; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.065;
Matches 11; Conservative 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSERVE LAW Offices of Peter Dehlinger STREET: 350 Cambridge Avenue, Suite 300 CITY: Palo Alco STATE: CA COUNTRY: USA ZIP: 94306 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION NUMBER: US/08/675,354 FILING DATE: 03-UL-1996 CLASSIFICATION NUMBER: US/08/675,354 FILING DATE: 1993-ADR-15 APPLICATION NUMBER: US/08/675,354 FILING DATE: 1993-ADR-15 APPLICATION NUMBER: US/08/675,354 FILING DATE: 1993-ADR-15 APPLICATION NUMBER: US/08/675,354 FILING DATE: 090-DEC-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/675,354
FILING DATE: 03-JUL-1996
APPLICATION NUMBER: 08/69/949
FILING DATE: 1993-APR-15
APPLICATION NUMBER: 05/0814,759
FILING DATE: 30-DEC-1991
ATTORNEY/ARENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REGISTRATION NUMBER: 5665-0009.30
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ČKLKGÓSČRKTSYDČČSGSČGŘSGKČ 26
TRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,774
                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: Inear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                   FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-742-774-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-675-354-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
```

```
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 586
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 650-324-0960 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                       COUNTRY: US
ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-298-017-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                   APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
      44.1%; Score 71; DB 2; Length 26; 42.3%; Pred. No. 0.065; tive 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 71; DB 2; Length 26;
Pred. No. 0.065;
4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/138,439 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1933-04-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A. REGISTRATION NUMBER: 34,44
REGISTRATION NUMBER: 34,44
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELEPHONE: (415) 324-080
TELEPHONE: (415) 324-080
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
                                                                                                            1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CKLKGQSCRKTSYDCCSGSCGRSGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 8, Application US/08613400A
                                                                                                                                                                                                      US-09-138-439-8
Sequence 8, Application US/09138439
Patent No. 5994305
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 42.3%;
Matches 11; Conservative
                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: NO
Query Match "Best Local Similarity Matches 11; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 19
US-08-613-400A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-138-439-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
44.1%; Score 71; DB 3; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.065;
Matches 11; Conservative 4; Mismatches 11; Indels
APPLICANT: Gadbois, Theresa APPLICANT: Gadbois, Theresa APPLICANT: Datter, R.; APPLICANT: Luther, Robert, R.; TITLE OF INVENTION: IMPROVED EPIDURAL TITLE OF INVENTION: METHOD OF PRODUCING ANALGESIA NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
US-08-613-400A-8
                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
COURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/613,400A
FILING DATE: 08-MAR-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
                                                                                                                                                                                                   ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CKLKGÓSCRKTSYDCCSGSCGRSGKC 26
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 38.8%; Score 62.5; DB 4; Length 36; Best Local Similarity 40.7%; Pred. No. 0.8; Matches 11; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

44.1%; Score 71; DB 3; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.065;
Matches 11; Conservative 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Resbina
APPLICANT: Shetty, Resbina
APPLICANT: Minenez, Elsie C.
APPLICANT: Minenez, Baldomero M.
APPLICANT: Warkins, Maren
APPLICANT: Warkins, Maren
APPLICANT: Warkins, Maren
APPLICANT: Wankins, Robert M.
APPLICANT: Shen, Greg S.
                                                                                                                                                                                                                                                                                                                                                                                                 ; INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
US-09-392-979A-8
                               ATTONNEY CAGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REPERRENCE/POCKET NUMBER: 5865-0009.30
TELECONWUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: I-Superfamily Conotoxins FILE REFERENCE: 2314-238
FULE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-10-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: Patentin version 3.0
SEQ ID NO 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 CLSLGQRCERH-SDCCGYLCCFYDKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 369, Application US/09894882
Patent No. 6767895
                                                                                                                                                                                                                                                                  26 amino acids
                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Conus betulinus
              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: 1 ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-894-882-369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-894-882-369
                                                                                                                                                                                                                                                                  LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 44.1%; Score 71; DB 3; Length 26; l Similarity 42.3%; Pred. No. 0.065; 11; Conservative 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: VALENTINO, FORES P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
                                      COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 APPLICATION DATA: US/09/298,017 PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatchtIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/392,979A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                           34,444
PP: 5865-0009.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,794
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-00
TELECOMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-04-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/09392979A
Patent No. 6136786
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-392-979A-8
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-298-017-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
```

셤

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                        5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                        38.5%; Score 62; DB 4; Length 76; 39.3%; Pred. No. 1.7; ive 6; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.9%; Score 61; DB 1; Length 26; 38.5%; Pred. No. 0.89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRODUCING ANALGESIA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 19930415
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 29, Application US/08049794
; Sequence 29, Application US/08049794
; Patent No. 5587454
; GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: GOHILL, KISHOR C
APPLICANT: GOHILL, KISHOR C
APPLICANT: MILJANICH, GEORGE P
: TITLE OF INVENTION: BEHANCING OPPREDICTION OF THE OF INVENTION: BEHANCING OPPREDICTION OF THE OF INVENTION: BHANCING OPPREDICTION OF THE OF INVENTION: BHANCING OPPREDICTION OF THE OFFICE OF THE OFFICE AND OFFICE SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METHODS OF PRODUCING ANALGENHANCING OPIATE ANALGESIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                  1 CRIXNQKCFQHLDDCCSRKCNRF-NKCV 27
                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE: SNX-230, FIGURE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 19930415
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 409
SOFTWARE: PatentIn version 3.0
SEQ ID NO 207
LENGTH: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                      Query Match
Best Local Similarity 39.34
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 37.9
Best Local Similarity 38.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                TYPE: PRT
; ORGANISM: Conus distans
US-09-749-637A-207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-049-794-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 62.5; DB 4; Length 73; Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Indels
                                                                                                                     APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Cartier, G. Edward
APPLICANT: Watkins, Maren
APPLICANT: Hillyard, David R.
APPLICANT: McIntosh, J. Michael
APPLICANT: Includent, J. Michael
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: O-Superfamily Conotoxin Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: University of Utah Research Foundation
                                                                                                                                                                                                                    APPLICANT: Machael Shetty, Reshma APPLICANT: Jimenez, Elsie C. APPLICANT: Jimenez, Elsie C. APPLICANT: Jimenez, Elsie C. APPLICANT: Jimenez, Baldomero M. APPLICANT: Olivera Baldomero M. APPLICANT: Gones, Robert M. APPLICANT: Shan, Greg S. TITLE OF INVENTION: 1-Superfamily Conotoxins TITLE OF INVENTION: 1-Superfamily Conotoxins CURRENT APPLICATION NUMBER: US 60/29 FRIOR APPLICATION NUMBER: US 60/243,410 FRIOR FILING DATE: 2000-11-08 FRIOR FILING DATE: 2000-11-14 FRIOR APPLICATION NUMBER: US 60/247,714 FRIOR APPLICATION NUMBER: US 60/264,256 FRIOR APPLICATION NUMBER: US 60/264,256 FRIOR FILING DATE: 2001-01-29 SOFTWARE: Patentin version 3.0 SEQ ID NO 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 2314-227
CURRENT APPLICATION NUMBER: US/09/749,637A
CURRENT FILING DATE: 2000-12-28
PRIOR PAPLICATION NUMBER: US 60/243,412
PRIOR PILING DATE: 2000-10-27
PRIOR PILING DATE: 2000-07-20
PRIOR PILING DATE: 2000-07-20
PRIOR PILING DATE: 2000-07-20
PRIOR PILING DATE: 2000-06-26
PRIOR PILING DATE: 2000-06-26
PRIOR PLICATION NUMBER: US 60/214,263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39 CLSLGQRCERH-SDCCGYLCCFYDKCV 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 207, Application US/09749637A Patent No. 6762165
                                                                                       Sequence 167, Application US/09894882
Patent No. 6767895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 40.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Conus betulinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-749-637A-207
                                                                         US-09-894-882-167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-894-882-167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
```

```
; Sequence 29, Application US/08675354
; Patent No. 5859186
; GENERAL INFORMATION:
; APPLICANT: UNSTICE, ALAN
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: WILDANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPLATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.9%; Score 61; DB 2; Length 26; 38.5%; Pred. No. 0.89; tive 4; Mismatches 12; Indels
                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,774
                                              Peter Dehlinger
                                                                                                                                                                                                                                                                                                                           SSEE: Law Offices of Peter Dehlinger
F: 350 Cambridge Avenue, Suite 300
Palo Alto
                                            SEE: Law Offices of Peter Dehling
: 350 Cambridge Avenue, Suite 300
Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | CKGKGAPCRKTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                   PC-DOS/MS-DOS
                                                                                                                    COUNTR:
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
METHR: IEM PC compatible
PC-DOS/MS-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 38.5°
Matches 10; Conservative
                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                            CA
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
STREET: 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-742-774-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-675-354-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                  Sequence 29, Application US/08496847
Patent No. 5795864
GENERAL INFORMATION:
APPLICANT: Ametuz, Gary A.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Golil, Kishorchandra
APPLICANT: Ariaensens, Peter I.
APPLICANT: Kristipati, Ramasharma
TITLE OF INVENTION: METHODS AND
TITLE OF INVENTION: METHODS AND
TITLE OF INVENTION: PORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Deblinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.9%; Score 61; DB 1; Length 26; 38.5%; Pred. No. 0.89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDION TYPE: Diskette
COMPUTER: Diskette
COMPUTER: TBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEG for Windows Version 2.0
CURRENARE: FastSEG for Windows Version 2.0
CURRENARE: DATE: 27-UNN-1995
CLASSIFICATION NUMBER: US/08/496,847
FILING DATE: 27-UNN-1995
CLASSIFICATION 514
ATTORNEY/AGENT INFORMATION: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.31
TELECOMMUNICATION INFORMATION: TELEPRAK: 650-324-0880
TELEFRAK: 650-324-0800
TELEFRAK: 650-324-0800
TELEFRAK: 650-324-0950
TELEFRAK: 650-324-0960
TELEFRAK: FORDING COLD NO: 29: COUNTH: 26 mino acid
TVPE: amino acid
TVPE: Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METHODS OF PRODUCING ANALGE ENHANCING OPIATE ANALGESIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
US-08-496-847-29
1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | CKGKGAPCRKTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: WALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
ITILE OF INVENTION: METHODS OF PF
TITLE OF INVENTION: ENHANCING OP:
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 29, Application US/08742774; Patent No. 5824645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTAIN ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.9.9.
Best Local Similarity 38.5'
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 27
US-08-742-774-29
                   g
```

g

ò

```
; INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
US-09-138-439-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 29, Application US/09138439 Patent No. 5994305
               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: aminc TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94306
                                                                                                                                                                                                              US-08-965-918-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 30
US-09-138-439-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 29, Application US/08965918

Sequence 29, Application US/08965918

Settent No. 5891849

GENERAL INFORMATION:
APPLICANT: Ametuz, Gary A.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Adriaensens, Peter I.
APPLICANT: Adriaensens, Peter I.
APPLICANT: Kristipati, Ramasharma
ITILE OF INVENTION: PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.9%; Score 61; DB 2; Length 26; 38.5%; Pred. No. 0.89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12; Indels
      CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/675,354

FILING DATE: 03-UJL-1996

CLASSIFICATION: 530

PRIOR APPLICATION NUMBER: US/08/049,794

FILING DATE: 1993-ARR-15

APPLICATION NUMBER: US 07/814,759

FILING DATE: 30-DEC-1991

ATTORNEY/AGENT INFORMATION:

NAME: Stratford, Carol A.

REGISTRATION NUMBER: 34.44

REFERENCY/DOCKET NUMBER: 5865-0009.30

TELEFONDE: (415) 324-0860

TELEFONDE: (415) 324-0960

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONTINENT LAN COMPACTION
OFFRATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,918
FILING DATE: 07-NOV-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAMME: MOAR. JUDY M.
REGISTRATION NUMBER: 38,563
REGISTRATION NUMBER: 38,563
REFERENCE/DOCKET NUMBER: 5865-0009.34
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE: SNX-230, FIGURE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CKGKGAPCRKTMYDCCSGSCGRRGKC 26
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 26 amino acida TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 38.5
Marches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 29
US-08-965-918-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-675-354-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 37.9%; Score 61; DB 2; Length 26; Best Local Similarity 38.5%; Pred. No. 0.89; Matches 10; Conservative 4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: SINGH, TEJINDER
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SOUDENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/138,439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Law Offices of Peter Dehlinger STREET: 350 Cambridge Avenue, Suite 300 CITY: Palo Alto STATE: CA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/049,794
FILING DATE: 1993-04-15
APPLICATION NUMBER: US/0814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 5865-0009.30
TELEPHONE: (415) 324-0860
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TOTAL CARLOS CONTRACTOR CARLOS 
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE; SNX-230, FIGURE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | CKGKGAPCRKTMYDCCSGSCGRRGKC 26
```

```
Query Match
Best Local Similarity
....hes 10; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-392-979A-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-298-017-29
                                                APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
      Score 61; DB 2; Length 26;
Pred. No. 0.89;
                                                                     12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.9%; Score 61; DB 3; Length 26; 38.5%; Pred. No. 0.89; Live 4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                      Sequence 29, Application US/08613400A
| Patent No. 605429
| GENERAL INFORMATION:
| APPLICANT: Bowercox, S. Scott
| APPLICANT: Gadbols, Theresa
| APPLICANT: Bettus, Mark, R. |
| APPLICANT: Luther, Nobert, R. |
| TITLE OF INVENTION: IMPROVED EPIDURAL |
| TITLE OF INVENTION: METHOD OF PRODUCING ANALGESIA |
| NUMBER OF SEQUENCES: 36 |
| CORRESPONDENE: 350 Cambridge Avenue, Suite 250 |
| CORRESPONDENE: SECUENCES: 36 |
| CORRESPONDENE: Behlinger & Associates |
| CORRESPONDER: Behlinger & Associates |
| C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/613,400A
FILING DATE: 08-MAR-1996
CLASSIFICATION: 514
PRIOR APPLICATION STA
                                                                     4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
US-08-613-400A-29
                                                                                                                               1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                      1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CKGKGAPCRKTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S.09-298-017-29 ". Sequence 29, Application US/09298017 Patent No. 6087091 GENERAL INFORMATION: APPLICANT: JUSTICE, ALAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A
REGISTRATION NUMBER: 34,444
REFRENCE/DOCKET NUMBER: 5865
TELECOMMUNICATION INFORMATION:
th 37.9%; l Similarity 38.5%; l0; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 650-327 CO. 29
INFORMATION FOR SEQ ID NO: 29
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 37.9
Best Local Similarity 38.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein HYPOTHETICAL: NO
                               Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
ZIP: 94306-1546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                          US-08-613-400A-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-298-017-29
Query Match
                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

```
37.9%; Score 61; DB 3; Length 26; ilarity 38.5%; Pred. No. 0.89; Conservative 4; Mismatches 12; Indels
                                                   METHODS OF PRODUCING ANALGESIA AND ENHANCING OPIATE ANALGESIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF PRODUCING ANALGESIA AND
                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/298,017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: METHODS OF PRODUCING ANALG
TITLE OF INVENTION: ENHANCING OPLATE ANALGESIA
NUMBER OF SEQUENCES: 34
                                           TITLE OF INVENTION: METHODS OF PRODUCING ANY TITLE OF INVENTION: ENHANCING OPIATE ANALGES NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger STREET: 350 Cambridge Avenue, Suite 300 CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5865-0009.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CKGKGAPCRKTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 29, Application US/09392979A; Patent No. 6136786; GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: OOHIL, KISHOR C
APPLICANT: VALENITNO, KAREN L
APPLICANT: MILJANICH, GEORGE P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,794
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTAATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-000
TELECOMMUNICATION INFORMATION:
TELEPANE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
VALENTINO, KAREN L
MILJANICH, GEORGE F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: C
```

94306

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Goodman, Corey,
APPLICANT: Goodman, Corey,
APPLICANT: Rid, Thomas
APPLICANT: Brose, Katja
APPLICANT: Tessier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/540,245A
CURRENT FILING DATE: 2000-03-31
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: 60/081,057
PRIOR FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 36.6%; Score 59; DB 3; Length 735; Best Local Similarity 45.0%; Pred. No. 28; Matches 9; Conservative 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Goodman, Corey
APPLICANT: Brose, Katja
APPLICANT: Brose, Katja
APPLICANT: Tebsier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REPERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/191,647
CURRENT APPLICATION NUMBER: 60/065,544
EARLIER FILING DATE: 1997-11-14
EARLIER FILING DATE: 1997-11-14
EARLIER FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Ratentin Ver. 2.0
SEG ID NO 9
LENGTH: 735
                                                                                                                                                                                                                                                                              12; Indels
                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                         Query Match 37.9%; Score 61; DB 1;
Best Local Similarity 38.5%; Pred. No. 0.97;
Matches 10; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                            1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                          1 : | | | | | | | | | 3 CKGKGAPCRKTMYDCCSGSCGRRGKC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/09540245A Patent No. 6270984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              254 CEKNIDDCVNSKCENGGKCV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/09191647
Patent No. 6046015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 CFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Caenorhabditis elegans US-09-191-647-9
                                                                                29 amino acids
                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
          202-962-8300
                                                                                                                                                MOLECULE TYPE: protein US-08-092-215-9
                                                                                                          TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-540-245A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 35
US-09-191-647-9
                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                              ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 61, DB 3; Length 26;
Pred. No. 0.89;
4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Olivera, Baldomero M.
APPLICANT: Hillyard, David R.
APPLICANT: Hillyard, Julita S.
APPLICANT: Imperial, Julita S.
APPLICANT: Monje, Virginia D.
TITLE OF INVENTION: w-Conotoxin Peptides
NUMBER OF SEQUENCES: 13
CORRESPONDENCES: 13
CORRESPONDENCES: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W., Suite 1000
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/392,979A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/092,215
                                                                                                                                                     PELLICALION
FILING DATE:
CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-04-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REGISTRATION NUMBER: 34,444
REGISTRATION NUMBER: S865-0009.30
TELECOMUNICATION INFORMATION:
TELECHONE: (415) 324-0960
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
"VUDE: amino acids
"VUDE: CLASSIFICATION acids
"VUDE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/ACENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107674
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
US-09-392-979A-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CKGKGAPCRKTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: DC
ZIP: 20005
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/08092215
Patent No. 5591821
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 38.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 34
US-08-092-215-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
```

ï

Gaps

```
Gaps
                                                                                                                                                                                                                                                                                                                    ٦,
                                                                                                                                                                                                                                      35.7%; Score 57.5; DB 4; Length 36; Best Local Similarity 37.0%; Pred. No. 2.9; Matches 10; Conservative 6; Mismarchen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 35.7%; Score 57.5; DB 4; Length 36; Best Local Similarity 37.0%; Pred. No. 2.9; Matches 10; Conservative 6; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AEPOLICANT: Walker, Craig S. APPLICANT: Research Foundation SAPPLICANT: University of Utah Research Foundation APPLICANT: Walker, Craig S. APPLICANT: Walker, Craig S. APPLICANT: Shetty, Reshma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Markins, Marken
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: 1-Superfamily Conctoxins
FILE REFERENCE: 2314-238
CURRENT FILING DATE: 2001-06-29
FRIOR APPLICATION NUMBER: US 60/
PRIOR APPLICATION NUMBER: US 60/
PRIOR APPLICATION NUMBER: US 60/
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR PILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 368
                                                                                                                                                                                                                                                                                                                                                     1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                    2 CLSLGQRCERH-SNCCGYLCCFYDKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CLSLGQRCGRH-SNCCGYLCCFYDKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
              PRIOR FILING DATE: 2000-11-14
PRIOR PEDLICATION NUMBER: US 60/264,256
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: Patentin version 3.0
SEQ ID NO 365
LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 371, Application US/09894882
; Patent No. 6767895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jimenez, Elsie C.
McIntosh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
                                                                                                                                                                                            ; ORGANISM: Conus betulinus
US-09-894-882-365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Conus betulinus
US-09-894-882-368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-894-882-371
                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . q
                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                          GENERAL INCOREATION:
APPLICANT: Goodman, Corey
APPLICANT: Goodman, Corey
APPLICANT: Brose, Katja
APPLICANT: Tessier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/540,153
CURRENT FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: 60/081,057
PRIOR APPLICATION NUMBER: 60/081,057
PRIOR PRILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 735
                                                                                                DB 3; Length 735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 36.6%; Score 59; DB 3; Length 735; Best Local Similarity 45.0%; Pred. No. 28; Matches 9; Conservative 4; Mismatches 7; Indels
                                                                                                                                           7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Shen, Greg S.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: 1-Superfamily Conotcxins
FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-10-27
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
                                                                                       Query Match
Best Local Similarity 45.0%; Pred. No. 28;
Matches 9; Conservative 4; Mismatches
                                                                                                                                                                                                            254 CEKNIDDCVNSKCENGGKCV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 365, Application US/09894882
; Patent No. 6767895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            254 CEKNIDDCVNSKCENGGKCV 273
                                                                                                                                                                                8 CFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/09540153
Patent No. 6270995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 CFQHLDDCCSRKCNRFNKCV 27
                  ORGANISM: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-540-153-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-894-882-365
                                            US-09-540-245A-9
                                                                                                                                                                                                                                                                                                                    US-09-540-153-9
TYPE: PRT
                                                                                                                                                                                ઠે
                                                                                                                                                                                                                           윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

ï

```
Gaps
                                                                                                                                 ;
                                                                           Score 57.5; DB 4; Length 36;
Pred. No. 2.9;
6; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            uvery Match
35.7%; Score 57.5; DB 4; Length 73;
Best Local Similarity 37.0%; Pred. No. 5.5;
Matches 10; Conservative 6; Mismatches 10. 1.2.2.
                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 164, Application US/09894882
Batent No. 6767895
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Galles, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I Superfamily Conotoxins FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US 09/894,882
CURRENT APPLICATION NUMBER: US 60/243,410
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/245,581
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-14
SROR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE PATENTIN VERSION 3.0
SOFTWARE PATENTIN VERSION 3.0
                                                                                                                                                                               1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                               2 CLSLGQRCERH-SNCCGYLCCFYDKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 CLSLGQRCERH-SNCCGYLCCFYDKCV 64
                                                                                                                                                                                                                                                                                                                                                           Sequence 155, Application US/09894882
Patent No. 6767895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jimenez, Elsie C.
McIntosh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jimenez, Elsie C.
McIntosh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
                                                                           Query Match
Best Local Similarity 37.0%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jones, Robert M.
Shen, Greg S.
, ORGANISM: Conus betulinus
US-09-894-882-372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Conus betulinus
                                                                                                                                                                                                                                                                                                                                           JS-09-894-882-155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 43
US-09-894-882-164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-894-882-155
                                                                                                                                                                                                                                  g
                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 57.5; DB 4;
Pred. No. 2.9;
6; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Shetty, Reshma
APPLICANT: Shetty, Reshma
APPLICANT: Minches, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: Watkins, Maren
                                                                                                                                                                                            TITLE OF INVENTION: 1-Superfamily Conotoxins FILE REFERENCE: 2314-238
FILE REFERENCE: 2314-238
FILE REFERENCE: 2314-238
FILE REPERION: 108/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR PLING DATE: 2000-06-30
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR PLICATION NUMBER: US 60/246,581
PRIOR PLICATION NUMBER: US 60/247,714
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR PLICATION NUMBER: US 60/264,256
PRIOR FILING DATE: 2000-11-19
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PATENTIN VETSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TILLE OF INVENTION: 1-Superfamily Conotoxins FILE REFERENCE: 2314-238
FILE REFERENCE: 2314-238
FILE REFERENCE: 2314-238
FILE REFERENCE: 2314-238
CURRENT FILING DATE: 2001-06-29
PRIOR PELING DATE: 2000-06-30
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-38
PRIOR FILING DATE: 2000-11-38
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-29
NUMBER: OS SEQ ID NOS: 506
SOFTWARE: PALENTIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLSLGQRCERH-SNCCGYLCCFYDKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 41
US-09-894-882-372
Sequence 372, Application US/09894882.
Patent No. 6767895
                                           Jimenez, Elsie C.
McIntosh, J. Michael
Olivera, Baldomero M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 37.0%;
Matches 10; Conservative (
                                                                                                                         Watkins, Maren
Jones, Robert M.
Shen, Greg S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jones, Robert M.
Shen, Greg S.
Walker', Craig S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Conus betulinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-894-882-371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 372
LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 371
```

ઠે g 39 CLSLGQRCERH-SNCCGYLCCFYDKCV 64

```
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 35.7%; Score 57.5; DB 4; Length 73; Best Local Similarity 37.0%; Pred. No. 5.5; Matches 10; Conservative 6; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: Shetty, Reshma
APPLICANT: Shetty, Reshma
APPLICANT: Mcntosh, U. michael
APPLICANT: Olivera, Baldomero M. APPLICANT: Olivera, Baldomero M. APPLICANT: Olivera, Markins, Maren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: 1-Superfamily Conotoxins FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2001-01-19
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 57.5; DF
Pred. No. 5.5;
6; Mismatches
        TITLE OF INVESTIGNT

UNRENT APPLICATION NUMBER: US/09/894, E82
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR PILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-10-27
PRIOR PILING DATE: 2000-11-08
PRIOR PILING DATE: 2000-11-14
PRIOR PILING DATE: 2001-11-14
PRIOR PILING DATE: 2001-11-14
PRIOR PILING DATE: 2001-01-29
PRIOR FILING DATE: 2001-01-29
SPRIOR FILING DATE: 2001-01-29
SPRIOR PILING DATE: 2001-01-29
SPRIOR PILING DATE: 2001-01-29
SPRIOR PILING DATE: 2001-01-29
SPRIOR PILING DATE: 2001-01-39
TITLE OF INVENTION: I-Superfamily Conotoxins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 CLSLGQRCGRH-SNCCGYLCCFYDKCV 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 173, Application US/09894882
Patent No. 6767895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 37.0%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jones, Robert M.
Shen, Greg S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Conus betulinus
US-09-894-882-164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Conus betulinus
US-09-894-882-173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-894-882-173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D ID NO 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

```
Sequence 18, Application US/08185432
Patent No. 5750652
GENERAL INFORMATION:
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Busseau, Isabelle
APPLICANT: Diederich, Robert J.
APPLICANT: Matsuno, Kenji
TITLE OF INVENTION: DELFEX PROTEINS, NUCLEIC ACIDS, AND
TITLE OF SEQUENCES: 23
CORRESPONDENCE ADDRESS: 23
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: PENNIE & EDMONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 35.7%; Score 57.5; DB 4; Length 73; Best Local Similarity 37.0%; Pred. No. 5.5; Matches 10; Conservative 6; Mismatches 10; Indels
                                                                                                              APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc. APPLICANT: Walker, Craig S. APPLICANT: Shetty, Reshma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IITLE OF INVENTION: I-Superfamily Conotoxins FILE REFERENCE: 2314-238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR PELING DATE: 2000-06-30
PRIOR PELING DATE: 2000-10-27
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-08
PRIOR PILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2001-11-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 CLSLGQRCERH-SNCCGYLCCFYDKCV 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3: PENNIE & EDMONDS
1155 Avenue of the Americas
Seguence 176, Application US/09894882
Patent No. 6767895
                                                                                                                                                                                                                                                                            Jimenez, Elsie C.
McIntosh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
Jones, Robert M.
Shen, Greg S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Conus betulinus
US-09-894-882-176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-185-432-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
```

۲;

```
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 2523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
CITY: WA
                                                                                                                                                                                                                                                                                                                                                                   US-08-937-236-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-899-232-3

Sequence 3, Application US/08899232

Sequence 3, Application US/08899232

Sequence 3, Application US/08899232

Sequence 3, Application

GENERAL INCORMATION:

APPLICANT: 01, Hullin

TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON

FILE REFERENCE: 7326-046

CURRENT APPLICATION NUMBER: US/08/899,232

CURRENT FILING DATE: 1997-07-23

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 48
US-09-121-457-3
US-09-121-457-3
Sequence 3, Application US/09121457
Patent No. 6692919
GENERAL INFORMATION:
APPLICANT: Artavanis-Tsakonas, S.
APPLICANT: Rand, M.
TITLE OF INVENTION:
FILE REFERENCE: 7326-673
CURRENT FILE OF INVENTION: US/09/121,457
CURRENT APPLICATION NUMBER: US/09/121,457
CURRENT FILE OF INVENTION: US/09-07-23
EARLIER APPLICATION NUMBER: 08/899,232
FARLIER PILLING DATE: 1997-07-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,432
FILING DATE: 21-JAN-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MASTOCK, S. Leblie
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 18,872
RELEFENCE/OFFORTION INFORMATION:
TELEFONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEFAX: (614) PERNIE
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 57; DB 4;
Pred. No. 1.4e+02
4; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 57; DB Pred. No. 1.4e 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249 SGONCEENIDDCPSNNCRNGGTCV 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249 SGONCEENIDDCPSNNCRNGGTCV 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 XNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 XNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 37.5%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                              2523 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 37.59
                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-08-185-432-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Xenopus sp.
US-08-899-232-3
                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 3
LENGTH: 2523
                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

```
GENERAL INFORMATION:
APPLICANT: MANN, BARBARA J.
APPLICANT: PETRI, MILLIAM A.
APPLICANT: PETRI, MILLIAM A.
APPLICANT: DODSON, JAMES M.
TITLE OF INVENTION: RECOMBINANT ENTAMOEBA HISTOLYTICA LECTIN
TITLE OF INVENTION: SUBUNIT PEPTIDES AND REAGANTS SPECIFIC FOR MEMBERS OF THE
TITLE OF INVENTION: 170 KD SUBUNIT MULTIGENE FAMILY
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                            ö
                                                                                                                                              Gaрв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gape
                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3; Length 1277;
                                                                                            Length 2523;
                                                                                                                                          11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C: 2000 PENNSYLVANIA AVENUE N.W., STE. 5500 WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA

ZIP: 200006-1812

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin Rc-los/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
                                                                                            Score 57; DB 4; I
Pred. No. 1.4e+02;
4; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         703 CSMGTDNIITYHDDCNSRKSQCGNFNGKCV 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 35.1%; Score 56.5; D
Best Local Similarity 43.3%; Pred. No. 87;
Matches 13; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CRIXNOKCFOHLDDCCSRK--CNRFN-KCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            291482000622
                                                                                                                                                                                                                     249 SGONCEENIDDCPSNNCRNGGTCV 272
                                                                                                                                                                                        4 XNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/569,214
FILING DATE: 16 SEPTEMBER 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08937236
Patent No. 6187310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: LIVNAT, SHMUEL
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: 2914
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFRX: (202) 887-0763
TELEF RX: 90-4030
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33,949
                                                                                            Query Match 35.4%;
Best Local Similarity 37.5%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1277 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TYPE: PRT
ORGANISM: Xenopus sp.
US-09-121-457-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
```

```
APPLICANT: MANN, BARBARA J.
APPLICANT: PETRI, MILLIAM A.
APPLICANT: PETRI, MILLIAM A.
APPLICANT: DODSON, JAMES M.
TITLE OF INVENTION: RECOMBINANT ENTAMOEBA HISTOLYTICA LECTIN
TITLE OF INVENTION: SUBUNIT PEPTIDES AND REAGANTS SPECIFIC FOR MEMBERS OF THE
TITLE OF INVENTION: 170 KD SUBUNIT MULTIGENE FAMILY
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Э,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3; Length 1292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE N.W., STE. 5500
CITY: WASHINGTON
                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 200006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,236
                                                                                                                                                                                   FILING WALE:

FILLING JALE:

PRIOR APPLICATION 1944

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/06890

FILING DATE: 17-JUN-1994

ATTORNEY/AGENT INFORMATION:

NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 9148-0006.21

TELEPHONE: (202) 887-1500

TELEPHONE: (202) 887-1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 56.5; D
Pred. No. 88;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CRIXNOKCFQHLDDCCSRK--CNRFN-KCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: 291482000622
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/569,214
FILING DATE: 16 SEPTEMBER 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/08937236
Patent No. 6187310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 1292 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 43.33
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (202) 887-076
TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: WASH
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                          APPLICANT: MANN, BARBARA J.
APPLICANT: PETRI, WILLIAM A.
TITLE OF INVENTION: RECOMBINANT ENTANDEBA HISTOLYTICA LECTIN
TITLE OF INVENTION: SUBUNIT PETPIDES AND REAGANTS SPECIFIC FOR MEMBERS OF THE
TITLE OF INVENTION: 170 KD SUBUNIT MULTIGENE FAMILY
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORALSON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE N.W., STE. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08569214
Patent No. 6165469
GENERAL INFORMATION:
APPLICANT: MANN, BARRARA J.
APPLICANT: PETRI, WILLIAM A.
TITLE OF INVENTION: RECOMBINANT ENTAMORBA HISTOLYTICA LECTIN
TITLE OF INVENTION: SUBUNIT PEPTIDES AND REAGANTS SPECIFIC FOR MEMBERS OF THE
TITLE OF INVENTION: 170 KD SUBUNIT MULTIGENE FAMILY
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
STREET: 2000-PENNSYLVANIA AVENUE N.W., STE. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1292;
                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
35.1%; Score 56.5; D
Best Local Similarity 43.3%; Pred. No. 88;
Matches 13; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                718 CSMGTDNIITYHDDCNSRKSQCGNFNGKCV 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06890
FILING DATE: 17-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 9148-0006.21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CRIXNOKCFOHLDDCCSRK--CNRFN-KCV 27
                                       Sequence 5, Application US/08569214
Patent No. 6165469
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1292 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-08-569-214-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200006-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 51
US-08-569-214-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
```

Gaps

```
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Drosophila sp.
                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-185-432-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 55
US-08-899-232-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-899-232-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-121-457-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                             5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 19, Application US/08185432

| Patent No. 5750652
| GENERAL INFORMATION:
| APPLICANT: Artavania-Teakonas, Spyridon APPLICANT: Buseau, Isaabelle APPLICANT: Diederich, Robert J. APPLICANT: Xu, Tian APPLICANT: Watsuno, Kenji TITLE OF INVENTION: DELFEX RECTEINS, NUCLEIC ACIDS, AND TITLE OF INVENTION: ANTIBODIES, AND RELATED.METHODS AND COMPOSITIONS OF SEQUENCES: 23
                                                                                                                                                                                                                                                           3;
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/09641612

Betent No. 6703221

GENERAL INFORMATION:

THORMATION:

TITLE OF INVENTION:

FILE REFERENCE: PPO-1602.002 / 200130.498

CURRENT FILIGN DATE: 2000-08-17

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 585
                                                                                                                                                                                                                     DB 3; Length 1292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 34.8%; Score 56; DB 4; Length 585; Best Local Similarity 37.9%; Pred. No. 50; Matches 11; Conservative 2; Mismatches 14; Indels
                                                                                                                                                                                                                                                         11; Indels
                                                                                                                                                                                                             35.1%; Score 56.5; DE
43.3%; Pred. No. 88;
tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                         1 CRIXNQKCFQHLDDCCSRK--CNRFN-KCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        377 CRAGFAGPRCEHDLDDCAGRACANAGTCV 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CR -- IXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            i LOCATION: (1)...(585)
i OTHER INFORMATION: Xaa = Any Amino Acid
US-09-641-612-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEF S 90-4030
INFORMATION FOR SEC ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1292 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                         13; Conservative
                                                                                                             ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-937-236-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 54
US-08-185-432-19
                                                                                                                                                                                                                                                                                                                                                                                           RESULT 53
US-09-641-612-5
                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

```
GENERAL INFORMATION:
APPLICANT: Arcavania-Trakonas, Spyridon
APPLICANT: Arcavania-Trakonas, Spyridon
TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS CHEREON
TITLE OF INVENTION: ACTIVATED FORMS
CURRENT APPLICATION NUMBER: US/08/899, 232
CURRENT FILING DATE: 1997-07-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Artavanis-Teakonas, S.
APPLICANT: Artavanis-Teakonas, S.
APPLICANT: A.H.
APPLICANT: Rand, M.
TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON FILE REFERENCE: 7326-073
CURRENT PAPLICATION NUMBER: US/09/121, 457
CURRENT FILING DATE: 1998-07-23
EARLIER APPLICATION NUMBER: 08/899, 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
34.8%; Score 56; DB 1; Length 2703;
Best Local Similarity 33.3%; Pred. No. 1.9e+02;
Matches 9; Conservative 5; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2703;
OFFRANTING SYSTEM: C-LUCY FGS-LUCS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,432
FILING DATE: 21-JAN-1994
CLASSIFICATION: 530
ATYONENY/AGENT INFORMATION:
NAME: MASTOCK S. Leslie
REGISTRATION NUMBER: 18,872
REFRENCE/DOCKET NUMBER: 7326-006
TELEPRAX: (212) 790-9090
TELEPRAX: (212) 790-9090
TELERAX: (212) 700-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 56; DB 4; 1
Pred. No. 1.9e+02;
5; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           822 TGÓKCETNIDDCVTNPCGNGGTCI 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                822 TGÓKCETNIDDCVTNPCGNGGTCI 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 XNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 XNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08899232
Patent No. 6436650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09121457
Patent No. 6692919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 34.8%;
Best Local Similarity 33.3%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2703 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 2703'
```

```
APPLICANT: Miljanich, George P.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Fox, James A.
APPLICANT: Fox, James A.
APPLICANT: Valentino, Karen L.
APPLICANT: Stanshiro, Donald H.
TITLE OF INVENTION: Delayed Treatment Method of Reducing TITLE OF INVENTION: Ischemia-Related Neuronal Damage CORRESPONDENCES. 28
CORRESPONDENCES. 28
CORRESPONDENCES. Daw Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

34.5%; Score 55.5; DB 1; Length 25;
Best Local Similarity 38.5%; Pred. No. 3.6;
Matches 10; Conservative 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: 194306

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: TEM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/07/789,913
FILING DATE: 19911112
CLASSIFFCATION: DATA:
APPLICATION NUMBER: US 07/561,766
FILING DATE: 02-AMG-1990
FILING DATE: 10-AMG-1990
FILING DATE: 22-NOV-1989
FILING DATE: 22-NOV-1989
FILING DATE: 22-NOV-1989
FILING DATE: 324-444
REFERENCE/DOCKET NUMBER: 3444

REFERENCE/DOCKET NUMBER: 5865-0005.30
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | CKGKGASCHRISYDCCTGSCNR-GKC 25
                                                                                                            Sequence 2, Application US/07789913
Patent No. 5559095
GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 2, Application US/08049794; Patent No. 5587454; GENERAL INPORMATION: APPLICANT: SINGH, TEJINDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 25 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: pe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                             JS-07-789-913-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-07-789-913-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-049-794-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          원
                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: MVIIB Omega conotoxin.
IDENTIFICATION METHOD: Direct peptide
IDENTIFICATION METHOD: sequencing of purified Conus magus venom
                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                          Query Match
34.8%; Score 56; DB 4; Length 2703;
Best Local Similarity 33.3%; Pred. No. 1.9e+02;
Matches 8; Conservative 5; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:

APPLICANT: David Hillyard

APPLICANT: Baldomero M. Olivera

TITLE OF INVENTION: Segregated Folding Determinants

TITLE OF INVENTION: for Small Disulfide-Rich Peptides

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Thorpe, No. 5231011th & Western

STREFT: 9035 South 700 East, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIREEL: 3033 SOULE (U.C.)

CITY: Sandy
STATE: Utah
COUNTRY: USA
ZIP: 84070
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage
COMPUTER: Compaq LTR/286
OPERATING SYSTEM: DOS 4.01
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/689,693B
FILING DATE: 19910418
CLASSIFTCATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: none
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
34.5%; Score 55.5; Di
Best Local Similarity 38.5%; Pred, No. 3.6;
Matches 10; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                       822 TGQKCETNIDDCVTNPCGNGGTCI 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CKGKGASCHRTSYDCCTGSCNR-GKC 25
                                                                                                                                                                                                                                                                                                          4 XNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/07689693B Patent No. 5231011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Western, M. Wayne
REGISTRATION NUMBER: 22,788
REFERENCE/DOCKET NUMBER: 9925
TELECOMMUNICATION INFORMATION:
TELEFAM: (801) 566-6730
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACIDS
TOPOLOGY: linear
EARLIER FILING DATE: 1997-07-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 2703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: na
ATTORNEY/AGENT INFORMATION:
                                                                                                                 TYPE: PRT
ORGANISM: Drosophila sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 57
US-07-689-693B-2
                                                                                                                                                                US-09-121-457-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-07-689-693B-2
                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
```

1;

Gaps

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 34.5%; Score 55.5; DB 1; Length 25; Best Local Similarity 38.5%; Pred. No. 3.6; Matches 10; Conservative 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: SINGH, TEJINDER
APPLICANT: GALEN, TESHORE
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
STRIET: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,774
                                                                                                             OPERATING STEM: COMPANDED OF STEM: DOS CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/08/496,847
FILING DATE: 27-JUN-1995
CLASSIFCATION: 514
ATTOMNEY/AGENT INFORMATION: NAME: Stratford, Carol A REGISTRATION NUMBER: 5865-0009.31
TELEROMMUNICATION INFORMATION: TELERAX: 650-324-0880
TELERAX: 650-324-0880
TELERAX: 650-324-0860
TELERAX: CHARACTERISTICS: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE: MVIIB/SNX-159, FIGURE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/675,354
FILING DATE: 03-JUL-1996
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-APR-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CKGKGASCHRTSYDCCTGSCNR-GKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08742774 Patent No. 5824645
                                                                                     COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stratford, Carol A
                                                                          Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . FILING DATE:
CLASSIFICATION:
                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08496847

Patent No. 5795864

GENERAL INFORMATION:
APPLICANT: Amstutz, Gary A.
APPLICANT: Gohil, Kiehorchandra
APPLICANT: Adriaenseens, Peter I.
APPLICANT: Adriaenseens, Peter I.
APPLICANT: Kristipati, Ramasharma
TITLE OF INVENTION: METHODS AND
TITLE OF INVENTION: PORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
APPLICANT: GOHÍL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: WALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 34.5%; Score 55.5; DB 1; Length 25; Best Local Similarity 38.5%; Pred. No. 3.6; Matches 10; Conservative 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/049,794

FILING DATE: 19930415

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/814,759

FILING DATE: 30-DEC-1991

ATTORNEY/AGENT INFORMATION:

NAME: Strafford, Carol A.

REGISTRATION NUMBER: $865-0009.30

TELECOMMUNICATION NUMBER: $865-0009.30

TELECOMMUNICATION NUMBER: $865-0009.30

TELECOMMUNICATION NUMBER: $865-0009.30

TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE: MVIIB/SNX-159, FIGURE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CKGKGASCHRISYDCCIGSCNR-GKC 25
                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94306-1546
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 60
US-08-496-847-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-049-794-2
```

ä

```
Query Match 34.5%; Score 55.5; DB 2; Length 25; Best Local Similarity 38.5%; Pred. No. 3.6; Matches 10; Conservative 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Amstuz, Gary A.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Gohil, Kishborchandra
APPLICANT: Gohil, Kishborchandra
APPLICANT: Adriaensens, Peter I.
APPLICANT: Kristipati, Ramasharma
TITLE OF INVENTION: METHODS AND FORMUATIONS FOR PREVEI
TITLE OF INVENTION: PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 36
CORRESPENDENCE ADDRESS:
ADDRESSE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.5%; Score 55.5; DB 2; 38.5%; Pred. No. 3.6; tive 4; Mismatches 11;
                   ; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: MVIIB/SNX-159, FIGURE 1
US-08-675-354-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Comparible
OPERATING SYSTEM: DOS
SOFTWARE: FastESQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,918
FILING DATE: 07-NOV-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: MVIIB/SNX-159, FIGURE 1
                                                                                                                                                                                                            1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                          |: : | : | | | CKGKGASCHRISYDCCIGSCNR-GKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08965918
Patent No. 5891849
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 64
US-009-168-168-2
'Sequence 2, Application US/09039168
'Patent No. 5965534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Mohr, Judy M.
REGISTRATION NUMBER: 38,563
REFRENCE/DOCKET NUMBER: 586:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 38.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US
ZIP: 94306-1546
                                                                                                                                                                                                                                                                                                                                                        US-08-965-918-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-965-918-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE:
                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                           Query Match 34.5%; Score 55.5; DB 2; Length 25; Best Local Similarity 38.5%; Pred. No. 3.6; Matches 10; Conservative 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: WALENTINO, KAREN L
APPLICANT: WILJANICH, GEORGE P
TITLE OF INVENTION: BNHANCING OPIATE ANALGESIA
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSES: LAW OFF:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
PELIGATION NUMBER: US/08/675,354
FLING DATE: 03-JUL-1996
CLASSIFICATION: 530
RIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-ARP-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                             ; INDIVIDUAL ISOLATE: MVIIB/SNX-159, FIGURE 1
US-08-742-774-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEE: Law Offices of Peter Dehlinger: 350 Cambridge Avenue, Suite 300 Palo Alto
                        REFERENCE/DOCKET NUMBER: 5865-0009.30 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CKGKGASCHRISYDCCTGSCNR-GKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CRIXNOKCFQHLDDCCSRKCNRFNKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
REGISTRATION NUMBER: 34,444
                                                                   TELEPHONE: (415) 324-0860
TELERAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 25 anino acids TYPE: amino acids TOPOLOGY: linear
                                                                                                                                                                                                                                     MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 25 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 62
US-08-675-354-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d
```

ä

Gaps

```
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Bowersox, S. Scott
APPLICANT: Gadbois, Theresa
APPLICANT: Gadbois, Theresa
APPLICANT: Gatbois, Mark, R.
APPLICANT: Luther, Robert, R.
TITLE OF INVENTION: IMPROVED EPIDURAL
TITLE OF INVENTION: METHOD OF PRODUCING ANALGESIA
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESSE:
ADDRESSE: ABORESSE:
CITY: Palo Alto
                 COMPUTER READABLE FORM:
MEDIUM TYPE: Flappy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/138,439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 34.5%; Score 55.5; DB 2; Best Local Similarity 38.5%; Pred. No. 3.6; Matches 10; Conservative 4; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US

ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/613,400A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE: NVIIB/SNX-159, FIGURE 1
                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-04-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REFERENCE/DOCKET NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION: NECRMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .ersa.
...ork: US/08/613,400A
08-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CKGKGASCHRTSYDCCTGSCNR-GKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08613400A
Patent No. 6054429
                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 324-0860
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-138-439-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                     TITLE OF INVENTION: The Use of w-Conctoxin Analogs For TITLE OF INVENTION: Treating Retinal and Optic Nerve Head Damage NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Alcon Laboratories, Inc. STREET: 6201 South Freeway, Patent Legal CITY: Fort Worth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.5%; Score 55.5; DB 2; Length 25; 38.5%; Pred. No. 3.6; tive 4; Mismatches 11; Indels
                                                                                                                                                                                                                               APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: VALENTINO, KAREN L
APPLICANT: WILJANITON, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: EMBANCING OPIATE ANALGESIA AND
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
    Pang, lok-Hou; Kapin, Michael and Hellberg,
Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/562,142
APPLICATION NUMBER: 08/5634ember 22, 1995
FILING DATE: NO. 596534ember 22, 1995
ATTORNEY/AGENT INFORMATION:
NAME: MAYO, MICHAEL C.
REGISTRATION NUMBER: 1462
TELECOMMUNICATION INFORMATION:
TELEPRAK: (817) 551-4610
INFORMATION FOR SEQ ID NO: 2:
SEQUERACE CHARACTERICATICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Law Offices of Peter Deblinger
350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 65
10S-09-138-439-2
1 Sequence 2, Application US/09138439
1 Patent No. 5994305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 38.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JUSTICE, ALAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: JUSTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Palo Alto
GENERAL INFORMATIÖN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-039-168-2
```

g

```
ä
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                              ;
                                                                                                                                                           Query Match 34.5%; Score 55.5; DB 3; Length 25; Best Local Similarity 38.5%; Pred. No. 3.6; Matches 10; Conservative 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: JUNCKALIUE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: GOHIL, KISHOR C
APPLICANT: GOHIL, KISHOR C
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/392,979A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34.5%; Score 55.5; DB 3; 38.5%; Pred. No. 3.6; tive 4; Mismatches 11;
                           ) ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: MVIIB/SNX-159, FIGURE 1
US-09-298-017-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INDIVIDUAL ISOLATE: MVIIB/SNX-159, FIGURE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-04-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 384444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (115) 3.24-0880
                                                                                                                                                                                                                                                                                       1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                         1 CKGKGASCHRTSYDCCTGSCNR-GKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 2, Application US/09392979A
; Patent No. 6136786
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 38.5:
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 68
US-09-392-979A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-392-979A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHL, KISHOR C
APPLICANT: WALENTINO, KAREN L
APPLICANT: MILANICH, GEORGE P
TITLE OF INVENTION: ENHANCING OPPRODUCING ANALGESIA
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Indels
                        | NAME: Stratford, Carol A | NAME: Stratford, Carol A | REGISTRATION NUMBER: 34,444 |
| REGISTRATION NUMBER: 34,444 |
| REFERENCE/DOCKET NUMBER: 566-0019 |
| TELECOMMUNICATION INPORMATION: TELEPHONE: 650-324-0860 |
| TELEPHONE: 650-324-0860 |
| TELEPAX: 650-324-080 |
| T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/298,017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 34.5%; Score 55.5; DB 3; Best Local Similarity 38.5%; Pred. No. 3.6; Matches 10; Conservative 4; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
FILING DATE:
CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,794
FILING DATE:
NAME: Strafford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELEPOMUNICATION INFORMATION:
TELEPAN: (415) 324-0960
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CKGKGASCHRTSYDCCTGSCNR-GKC 2.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09298017
Patent No. 6087091
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 67
US-09-298-017-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
```

```
FILING DATE: 22-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 72
5189020-1
;Patent No. 5189020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5424218-2
;Patent No. 5424218
                                                          . LENGTH: 25
5424218-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 25
                             SEQ ID NO:2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO:2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5189020-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5189020-2
                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 71
5424218-2
Patent No. 5424218
PAPLICANT: MILJANICH, GEORGE P.; BITNER, ROBERT S.; BOWERSOX,
STEPHEN S.; FOX, JAMES A.; VALENTINO, KAREN L.; YAMASHIRO, DONALD H.
TITLE OF INVENTION: SCREENING METHOD FOR NEUROPROTECTIVE COMPOUNDS;
                                                                                            APPLICANT: Milijanich, George P.; Bitner, Robert S.; Bowersox,
Stephon S.; Fox, James A.; Valentino, Karen L.; Yamashiro, Donald
; H.; Teubokawa, Makoto
; TITLE OF INVENTION; METHOD OF REDUCING NEURONAL DAMAGE USING; OMEGA CONOTONIN PEPTIDES
; MARBER OF SEQUENCES: 29
; CURRENT APPLICATION DATA;
; APPLICATION NUMBER: US/07/561,766
; FILING DATE: 02-AUG-1990
; PRIOR APPLICATION DATA:
; REPLICATION NUMBER: 440,094
; SEQ ID NO:1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H., Teubokawa, Makoto
M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 5189020; APPLICANT: Milijanich, George P.;Bitner, Robert S.;Bowersox, Stephen S.;Fox, James A.;Valentino, Karen L.;Yamashiro, Donald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.5%; Score 55.5; DB 6; Length 25; 38.5%; Pred. No. 3.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 34.5%; Score 55.5; DB 6; Best Local Similarity 38.5%; Pred. No. 3.6; Matches 10; Conservative 4; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CKGKGASCHRTSYDCCTGSCNR-GKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CKGKGASCHRTSYDCCTGSCNR-GKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 21
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,714
FILLING DATE: 04-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 855,269
FILING DATE: 23-WAR-1992
APPLICATION NUMBER: 561,766
FILING DATE: 02-AUG-1990
APPLICATION NUMBER: 440,094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 440,094
FILING DATE: 22-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 38.5<sup>3</sup>
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO:2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 70
5189020-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5189020-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5189020-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
```

```
ä
                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Milijanich, George P.;Bitner, Robert S.;Bowersox, ;Stephen S.;Fox, James A.;Valentino, Karen L.;Yamashiro, Donald; H.;Tsubokawa, Makoto ; TITLE OF INVENTION: METHOD OF REDUCING NEURONAL DAMAGE USING;OMEGA CONOTOXIN PEPTIDES NUMBER OF SEQUENCES: 29 ; CURRENT APPLICATION NUMBER: US/07/561,766 ; RILING DATE: 02-AUG-1990 ; PRIOR APPLICATION DATA: 20 ; RILING APPLICATION DATA: 20 ; RILIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 55.5; DB 6; Length 25;
Pred. No. 3.6;
4; Mismatches 11; Indels
Score 55.5; DB 6; Length 25;
Pred. No. 3.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 55.5; DB 6; Length 25; Pred. No. 3.6;
                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                      11;
                                                                                                      4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
                                                                                                                                                                                                                                            1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CKGKGASCHRTSYDCCTGSCNR-GKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CKGKGASCHRTSYDCCTGSCNR-GKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 440,094
FILING DATE: 22-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 38.5%;
Matches 10; Conservative 4
                 Query Match
Best Local Similarity 38.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 38.5%;
Matches 10; Conservative
```

```
,
US-07-689-693B-1
                                                                                                                                                                                                                                                                                                                                    US-08-937-236-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-569-214-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 77
                                                                                                                                                                                            ò
                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
APPLICANT: MILJANICH, GEORGE P.; BITNER, ROBERT S.; BOWERSOX,
TITLE OF INVENTION: SCREENING, KAREN L.; YAMASHIRO, DONALD H.
TITLE OF INVENTION: SCREENING METHOD FOR NEUROPROTECTIVE COMPOUNDS
TUTNER OF SEQUENCES: 21
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,714
FILING DATE: 04-00V-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 855,269
FILING DATE: 23-MAR-1992
APPLICATION NUMBER: 561,766
FILING DATE: 02-MG-1990
APPLICATION NUMBER: 561,766
FILING DATE: 22-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: David Hillyard
APPLICANT: Baldomero M. Olivera
TITLE OF INVENTION: Segregated Folding Determinants
TITLE OF INVENTION: Segregated Folding Determinants
TITLE OF INVENTION: Los Small Disulfide-Rich Peptides
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thorpe, No. 5231011th & Western
STREET: 9035 South 700 East, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage COMPUTER: Compag LTE/286
COMPUTER: DOS 4.01
SOFTWARE: Word Perfect 5.1
SOFTWARE: Word Perfect 5.1
SOFTWARE: 19910418
FILING DATE: 19910418
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: none
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Prepropeptide sequence for four-loop
NAME/KEY: MVIIB Omega conotoxin from Conus magus.
IDENTIFICATION METHOD: Libraries were created
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

34.5%; Score 55.5; DB 6;
Best Local Similarity 38.5%; Pred. No. 3.6;
Matches 10; Conservative 4; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PILING DATE: na
ATTORNEY/AGENT INFORMATION:
NAME: WASTERNIN W. WAYNE
REGISTRATION NUMBER: 22,788
REFERENCE/DOCKET NUMBER: 9925
TELECOMMUNICATION INFORMATION:
TELEPHONE: (801) 566-0750
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/07689693B
Patent No. 5231011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: , peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Sandy
STATE: Utah
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                       LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 75
US-07-689-693B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                 SEQ ID NO:2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE
                                                                                                                                                                                                                                                                                                                                                                             5424218-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

```
APPLICANT: MANN, BARBARA J.
APPLICANT: PETRI, WILLIAM A.
APPLICANT: PETRI, WILLIAM A.
APPLICANT: POSSON, JAMES M.
TITLE OF INVENTION: RECOMBINANT ENTAMOEBA HISTOLYTICA LECTIN
TITLE OF INVENTION: SUBUNIT PEPTIDES AND REAGANTS SPECIFIC FOR MEMBERS OF THE
TITLE OF INVENTION: 170 KD SUBUNIT MULTIGENE FAMILY
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
IDENTIFICATION METHOD: using oligo-dT primed pUC13 vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1276;
                                                                                Length 71;
                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE N.W., STE. 5500
CITY: WASHINGTON
                                                                                                                           11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PRELICATION NUMBER: US/08/937,236
FILING DATE:
                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

34.5%; Score 55.5; DB 3;
Best Local Similarity 40.0%; Pred. No. 1.1e+02;
Matches 12; Conservative 4; Mismatches 11;
                                                                                                                         4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
34.5%; Score 55.5;
Best Local Similarity 38.5%; Pred. No. 9;
Matches 10; Conservative 4; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CRIXNOKCFQHLDDCCSRK--CNRFN-KCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 291482000622
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
                                                                                                                                                                                             1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPATIBLE: FLOPPY disk
MEDIUM TYPE: FLOPPY disk
                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08937236
Patent No. 6187310
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/569,214
FILING DATE: 16 SEPTEMBER 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08569214
Patent No. 6165469
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33,949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 3;
SEQUENCE CHARACTERISTICS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1276 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: LIVNAT, SHMUEL REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: amino acid
; STRANDEDNESS: sin
; TOPOLOGY: linear
US-08-937-236-3
```

```
GENERAL INFORMATION:
APPLICANT: MANN, BARBARA J.
APPLICANT: PETRI, WILLIAM A.
TITLE OF INVENTION: RECOMBINANT ENTAMOEBA HISTOLYTICA LECTIN
TITLE OF INVENTION: SUBINIT PEPTIDES AND REAGANTS SPECIFIC FOR MEMBERS OF THE
TITLE OF INVENTION: 1.70 KD SUBUNIT MULTIGENE FAMILY
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34.5%; Score 55.5; DB 3; Length 1291;
40.0%; Pred. No. 1.1e+02;
tive 4; Mismatches 11; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE N.W., STE. 5500
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/569,214
                                                                                                                                   CLASSIPTOATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/569,214
FILING DATE: 16 SEPTEMBER 1997
ATTORNEY/AGENT INFORMATION:
NAME: LIVNAT, SHMUEL
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: 291482000622
TELEPHONE: (202) 887-1500
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  717 CSMGTDNIITYHDDCNSRKSQCGNFNGKCI 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CRIXNQKCFQHLDDCCSRK--CNRFN-KCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06890
FILING DATE: 17-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: MUNASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9148-0006.21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 200006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08569214
Patent No. 6165469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 91
TELECOMMUNICATION INPORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1291 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 40.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LITY: WASHINGTON STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino
TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-569-214-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                    APPLICANT: PETRI, WILLIAM A.

TITLE OF INVENTION: RECOMBINANT ENTAMOEBA HISTOLYTICA LECTIN

TITLE OF INVENTION: SUBUNIT PEPTIDES AND REAGANTS SPECIFIC FOR MEMBERS OF THE

TITLE OF INVENTION: 170 KD SUBUNIT MULTIGENE FAMILY

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 2000 PENNSYLVANIA AVENUE N.W., STE. 5500

CITY: MASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RECOMBINANT ENTAMOEBA HISTOLYTICA LECTIN
SUBUNIT PEPTIDES AND REAGANTS SPECIFIC FOR MEMBERS OF THE
170 KD SUBUNIT MULTIGENE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: MORRISON & FOERSTER
2000 PENNSYLVANIA AVENUE N.W., STE. 5500
                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.5%; Score 55.5; DB 3; 40.0%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               717 CSMGTDNIITYHDDCNSRKSQCGNFNGKCI 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION: 424
PRIOR APPLICATION DATA;
APPLICATION NUMBER: PCT/US94/06890
FILING DATE: 17-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: WURASHIGE, KATE H.
REGISTRATION WUMBER: 29,959
REFERENCE/DOCKET NUMBER: 9148-0006.21
TELEFRANCE/ORDER INFORMATION:
TELEFRANCE/CATION INFORMATION:
TELEFRANCE/CATION INFORMATION:
TELEFRANCE/CATION 10FORMATION:
TELEFRANCE/CATION 10FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CRIXNQKCFQHLDDCCSRK--CNRFN-KCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 200006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08937236 Patent No. 6187310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: MANN, BARBARA J.
APPLICANT: PETRI, WILLIAM A.
APPLICANT: DODSON, JAMES M.
TITLE OF INVENTION: RECOMBINANT
TITLE OF INVENTION: 170 KD SUBINIT PER
TITLE OF INVENTION: 170 KD SUBINIT PER
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
       MANN', BARBARA J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1291 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 40.0°
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (202) 887-076
TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: Bir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
US-08-569-214-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: ZUUC
TTY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 78
US-08-937-236-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

Gaps

ë

us-10-627-685a-26.rai

```
US-08-496-847-21

Sequence 21, Application US/08496847

Patent No. 5795864

GENERAL INFORMATION:
APPLICANT: Amstutz, Gary A.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Gohil, Kishorchandra
APPLICANT: Gohil, Kishorchandra
APPLICANT: Kristipati, Ramasharma
ITTLE OF INVENTION: METHODS AND
ITTLE OF INVENTION: FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 36
CORRESPONDENCES: 36
CORRESPONDENCES: 36
STREET: 350 Cambridge & Associates
STREET: 350 Cambridge Avenue
CITY: Palo alt-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.2%; Score 55; DB 1; Length 26; 47.4%; Pred. No. 4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 7
OTHER INFORMATION: /note= "where X is hydroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONTIGET IN COMPARIATION OF SECULAR OF STATEM COMPARIATION DATA:
SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,847
FILING DATE: 27-UN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAMME: Stratford, Carol A
REGISTRATION NUMBER: 34,444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 5865-0009.31
TELECOMUNICATION INFORMATION:
TELEPHONE: 650-324-0860
TELEFAX: 650-324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 21, Application US/08742774
Patent No. 5824645
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: GOHIL, KISHOR C
                        8 CFOHLDDCCSRKCNRFNKC 26
                                                  8 CRKTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 CFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 CRKTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 47.41
Best Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-496-847-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-742-774-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 82
                                                       Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                  Score 55.5; DB 3; Length 1295;
Pred. Nc. 1.1e+02;
4; Mismatches 11; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                                                                                                                                                       Sequence 21, Application US/08049794

Patent No. 5587454

GENERAL INFORMATION:

APPLICANT: JUSTICE, ALAN

APPLICANT: GOHIL, KISHOR C

APPLICANT: GOHIL, KISHOR C

APPLICANT: MILJANICH, GEORGE P

TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND

TITLE OF INVENTION: BHANCING OPIATE ANALGESIA AND

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: 7
; OTHER INFORMATION: /note= "where X is hydroxyproline"
US-08-049-794-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DUS/MB-DUS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PEDICATION NUMBER: US/08/049,794
FILING DATE: 19930415
CLASSIFICATION: 514
PRICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATFORNEY/AGENT INFORMATION:
NAME: STRATION NUMBER: 34,444
REGISTRATION NUMBER: 34,444
REGISTRATION NUMBER: 34,444
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELEPRATION INFORMATION:
TELEPRACE (415) 324-0960
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LEMGTH: 26 amino acids
LYYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124.2%; Score 55; DB 1; ity 47.4%; Pred. No. 4.3; servative 2; Mismatches
                                                                                                                                                                                                                                        117 CSMGTDNIITYHDDCNSRKSQCGNFNGKCI 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Law Offices of Peter Dellinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                           1 CRIXNQKCFQHLDDCCSRK--CNRFN-KCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                Query Match
34.5%;
Best Local Similarity 40.0%;
Matches 12; Conservative
    1295 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Modified-site

// TYPE: amino acid
// TOPOLOGY: linear
// MOLECULE TYPE: protein
US-08-569-214-2

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 47.4
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                     US-08-049-794-21
LENGTH:
                                                                                                                              Query Match
                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                   g
```

```
Sequence 21, Application US/08965918
Fatent No. 5891849
Fatent No. 5891849
Fatent No. 5891849
FAPPLICANT: Bowersox, Stephen S.
FAPPLICANT: Gary A.
FAPPLICANT: Advisorsesnes, Peter I.
FAPPLICANT: Kristipati, Ramasharma
FITLE OF INVENTION: METHODS AND FORMULATIONS FOR PREVENTING
FITLE OF INVENTION: PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
FORRESPONDENCE ADDRESS FORRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 34.2%; Score 55; DB 2; Length 26; Best Local Similarity 47.4%; Pred. No. 4.3; Matches 9; Conservative 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 7
OTHER INFORMATION: /note= "where X is hydroxyproline"
                                                                                                                                                           COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENT PRESSENT PRESSENT PAPLICATION DATA:
APPLICATION NUMBER: US/08/675,354
FILING DATE: 03-UL.1996
CLASSIFICATION NUMBER: US/08/049,794
FILING DATE: 1993-ARR-15
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-ARR-15
APPLICATION NUMBER: US/08/049,794
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: STRAEFORY, CAROL AS REGISTRATION NUMBER: 34,44
REFERENCE/DOCKET NUMBER: 34,44
REFERENCE/DOCKET NUMBER: 3865-0009.30
TELEPHONE: (415) 324-0960
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acide
TYPE: amino acide
TYPE: amino acide
TYPE: amino acide
TYPE: APPENDENCE
NUMBER: POTCEIN
HYPOTHETICAL: NO
              i: Law Offices of Peter Dehlinger
350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 CFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B CRKTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
              ADDRESSEE: Law C
STREET: 350 Camb
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-675-354-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-965-918-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.2%; Score 55; DB 2; Length 26; 47.4%; Pred. No. 4.3; tive 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; · · LOCATION: 7
; OTHER INFORMATION: /note= "where X is hydroxyproline"
US-08-742-774-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: GOHIL, KISHOR C
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA AND
TITLE OF INVENTION: SHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:

PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/675,354
FILING DATE: 03-JUL-1996
APPLICATION NUMBER: 08/049,794
FILING DATE: 1993-APR-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: STEATEGAG CAROL A.
REGISTRATION NUMBER: 5865-0009.30
TELEPHONE: (415) 324-0960
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-675-354-21
; Sequence 21, Application US/08675354
; Patent No. 5859186
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 CFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 CRKTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 47.4%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 83
```

Gaps

```
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/613,400A
FILING DATE: 08-MAR-1996
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: SLEACFORD, CAROL A
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0019
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
34.2%; Score 55; DB
Best Local Similarity 47.4%; Pred. No. 4.3;
Matches 9; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                              SNX-231, FIGURE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 21, Application US/08613400A
Patent No. 6054429
                                           NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFRENCE/DOCKET NUMBER: 5865.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 CRKTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 CFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Modified-site LOCATION: 7
                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  650-324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RY: US
94306-1546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: C. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

34.2%; Score 55: DB 2; Length 26;
Best Local Similarity 47.4%; Pred. No. 4.3;
Matches 9; Conservative 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: /note= "where X is hydroxyproline"
US-08-965-918-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHLL, KISHOR C
APPLICANT: GOHLL, KISHOR C
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA AND
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Vereion 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,918
FILING DATE: 07-00-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MOHA: JUMP 83 563
REFERENCE/DOCKET NUMBER: 5865-0009.34
REGISTRATION NUMBER: 5865-0009.34
TELEPHONE: 650-324-0880
INFORMATION FOR SED ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Law Offices of Peter Dehlinger
350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-04-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21, Application US/09138439
Patent No. 5994305
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 CFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: Modified-site
LOCATION: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Law Of
STREET: 350 Cambi
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-138-439-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

```
Gaps
                                                                                                                     ö
                                                                       Length 26;
                                                                                                                     8; Indels
; OTHER INFORMATION: /note= "where X is hydroxyproline"
US-09-138-439-21
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bowersox, S. Scott
APPLICANT: Gadbois, Theresa
APPLICANT: Gadbois, Theresa
APPLICANT: Duther, Robert, R.
APPLICANT: Luther, Robert, R.
TITLE OF INVENTION: IMPROVED EPIDURAL
TITLE OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Ralo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
```

ö

```
APPLICANT: JUSTICE, ALAN
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: VALENTINO, KAREN C
APPLICANT: WALENTINO, KAREN D
APPLICANT: MILANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 55, DB 3; Length 26; Pred. No. 4.3; 2; Mismatches 8; Indels
    DB 3; Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 7
OTHER INFORMATION: /note= "where X is hydroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:

ZIP: 94306
COMPUTER HEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/392,979A
FILING DATE:
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-04-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-190:
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
PUERPERNCE/DOCKET NUMBER: 5865-0009.30
  Query Match
34.2%; Score 55; DB 3
Best Local Similarity 47.4%; Pred. No. 4.3;
Matches 9; Conservative 2; Mismatches
                                                                                                                                                                                                                                                      Sequence 21, Application US/09392979A Patent No. 6136786 GENERAL INFORMATION:
                                                                                              8 CFQHLDDCCSRKCNRFNKC 26
                                                                                                                           8 CRKTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 CFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B CRKTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION
TELEPHONE; (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 26 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Palo Alto
                                                                                                                                                                                                                                   JS-09-392-979A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-392-979A-21
                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                     Length 26;
                                                                                                                                       LOCATION: 7
CTHER INFORMATION: /note= "where X is hydroxyproline"
US-08-613-400A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: GOHIL, KISHOR C
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
MUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         i LOCATION: 7

CTHER INFORMATION: /note= "where X is hydroxyproline"
US-09-298-017-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIR Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/298,017
                                                                                                                                                                                                                                Score 55; DB 3;
Pred. No. 4.3;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Law Offices of Peter Dehlinger STREET: 350 Cambridge Avenue, Suite 300 CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,794
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 34,444
REPERENCA/DOCKET NUMBER: 5865-0009.30
TELEPHONE: (415) 324-0880
TELEPHONE: (415) 324-0880
INFORMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acide
TTPE: amino acide
                                           ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-231, FIGURE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOUNCE:
INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21, Application US/09298017
Pacent No. 6087091
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TELINDER
APPLICANT: GOHIL, KISHOR C
                                                                                                                                                                                                                                                                                                                                                         CRKTMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                              8 CFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                   Query Match
Best Local Similarity 47.4%;
Matches 9; Conservative ;
                                                                                                               NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Modified-site
MOLECULE TYPE: 'protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 87
US-09-298-017-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
```

ö

Gaps

. 0

```
Query Match
33.9%; Score 54.5; DB 1; Length 25;
Best Local Similarity 38.5%; Pred. No. 4.7;
Matches 10; Conservative 5; Mismatches 10; Indels
          Delayed Treatment Method of Reducing
Ischemia-Related Neuronal Damage
28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bowless, Stephen S. APPLICANT: Bowless, Stephen S. APPLICANT: Pox, James A. APPLICANT: Pox, James A. APPLICANT: Pathtino, Karen L. APPLICANT: Stiner, Robert S. Tarlic OF INVENTION: Delayed Treatment Method of Reducing TITLE OF INVENTION: Ischemia-Related Neuronal Damage CORRESPONDENCE ADDRESS: 28
ADDRESSEE: Law Offices of Peter Dehlinger
                                                                                                                                                                                                                                                                                                                               CURREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/789,913
FILING DATE: 19911112
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
FILING DATE: 02-A004-1990
FILING DATE: 02-A004-1990
FILING DATE: 02-A007-1990
FILING DATE: 22-A007-1990
FILING DATA:
APPLICATION NUMBER: US 07/440,094
FILING DATE: 22-A007-1990
FILING DATE: 32-A07-1990
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0005.30
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TITLE OF INVENTION: Delayed Treatment Metho TITLE OF INVENTION: Ischemia-Related Neuron NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger STREET: 350 Cambridge Avenue, Suite 300 CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Law Offices of Peter Dehlinger 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | CKGKGAKCSRLMYDCCTGSC-RSGKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 92
US-07-789-913-9
; Sequence 9, Application US/07789913
; Patent No. 5559095
                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORPATING SYSTEM: PC-DOS/MS-
SOFTWARE: Patentin Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Miljanich, George P.
Bowersox, Stephen S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 350 CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Miljan
                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                       94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-07-789-913-1
                                                   Sequence 9481, Application US/09949016
| Patent No. 681339
| GENERAL INFORMATION:
| PATENT NEWARTION:
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| CURRENT FILING DATE: 2000-04-14
| PRIOR PILING DATE: 2000-10-20
| PRIOR PILING DATE: 2000-10-03
| PRIOR FILING DATE: 2000-10-03
| PRIOR FILING DATE: 2000-09-08
| NUMBER OF SEQ ID NOS: 207012
| SOFTWARE: FASESEQ for Windows Version 4.0
| SEQ ID NO 9481
| LENGTH: 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2. Application US/09641612

Sequence 2. Application US/09641612

GENERAL INFORMATION:

APPLICANT: Vivien Chan et al.

TITLE OF INVENTION: NOTCH RECEPTOR LIGANDS AND USES THEREOF

FILE REPERENCE: PPO-1602.002 / 200130.458

CURRENT APPLICATION NUMBER: US/09/641,612

CURRENT FILING DATE: 2000-08-17

NUMBER: FSEC ID NOS: 10

SOFTWARE: FSECSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 583

TYPE: PRT

TYPE: PRT

COGANISM: Homo sapiens

US-09-641-612-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.2%; Score 55; DB 4; Length 473; 44.0%; Pred. No. 54; cive 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 37.9%; Pred. No. 65;
Matches 11; Conservative 2; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              375 CRAGFAGPRCEHDLDDCAGRACANGGTCV 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CR--IXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 RIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fox, James A.
Valentino, Karen L.
Bitner, Robert S.
Yamashiro, Donald H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 91
US-07-789-913-1
; Sequence 1, Application US/07789913
; Patent No. 5559095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Miljanich, George P. Bowersox, Stephen S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 11; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Miljani,
APPLICANT: Bowers
APPLICANT: Fox, Jan
APPLICANT: Valenti,
APPLICANT: Pitner,
APPLICANT: Yamashi,

; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-641-612-2
```

셤

```
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C.
APPLICANT: VALENTINO, KAREN L.
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 33.9%; Score 54.5; DB 1; Length 25; Best Local Similarity 38.5%; Pred. No. 4.7; Matches 10; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUW TYPE: RIJOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 19930415
CLASSIFICATION NUMBER: US 07/814,759
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REFERENCE/DOCKET NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
OIGHIAN ISOURCE:
RIDIVIDUAL ISOLATE: MVIIA/SNX-111, FIGURE 1
                                          ATTORNEY AGENT 1070 DEC-1991
ATTORNEY AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34 44
REGISTRATION NUMBER: 5865-0009.30
TELEPHONE: (415) 324-0860
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 1:
LENGTH: 25 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/08049794
Patent No. 5587454
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 30-DEC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                       TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 350 Camb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-049-794-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-049-794-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
33.9%; Score 54.5; DB 1; Length 25;
Best Local Similarity 38.5%; Pred. No. 4.7;
Matches 10; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: GOHIL, KISHOR C
APPLICANT: MILANINO, KAREN L
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices C
CITVET: 350 C-C
CITVET: SINGH CONTROLLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTKI: C. ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: TEM PC compatible
COPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/789,913
FILING DATE: 19911112
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/561,766
FILING DATE: 02-MG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/440,094
FILING DATE: 22-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0005.30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Law Offices of Peter Dehlinger STREET: 350 Cambridge Avenue, Suite 300 CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 93
US-08-049-794-1
; Sequence 1, Application US/08049794
; GENERAL INFORMATION:
; APPLICANT: UNSTICE, ALAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: C. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-07-789-913-9
```

ð

```
Sequence 9, Application US/08496847

Patent No. 5795864

GENERAL INFORMATION

APPLICANT: Ametutz, Gary A.

APPLICANT: Bowersox, Stephen S.

APPLICANT: Gohil, Kishorchandra

APPLICANT: Adriaenseens Peter I.

APPLICANT: Kristipati, Ramabharma

TITLE OF INVENTION: METHODS AND

TITLE OF INVENTION: PORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Deblinger & Associates

STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 33.9%; Score 54.5; DB 1; Length 25; Best Local Similarity 38.5%; Pred. No. 4.7; Matches 10; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08742774

Patent No. 5824645

GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: GOHIL, KISHOR C
APPLICANT: MLENTINO, KAREN C
APPLICANT: MLENTINO, KAREN C
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND TITLE OF INVENTION: BHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US

ZIP: 94306-1546

ZIP: 94306-1546

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: BE COMPUTED:
COMPUTER: DISKETTE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,847
FILING DATE: 27-TUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: STRETEORY
CLASSIFICATION: 34,444

REGISTRATION: ARANGE: 3665-0009.31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; INDIVIDUAL ISOLATE: SNX-190, FIGURE 2
US-08-496-847-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CKGAGAKCSRLMYDCCTGSC-RSGKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-742-774-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DP
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Mastuz, Gary A.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Golil, Kishorchandra
APPLICANT: Adriaenssens, Peter I.
APPLICANT: Kristipati, Ramasharma
TITLE OF INVENTION: METHODS AND
TITLE OF INVENTION: FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ij
                                                                                                                                                                                                                1;
                                                                                                                                                                 Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 25
                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                         10;
                                                                                                                                                Query Match
33.9%; Score 54.5; DB 1;
Best Local Similarity 38.5%; Pred. No. 4.7;
Matches 10; Conservative 5; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,847
FILING DATE: 27-JUN-1995
CLASSIFICATION: 514
ATTOMNEY/AGENT INFORMATION:
NAME: Stratford, Carol A
REGISTRATION NUMBER: 34,444
REPERBENCE/DOCKET NUMBER: 5865-0009.31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.9%; Score 54.5; DB 1; 38.5%; Pred. No. 4.7; ttive 5; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INDIVIDUAL ISOLATE: MVIIA/SNX-111, FIGURE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Deblinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                           ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: SNX-190, FIGURE 2
US-08-049-794-9
                                                                                                                                                                                                                                             1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                       1 CKGAGAKCSRLMYDCCTGSC-RSGKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CKGKGAKCSRLMYDCCTGSC-RSGKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08496847
Patent No. 5795864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTAL
ZIP:
4306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 650-344-001 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: TENGTH: 25 amino acids
              MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 38.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein HYPOTHETICAL: NO
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ns
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: P
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-496-847-1
                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
```

1: Law Offices of Peter Dehling 350 Cambridge Avenue, Suite 300

Palo Alto

RESULT 96

ADDRESSEE:

STREET:

```
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Law Offices of Peter Dehlinger STREET: 350 Cambridge Avenue, Suite 300 CITY: Palo Alto
                                  FILING DATE: 03-JUL-1996
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-APR-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REEFERNECE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
INFORMATION FOR SEQ 1D NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 33.9%; Score 54.5; Best Local Similarity 38.5%; Pred. No. 4. Matches 10; Conservative 5; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-190, FIGURE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 5865-0009.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRICE APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-APR-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/675,354
FILING DATE: 03-JUL-1996
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08675354
Patent No. 5859186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Stratford, Carol A REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                        25 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
PRIOR APPLICATION DATA APPLICATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-742-774-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 54.5; DB 2; Length 25; Pred. No. 4.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PILICATION NUMBER: US/08/742,774
FILING DATE:
                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
PILICATION NUMBER: US/08/742,774
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: UUSTICE, ALAN
APPLICANT: USINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: MILANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGE;
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: MVIIA/SNX-111, FIGURE 1
US-08-742-774-1
                                                                                                                                                                                      FILING TABLE

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/675,354
FILING DATE: 03-JUJ-1996
APPLICATION NUMBER: 08/08/049,794
FILING DATE: 1393-APR-15
APPLICATION NUMBER: US 0/814,759
FILING DATE: 30-DEC-1991
ATTOMENY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
FELECOMMUNICATION INFORMATION:
TELEPAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CRIXNOKCFQHLDDCCSRKCNRFNKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/08742774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 10; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-742-774-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 98
```

```
ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SERVERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHL, KISHOR C
APPLICANT: GOHL, KISHOR C
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: ENTHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENTHODS OF PRODUCING ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: BM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PETENTIN BATA:

APPLICATION NUMBER: US/08/675,354

FILING DATE: 03-011-1996

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/049,794

FILING DATE: 30-DEC-1991

ATTORNEY AGENT INFORMATION:

NAME: Stratford, Carol A.

REGISTRATION NUMBER: 3865-0009,30

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0960

INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHRACTERISTICS:

LENGTH: 25 amino acide

TOPPING AGENT INFORMATION:

TELEPAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHRACTERISTICS:

LENGTH: 25 amino acide

TOPPING AGENT INFORMATION:

TOPPING AGENT INFORMATION:

TELEPAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHRACTERISTICS:

LENGTH: 25 amino acide

TOPPING AGENT INFORMATION:

TOPPING AGENT INFORMATION:

TOPPING AGENT INFORMATION:

TOPPING AGENT INFORMATION:

TOPPING AGENT INFORMATION: 9: SEQUENCE CHRACACERISTICS:

LENGTH: 25 amino acide

TOPPING AGENT INFORMATION:

TOPPING AGENT IN
                                  TELEFA: (415) 324-0880

INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acids
TOPOLGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
CNIGITAL SOURCE:
INDIVIDUAL ISOLATE: MVIIA/SNX-111, FIGURE 1
US-08-675-354-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
33.9%; Score 54.5; DB 2;
Best Local Similarity 38.5%; Pred. No. 4.7;
Matches 10; Conservative 5; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLAGY: lipear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-190, FIGURE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | CKGKGAKCSRLMYDCCTGSC-RSGKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application US/08675354
Patent No. 5859186
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
```

Search completed: April 18, 2005, 20:39:52 Job time : 31.5 secs

ή:

Appli Appli Appli Appli Appli Appli

Sequence Sequence Sequence Sequence Sequence Sequence

Sequence 1

Sequence

```
Sequence 384, App Sequence 223, App Sequence 228, App Sequence 258, App Sequence 268, App Sequence 218, App Sequence 318, App Sequence 318, App Sequence 350, App Sequence 34, App Sequence 224, App Sequence 234, App Sequence 234,

      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0
      0

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.9
37.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
683.85
68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
         4 M _{2} M _{2} M _{2} M _{3} M _{2} M _{3} M _{2} M _{3} M _{3}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13, Appl
23, Appl
4, Appli
                                                                                                                                                                                                 April 18, 2005, 20:29:42; Search time 91.5 Seconds (without alignments) 98.077 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published Applications AA:*

1: \cgn2_6/ptodata/1/pubpaa/NSO7 PUBCOMB.pep:*

2: \cgn2_6/ptodata/1/pubpaa/PCT NEW PUB.pep:*

3: \cgn2_6/ptodata/1/pubpaa/NSO6 NEW PUB.pep:*

4: \cgn2_6/ptodata/1/pubpaa/NSO6 NEW PUB.pep:*

5: \cgn2_6/ptodata/1/pubpaa/NSO7 NEW PUB.pep:*

6: \cgn2_6/ptodata/1/pubpaa/NSO7 NEW PUB.pep:*

7: \cgn2_6/ptodata/1/pubpaa/NSO8_NEW PUB.pep:*

8: \cgn2_6/ptodata/1/pubpaa/NSO8_NEW PUB.pep:*

9: \cgn2_6/ptodata/1/pubpaa/NSO8_PUBCOMB.pep:*

10: \cgn2_6/ptodata/1/pubpaa/NSO8_PUBCOMB.pep:*

11: \cgn2_6/ptodata/1/pubpaa/NSO8_PUBCOMB.pep:*

12: \cgn2_6/ptodata/1/pubpaa/USO9_NEW PUB.pep:*

13: \cgn2_6/ptodata/1/pubpaa/USO9_NEW PUB.pep:*

14: \cgn2_6/ptodata/1/pubpaa/USO9_NEW PUB.pep:*

15: \cgn2_6/ptodata/1/pubpaa/USO9_NEW PUB.pep:*

16: \cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

16: \cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

17: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*

18: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*

18: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*

19: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*

19: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*

10: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*

10: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*

10: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*

10: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*

10: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1421835
                                 5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-352-254-24
US-10-627-685-24
US-10-352-254-19
US-10-352-254-12
US-10-627-685-9
US-10-627-685-12
US-10-627-685-18
US-10-627-685-18
US-10-627-685-18
US-10-627-685-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-627-685-13
US-10-627-685-23
US-10-352-254-4
                                                                                                                                                                                                                                                                                                                   US-10-627-685A-26
161
1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1421835 segs, 332370683 residues
                                 GenCore version
(c) 1993 - 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 0%
Match 100%
first 100 summaries
                                                                                                                                             protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                         BLOSUM62DX
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54445445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                            Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum Maximum Maximum N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match 1
```

Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence 3

Post-processing:

Database

Title: Perfect score:

Sequence:

.

OM protein

ü ü

Run

Scoring table:

Searched:

Sequence 1 Sequence 1 Sequence 1

Sequence Sequence Sequence

Sequence

Sequence

Seguence

Sequence Sequence Sequence Sequence

Sequence

Sequence

Sequence 1 Sequence 1 Sequence 1

Sequence 359, App Sequence 359, App Sequence 5, Appli Sequence 5, Appli Sequence 26, Appli

1000.0 98.1 98.1 98.1 98.1 98.1 98.1 97.5 97.5

161 158 158 158 158 158 157 157 157

Score

Result No.

```
APPLICANT: Jones, Robert M. APPLICANT: Jones, Robert M. APPLICANT: Temple, Davis APPLICANT: Temple, Davis APPLICANT: Pemple, Davis McIncael, J. Michael APPLICANT: Oliveza, Baldomero M. TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants FILE REFERENCE: 2314-254 CURRENT APPLICATION NUMBER: US/10/352,254 CURRENT FILING DATE: 2002-01-29 PRIOR APPLICATION NUMBER: US 60/352,219 PRIOR APPLICATION NOWER: US 60/352,219 PRIOR PILING DATE: 2002-01-29 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Pemberton Goodman, Karen
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: Olivera, Baldomero M.
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                  Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 27;
                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                             ; Score 161; DB 15;
Pred. No. 1.2e-12;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.1%; Score 158; DB 15; I
96.3%; Pred. No. 2.8e-12;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: Pemberton-Goodman, Karen
                                                                                                                                                                                                                                                                                                                        1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                               1 CRIANQKCFQHLDDCCSRKCNRFNKCV 27
            PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/155,135
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 24
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CKIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/10352254
Publication No. US20030224343Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/10352254
Publication No. US20030224343A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                           100.0%;
96.3%; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEATURE: COLLE PALPAGECEIS

NAME/KEY: PEPTIDE
LOCATION: (1)..(27)

OTHER INFORMATION: Xaa is Hyp
US-10-352-254-9
                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Conus purpurascens
US-10-627-685-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                            Best Local Similarity 96.33
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 96.35
Matches 26; Conservative
                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: COGNELY, Inc.

APPLICANT: COGNELY, Inc.

APPLICANT: Cognetix, Inc.

APPLICANT: University of Utah Research Foundation

APPLICANT: University of Utah Research Foundation

APPLICANT: Demberton-Goodman, Karen

APPLICANT: Temple, Davis

APPLICANT: Temple, Davis

APPLICANT: MoIntera, Baldomero M.

TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants

FILE REFERENCE: 2314-254

CURRENT APPLICATION NUMBER: US/10/352,254

CURRENT FILING DATE: 2003-01-29

PRIOR FILING DATE: 2003-01-29

PRIOR FILING DATE: 2002-01-29

NUMBER OF SEO ID NOS: 28

SOFTWARE: PatentIn Ver. 2.0

LENGTH: 27
                                                                                                                                                      Sequence 391, 2
Sequence 392, 2
Sequence 391, 2
                                                                                           Sequence 235,
Sequence 6999,
Sequence 9, A
                               Sequence 236,
Sequence 390,
Sequence 235,
                                                                                                                                                                                                                Sequence 392
Sequence 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                        Sequence 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 1f1; DB 15; Length 27; 96.3%; Pred. No. 1.2e-12; iive 1; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Pemberton, Karen E.
APPLICANT: Pemple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: Cones, Robert M.
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION UNMER: US/10/627,685
    US-09-910-082A-390
US-10-755-926-236
US-10-755-926-390
US-09-910-082A-235
US-10-765-926-235
US-10-269-93-6999
US-10-269-776-9
US-09-910-082A-391
US-09-910-082A-391
US-09-910-082A-392
US-10-765-926-392
US-10-765-926-392
US-09-910-082A-238
US-09-910-082A-238
US-09-910-082A-238
US-09-910-082A-238
                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION VINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/219,438
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 24, Application US/10352254
Publication No. US20030224343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24, Application US/10627685
Publication No. US20040092447A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Publication No. US20030224343A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 96.3
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         -10-352-254-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-352-254-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-627-685-24
    Query Match
g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Tember Out, Agree B.
APPLICANT: Tember Out, Agree B.
APPLICANT: Tember Out, Agree B.
APPLICANT: Layer, Richard T.
APPLICANT: Jones, Robert M.
APPLICANT: Jones, Robert M.
APPLICANT: Gonetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/10/627,685
CURRENT FILING DATE: 2003-07-28
PRIOR PILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO. 12
LEMETH: 27
LEM
                                                                                                              APPLICANT: COGNES, ADDECTOR.

TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/10/627,685
CURRENT FILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 1999-09-22
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VET. 2.0
ENGTHARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.1%; Score 158; DB 15;
96.3%; Pred. No. 2.8e-12;
tive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 98.1%; Score 158; DB 15; Best Local Similarity 96.3%; Pred. No. 2.8e-12; Matches 26; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CKIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/10627685
Publication No. US20040092447A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
CTHER INFORMATION: Xaa is Hyp
US-10-627-685-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Conus purpurascens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 96.33
Matches 26, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Concerts, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Pemberton-Goodman, Karen
APPLICANT: Jones, Robert M.
APPLICANT: Temple, Davis
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conctoxins as Organ Protectants
CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT FILING DATE: 2003-01-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 98.1%; Score 158; DB 15; Length 27; Best Local Similarity 96.3%; Pred. No. 2.8e-12; Matches 26; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
98.1%; Score 158; DB 15;
Best Local Similarity 96.3%; Pred. No. 2.8e-12;
Matches 26; Conservative 1; Mismatches 0;
PRIOR APPLING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 60/352,219
PRIOR FILING DATE: 2003-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 27
TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CRIXNOKCYQHLDDCCSRKCNRFNKCV 27
                                                  CURRENT APPLICATION NUMBER: US/10/352,254 CURRENT FILING DATE: 2003-01-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CRIXNQKCFQHLDDCCARKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/352,219 PRIOR FILING DATE: 2002-01-29 NUMBER OF SEQ ID NOS: 28 SOFTWARE: PATENTIN VEY: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 18, Application US/10352254; Publication No. US20030224343A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/10627685
Publication No. US20040092447A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cornell-Bell, Ann H. APPLICANT: Pemberton, Karen E. APPLICANT: Temple Jr., Davis L. APPLICANT: Layer, Richard T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
COTHER INFORMATION: Xaa is Hyp
US-10-352-254-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     i LOCATION: (1)...(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-12
                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 18
LENGTH: 27
```

```
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
CURRENT APPLICATION NUMBER: US,10/352,254
CURRENT PILING DATE: 2003-01-28
FRIOR APPLICANTON NUMBER: US 60/352,219
PRIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 98.1%; Score 158; DB 15; Length 27; Best Local Similarity 96.3%; Pred. No. 2.8e-12; Matches 26; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                             APPLICANT: Temple Jr., Davis L.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: MoCabe, R. Tyler
APPLICANT: Jones, Robert M.
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REPRENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/10/627,685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: Pemberton-Goodman, Karen
APPLICANT: Jones, Robert M.
1 CRIXNQKCYQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VET: 2.0
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18, Application US/10627685
Publication No. US20040092447A1
GENERAL INFORMATION:
APPLICANT: Cornell Bell, Ann H.
APPLICANT: Pemberton, Karen E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13, Application US/10352254
Publication No. US20030224343A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
FORTER INFORMATION: Xaa is Hyp
US-10-627-685-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: PEPTIDE
                                                                                                                10-627-685-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-352-254-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 13
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Pemberton-Goodman, Karen
APPLICANT: Temple, Machael
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
CURRENT APPLICANTON NUMBER: US/10/352,254
CURRENT APPLICATION NUMBER: US 60/352,219
PRIOR APPLICATION NUMBER: US 60/352,219
PRIOR APPLICATION NUMBER: US 60/352,219
PRIOR PLING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 23
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 27;
                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: Cornell-Bell, Ann H.

APPLICANT: Pemberton, Karen E.

APPLICANT: Temple Jr., Davis L.

APPLICANT: Layer, Richard T.

APPLICANT: Layer, Richard T.

APPLICANT: McCabe, R. Tyler

APPLICANT: McCabe, R. Tyler

APPLICANT: Cognetix, Inc.

TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA

FILE REFERENCE: Kappa-PVIIA

CURRENT APPLICATION NUMBER: US/10/627,685

CURRENT APPLICATION NUMBER: US/09/666,837

PRIOR FILING DATE: 2000-09-21

PRIOR FILING DATE: 2000-09-21

PRIOR FILING DATE: 2000-09-21

PRIOR FILING DATE: 2000-09-20

PRIOR FILING DATE: 2000-09-20

PRIOR FILING DATE: 2000-07-20
                                                                                                         Ouery Match

97.5%; Score 157; DB 15;
Best Local Similarity 96.3%; Pred. No. 3.7e-12;
Matches 26; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 97.5%; Score 157; DB 15; L Similarity 100.0%; Pred. No. 3.7e-12; 26; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                         1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                      1 CQIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                          Application US/10352254
No. US20030224343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13, Application US/10627685
Publication No. US20040092447A1
GENERAL INFORMATION:
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
CHER INFORMATION: Xaa is Hyp
US-10-352-254-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                      10-352-254-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-627-685-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local
Matches 2
```

```
Pag

"" FulCANT: Jones, Robert M.
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: Maintensh, J. Michael
APPLICANT: Olivera, Baldomero M.
ITILE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT FILING DATE: 2003-01-28
BRIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cognetix, Inc.

APPLICANT: Cognetix, Inc.

APPLICANT: University of Utah Research Foundation

APPLICANT: University of Utah Research Foundation

APPLICANT: Tomes, Robert M.

APPLICANT: Temple, Davis

APPLICANT: Temple, Davis

APPLICANT: McIncosh, J. Michael

APPLICANT: McIncosh, J. Michael

APPLICANT: McIncosh, J. Michael

APPLICANT: McIncosh, J. Michael

TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants

FILE REFERENCE: 2314-254

CURRENT FILING DATE: 2003-01-28

CURRENT FILING DATE: 2002-01-29

NUMBER: PALCATION NUMBER: US 60/352,219

PRIOR FILING DATE: 2002-01-29

NUMBER: PALCHIN Ver. 2.0

SEQ ID NO 20

LENTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 156; DB 15; Length 27; Pred. No. 4.9e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 96.9%; Score 156; DB 15; Best Local Similarity 96.3%; Pred. No. 4.9e-12; Matches 26; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CRAXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CRIXNQKCFQHADDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20, Application US/10352254 Publication No. US20030224343A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
US-10-627-685-4
; Sequence 4, Application US/10627685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: (1)...(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1)..(27)
COTHER INFORMATION: Xaa is Hyp
US-10-352-254-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 96.3%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 157; DB 15; Length 27;
Pred. No. 3.7e-12;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 97.5%; Score 157; DB 15; Length 27; Best Local Similarity 100.0%; Pred. No. 3.7e-12; Matches 26; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 23, Application US/10627685
| Publication No. US20040092447A1
| GENERAL INFORMATION:
| APPLICANT: Cornell-Bell, Ann H.
| APPLICANT: Cornell-Bell, Ann H.
| APPLICANT: Temple Jr., Davis L.
| APPLICANT: Layer, Richard T.
| APPLICANT: McCabe, R. Tyler
| APPLICANT: McCabe, R. Tyler
| APPLICANT: McCabe, R. Tyler
| APPLICANT: Gonetix, Inc.
| TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
| FILE REFERENCE: Kappa-PVIIA
| CURRENT FILLNG DATE: 2003-07-28
| PRIOR APPLICATION NUMBER: US 60/219/438
| PRIOR PILING DATE: 2000-09-20
| PRIOR APPLICATION NUMBER: US 60/155,135
| PRIOR FILING DATE: 1999-09-22
| NUMBER OF SEQ ID NOS: 25
| SOFTWARE: PALENTIN VET. 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/10352254
Publication No. US20030224343A1
GENERAL INFORMATION:
APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: Pemberton-Goodman, Karen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                 ; LUCCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-13
                                                                                                                                                                                                                                                                                                                                                                                                                                  97.5%;
                                                                                                                                  PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (1)...(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-23
                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 96.3
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                     NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
US-10-627-685-23
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
```

ö

Gaps

```
APPLICANT: Cognetax, Inc.

APPLICANT: Cognetax, Inc.

APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Temple, Davis
APPLICANT: McIncal Michael
APPLICANT: McIncal Jaidomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
CURRENT FILING DATE: 2003-01-28
CURRENT APPLICATION NUMBER: US 60/352,219
PRIOR PLING DATE: 2003-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: Pemberton-Goodman, Karen
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: Morincosh, J. Michael
APPLICANT: Morincosh, J. Michael
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REPERBENC: 2314-254
CURRENT FILING DATE: 2003-01-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                            Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 27;
                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                          Query Match 96.9%; Score 156; DB 15; Best Local Similarity 96.3%; Pred. No. 4.9e-12; Matches 26; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 155; DB 15;
Pred. No. 6.5e-12;
0; Mismatches 1;
                                                                                                                                                                                      1 CRIXNQKCFQHADDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 2003-01-28
FRICA APPLICATION NUMBER: US 60/352,219
FRIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/10352254
Publication No. US20030224343A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/10352254
Publication No. US20030224343A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT

GRANISM: Conus purpurascens
FEATURE:
NAME/KEY: PEPTIDE
J. COCATION: (1)...(27)
CTHER INFORMATION: Xaa is Hyp
US-10-352-254-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 96.3%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 3
LENGTH: 27
                                                                                                                                                   ð
                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                            APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: McCabe, R. Tyler
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REPERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/10/627,685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: Jones, Robert M.
APPLICANT: Jones, Robert M.
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotcxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT PFLING DATE: 2003-07-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match

96.9%; Score 156; DB 15;
Best Local Similarity 96.3%; Pred. No. 4.9e-12;
Matches 26; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 2003-07-28
PRIOR PLICATION NUMBER: US/09/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR PLILNG DATE: 2000-07-20
PRIOR PLILNG DATE: 1999-09-22
PRIOR PLILNG DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VOY: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US/9/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR FILING DATE: 2000-07-20
PRIOR PILING DATE: 1999-09-22
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRAXNORCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20, Application US/10627685
Publication No. US20040092447A1
GENERAL INFORMATION:
Publication No. US20040092447A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (1)...(27)
COTHER INFORMATION: Xaa is Hyp
US-10-627-685-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
```

```
APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: Pemberton-Goodman, Karen
                                                                                                                                                                                                                                                                Score 155; DB 15;
Pred. No. 6.5e-12;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
96.3%; Score 155; DB 15;
Best Local Similarity 96.3%; Pred. No. 6.5e-12;
Matches 26; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                          1 CAIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                              1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CRIXNOKCFOHLDDCCSRKCNRFNACV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10, Application US/10352254 Publication No. US20030224343A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/10352254
Publication No. US20030224343A1
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 27
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
NAME/KEY: PEPTIDE
                                                                                                                                                                    ; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-6
                                                                                                                                                                                                                                                                     96.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: PEPTIDE

: DCATTON: (1)..(27)

: THER INFORMATION: Xaa is Hyp

US-10-352-254-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Conus purpurascens FEATURE:
                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 96.34
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-352-254-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Pembercon-Goodman, Karen
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: MoIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
CURRENT FILING DATE: 2003-01-28
FRIOR APPLICATION NUMBER: US 60/352,219
FRIOR APPLICATION NUMBER: US 60/352,219
FRIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: University, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: Demberton-Goodman, Karen
APPLICANT: Pemberton-Goodman, Karen
APPLICANT: Tones, Robert M.
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 60/352,219
PRIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                             96.3%; Score 155; DB 15; Length 27; 96.3%; Pred. No. 6.5e-12; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 155; DB 15; Length 27;
Pred. No. 6.5e-12;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                            1 CRIXNQKCFQHLDDCCSRKCNAFNKCV 27
                                                                                                                                                                                                                                              1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CRIXNOKCFQHLDDCCSRACNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/10352254 Publication No. US20030224343A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 5, Application US/10352254; Publication No. US20030224343A1; GENERAL INFORMATION:
                                               ; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 96.3%;
1 Similarity 96.3%;
26; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LUCCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp. US-10-352-254-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Conus purpurascens
                                                                                                                                                                      Best Local Similarity 96.3
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                        NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                   RESULT 19
US-10-352-254-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 5
LENGTH: 27
                                                                                                                                                  Query Match
    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d
                                                                                                                                                                                                                                                 ઠે
```

```
ô
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Raren
APPLICANT: Jones, Robert M.
APPLICANT: Temple, Davis
APPLICANT: Meintosh, J. Michael
APPLICANT: Meintosh, J. Michael
APPLICANT: Mirvara, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT FILING DATE: 2003-01-28
PRIOR FILING DATE: 2002-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Jones, Robert M.
APPLICANT: Temple, Davis
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivers Baldomero M.
APPLICANT: Olivers Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
.
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
```

```
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
TITLE OP INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REPERENCE: 2314-254
CURRENT PAPLICATION NUMBER: US/10/352,254
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 60/352,219
PRIOR FILING DATE: 2002-01-29
SOFTWARE: PATENTING DATE: 2002-01-29
SOFTWARE: PATENTING DATE: 2002-01-29
TYPE: PRIOR DATE: 2002-01-29
SOFTWARE: PATENTING DATE: 2008-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: Pemberton-Goodman, Karen
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
CURRENT APPLICATION NUMBER: 2003-01-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
96.3%; Score 155; DB 15;
Best Local Similarity 96.3%; Pred. No. 6.5e-12;
Matches 26; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
96.3%; Score 155; DB 15;
Best Local Similarity 96.3%; Pred. No. 6.5e-12;
Matches 26; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CRIXNAKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 2003-01-28
PRIOR FILING DATE: 2002-01-28
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
LENTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CRIXNOKCFAHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 22, Application US/10352254
Publication No. US20030224343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 2, Application US/10627685
; Publication No. US20040092447A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Conus purpurascens
                                       Temple, Davis
                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 26
US-10-627-685-2
                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: Discrept of Utah Research Foundation
APPLICANT: Pemberton-Goodman, Karen
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT APPLICATION NUMBER: US 60/352,219
PRIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 96.3%; Score 155; DB 15; Length 27; Best Local Similarity 96.3%; Pred. No. 6.5e-12; Matches 26; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 96.3%; Pred. No. 6.5e-12;
Matches 26; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RMATION:
Cognetix, Inc.
University of Utah Research Foundation
Pemberton-Goodman, Karen
CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 60/352,219
FRIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 27
TYPE: PRT
ORGANISM: CONUS PUTPULASCENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CRIXNQACFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CRIXNOKCMOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 11, Application US/10352254
; Publication No. US20030224343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16, Application US/1035254
Publication No. US20030224343A1
GENERAL INFORMATION:
APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah ReservationTHT: Pemberton-Goodman, Karer APPLICANT: Jones, Robert M.
                                                                                                                                                                                                                                                                                                              ; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -10-352-254-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 24
US-10-352-254-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
   Score 155; DB 15; Length 27;
Pred. No. 6.5e-12;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFOWATION:
APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: Jones, Robert M.
APPLICANT: Ones, Robert M.
APPLICANT: Cognetix, Inc.
ITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT FILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR PILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ TO NO.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Pemberton, Karen E.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: Layer, Richard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: Jones, Robert M.
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT FILING DATE: 2003-07-28
PRIOR PLLING DATE: 2000-09-21
PRIOR PLLING DATE: 2000-09-21
PRIOR PPLICATION NUMBER: US 60/219,438
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR PLLING DATE: 2000-07-20
PRIOR PLLING DATE: 2000-07-20
PRIOR PLLING DATE: 2000-07-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 155; DB 15;
Pred. No. 6.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 96.3%; Score 155; DB Best Local Similarity 96.3%; Pred. No. 6.5e Matches 26; Conservative 0; Mismatches
                                                                                                                                                  1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                    1 CRIXNOKCFOHLDDCCSRKCNAFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CRIXNOKCFQHLDDCCSRACNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/10627685 Publication No. US20040092447A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/10627685
Publication No. US20040092447A1
GENERAL INFORMATION:
96.3%;
Local Similarity 96.3%;
les 26; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
JOHER INFORMATION: Xaa is Hyp
US-10-627-685-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Conus purpurascens
FEATURE:
              Query Match
                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                  APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: McCabe, R. Tyler
APPLICANT: Jones, Robert M.
APPLICANT: Jones, Robert M.
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/10/666,837
FRIOR PRING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 1999-09-22
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Temple Jr. Chard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: Mores, Robert M.
APPLICANT: Ognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT FILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-20
PRIOR FILING DATE: 1999-09-22
NUMBER OF EEQ ID NOS: 25
NUMBER OF EEQ ID NOS: 25
NUMBER OF EEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 155; DB 15;
Pred. No. 6.5e-12;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CRIXNQKCFQHLDDCCSAKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/10627685
Publication No. US20040092447A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 96.3%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEC ID NO 2
LENGTH: 27
TYPE: PRT
ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: PEPTIDE LOCATION: (1)..(27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

PRIOR FILING DATE: 1999-09-22

```
96.3%; Score 155; DB 15; Length 27; 96.3%; Pred. No. 6.5e-12; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 96.3%; Score 155; DB 15; Length 27; Best Local Similarity 96.3%; Pred. No. 6.5e-12; Matches 26; Conservative 0; Mismatches 1; Indels
                                                                     APPLICANT: Cognetix, Inc.

TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILLS REPERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/10/627,685
CURRENT APPLICATION NUMBER: US/09/666,837
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 1990-09-22
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 27
TUDE: DATE
T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/10627685
Publication No. US20040092447A1
GENERAL INFORMATION:
APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Layer, Richard T.
APPLICANT: Layer, Richard T.
APPLICANT: Layer, Richard T.
APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/10/627,685
CURRENT FILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO II LEMENT: 27
LEMENT: 27
LEMENT: 27
LEMENT: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CRIXNQACFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
CTHER INFORMATION: Xaa is Hyp
US-10-627-685-10
   Layer, Richard T.
McCabe, R. Tyler
Jones, Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: PEPTIDE

; LOCATION: (1)..(27)

; OTHER INFORMATION: Xaa is Hyp

US-10-627-685-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 96.33
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-627-685-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                              Query Match 96.3%; Score 155; DB 15; Length 27; Best Local Similarity 96.3%; Pred. Nc. 6.5e-12; Matches 26; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , DB 15;
6.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
96.3%; Score 155; DB
Best Local Similarity 96.3%; Pred. No. 6.5e
Matches 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/10627685
Publication No. US20040092447A1
GENERAL INFORMATION:
                                                                                                                                                                  FEATURE:

NAME/KEY: PEPTIDE

LOCATION: (1) ..(27)

OTHER INFORMATION: Xaa is Hyp
US-10-627-685-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cornell-Bell, Ann H. APPLICANT: Pemberton, Karen E. APPLICANT: Temple Jr., Davis L.
                                                                                                            TYPE: PRT ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    i LOCATION: (1)..(27)
i OTHER INFORMATION: Xaa is Hyp
US-10-627-685-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Conus purpurascens
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-627-685-10
                                                            SEQ ID NO 6
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

ö

.. 0 ö

Gaps

; 0

ď

ઠે

```
Sequence 7, Application US/1035254

Sequence 7, Application US/1035254

Publication No. US20030224343A1

GENERAL INFORMATION:
APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: Tonge, Robert M.
APPLICANT: Tonge, Robert M.
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254

CURRENT FILING DATE: 2003-01-28

CURRENT FILING DATE: 2002-01-29

NUMBER OF SEQ ID NOS: 28

SOFTWARE: PATENTIN VET. 2.0

SEQ ID NO 7

LENGTH: 27
                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-252.
CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT FILING DATE: 2003-01-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 27
                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: Pemberton-Goodman, Karen
APPLICANT: Jones, Robert M.
APPLICANT: Temple, Davis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 95.0%; Score 153; DB 15;
Best Local Similarity 96.3%; Pred. No. 1.1e-11;
Matches 26; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                  Query Match 96.3%; Score 155; DB 15; Best Local Similarity 96.3%; Pred. No. 6.5e-12; Matches 26; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CRIXNQKCAQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                           1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CRIXNOKCFAHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15, Application US/10352254 Publication No. US20030224343A1
                                                                                    FEATURE:

NAME/KEY: PEPTIDE

LOCATION: (1)..(27)

OTHER INFORMATION: Xaa is Hyp
US-10-627-685-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
OTHER INFORMATION: Xaa is Hyp
US-10-352-254-7
                            TYPE: PRT ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-352-254-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; DB 15; Length 27;
6.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                        APPLICANT: Pemberton, Karen E.
APPLICANT: Pemberton, Karen E.
APPLICANT: Pemple Jr., Davis L.
APPLICANT: Tayer, Richard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: Cagnetix, Inc.
TILLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-TVIIA
CURRENT APPLICATION NUMBER: US/10/627,685
CURRENT APPLICATION NUMBER: US/09/666,837
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/155,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Temple Jr., Maris L.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: Mocabe, R. Tyler
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Ubes of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT PILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 1999-09-22
NUMBER: OF SEQ ID NOS: 25
SOFTWARE: PATCHIN Ver. 2.0
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 96.3%; Score 155; DE
Best Local Similarity 96.3%; Pred. No. 6.5e
Matches 26; Conservative 0; Mismatches
CRIKNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CRIXNAKCFQHLDDCCSRKCNRFNKCV 27
                                                        CRIXNOKCMOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                    Sequence 16, Application US/10627685; Publication No. US20040092447A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 22, Application US/10627685; Publication No. US20040092447A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cornell-Bell, Ann H. APPLICANT: Pemberton, Karen E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (1)..(27)
CTHER INFORMATION: Xaa is Hyp
US-10-627-685-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: PEPTIDE
                                                                                                                                               RESULT 33
US-10-627-685-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 34
US-10-627-685-22
```

g

ઠે

```
## APPLICANT: Olivera, Baldomero M.

TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
| FILE REFERENCE: 2314-254 |
| CURRENT APPLICATION NUMBER: US/10/352,254 |
| PRIOR APPLICATION NUMBER: US 60/352,219 |
| PRIOR PILING DATE: 2002-01-29 |
| PRIOR PILING DATE: 2002-01-29 |
| WUMBER OF SEQ ID NOS: 28 |
| SOFTWARE: Patentin Ver. 2.0 |
| SOFTWARE: Patentin Ver. 2.0 |
| IENGTH: 27 |
| TYPE: PRT |
| ORGANISM: Conus purpurascens |
| FRATURE: |
| NAMMS KEY: PEPTIDE: |
| NAMMS KEY: PEPTIDE: |
| NAMMS KEY: PEPTIDE: |
| OTHER INFORMATION: Xaa is Hyp |
| US-10-352-254-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | GENERAL INFORMATION | W. 19244343A1 |
| GENERAL INFORMATION | W. 19244343A1 |
| APPLICANT: Cognetix, Inc. |
| APPLICANT: University of Utah Research Foundation |
| APPLICANT: Pember Goodman, Karen |
| APPLICANT: Pember B. Baldoman, Karen |
| APPLICANT: Temple, Davis |
| APPLICANT: McIntosh, J. Michael |
| TILLE OF INTENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants |
| TILLE OF INTENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants |
| TILLE OF INTENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants |
| TILLE OF INTENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants |
| TILLE OF INTENTION NOTHER: US 60/352,219 |
| PRIOR PILING DATE: 2003-01-29 |
| WUMBER OF SEQ ID NOS: 28 |
| SOFTWARE: PatentIn Ver. 2.0 |
| SEQ ID NO 21 |
| LENGTH: 27 |
| LENGTH: 27 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
95.0%; Score 153; DB 15;
Best Local Similarity 96.3%; Pred. No. 1.1e-11;
Matches 26; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

95.0%; Score 153, DB 15;
Best Local Similarity 96.3%; Pred. No. 1.1e-11;
Matches 26; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CRIXNORCFQHLDDCCSRKCNRFAKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CRIXNORCFQHLADCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21, Application US/10352254
Publication No. US20030224343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 25, Application US/10352254
Publication No. US20030224343A1
GENERAL INFORMATION:
APPLICANT: Cognetix, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
CTHER INFORMATION: Xaa is Hyp
US-10-352-254-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 39
US-10-352-254-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-352-254-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17, Application US/10352254
Publication No. US20030224343A1
GENERAL INFORMATION;
APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: Pemberton-Goodman, Karen
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
TITLE OF INVERTION; Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT FILING DATE: 2003-01-28
RAIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                Query Match

95.0%; Score 153; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 1.1e-11;
Matches 26; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 153; DB 15; Length 27; Pred. No. 1.1e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19, Application US/10352254
Publication No. US20030224343A1
APREAT INFORMATION:
APPLICANT: Cognetix, Inc.
APPLICANT: University.of Utah Research Foundation
APPLICANT: Pemberton-Goodman, Karen
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: MCINtosh, J. Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CRIXNOKCFQHLDACCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CRIXNQKCFQHLDDCCSRKCARFNKCV 27
                     60/352,219
PRIOR APPLICATION NUMBER: US 60, PRIOR FILING DATE: 2002-01-29 NUMBER OF SEQ ID NOS: 28 SOFTWARE: Patentin Ver. 2.0 LENGTH: 27 TYPE: PRT TYPE: PRT TYPE: PRT ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                            COATION: (1) (27)
COTHER INFORMATION: Xaa is Hyp
US-10-352-254-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Temple, Davis
McIntosh, J. Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LUCATION: (1)...(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 96.3
Matches 26; Conservative
                                                                                                                                                                                                                                       NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 37
US-10-352-254-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 38
US-10-352-254-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
```

```
1 CRIXNQKCAQHLDDCCSRKCNRFNKCV 27
                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
APPLICANT: Memple, Davis

APPLICANT: Methods

TITLE OF INVENTION: Kappa-VIIA-Related Conctoxins as Organ Protectants

FILE REFERENCE: 2314-254

CURRENT FILING DATE: 2003-01-28

FRIOR FILING DATE: 2003-01-29

PRIOR FILING DATE: 2002-01-29

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 25

TYPE

TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 95.0%; Score 153; DB 15; Length 27; Best Local Similarity 96.3%; Pred. No. 1.1e-11; Matches 26; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 15; Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Pemberton, Karen E.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Iayer, Richard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: McCabe, R. Tyler
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/09/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATCHTIN VUMBER: US 60/155,135
PRIOR FILING DATE: 1999-09-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 95.0%; Score 153; DB Best Local Similarity 96.3%; Pred. No. 1.1e Matches 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 7, Application US/10627685; Publication No. US20040092447A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCATION: (1)..(27)
CTHER INFORMATION: Xaa is Hyp
US-10-352-254-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (1)..(27)
OTHER INFORMATION: Xaa is Hyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 7
LENGIH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                 APPLICANT: Temple Jr., Davis L.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: Mocabe, R. Tyler
APPLICANT: Gonetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REPRENCE: Kappa-PVIIA
CURRENT PILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR FILING DATE: 2000-07-20
PRIOR PILING DATE: 2000-07-20
PRIOR PILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO SEQ ID NOS: 25
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Pemberton, Karen E.
APPLICANT: Temple Jr., Baris L.
APPLICANT: Temple Jr., Baris L.
APPLICANT: Layer, Richard T.
APPLICANT: Layer, Richard T.
APPLICANT: Gones, Robert M.
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/10/627,685
CURRENT FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US 60/155,135
PRIOR RIBER DE SEQ ID NOS: 25
PRIOR APPLICATION NUMBER: US 60/155,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

95.0%; Score 153; DB 15;
Best Local Similarity 96.3%; Pred. No. 1.1e-11;
Matches 26; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CRIXNOKCFOHLDACCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5-10-627-685-17
Sequence 17, Application US/10627685
Publication No. US20040092447A1
Sequence 15, Application US/10627685 Publication No. US20040092447A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
OTHER INFORMATION: Xaa is Hyp
US-10-627-685-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Conus purpurascens
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 95.0%; Score 153; DB 15; Length 27; Best Local Similarity 96.3%; Pred. No. 1.1e-11; Matches 26; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Corneal-Bell, Ann H.
APPLICANT: Pemberton, Karen E.
APPLICANT: Pemberton, Karen E.
APPLICANT: Pemple Jr., Davis L.
APPLICANT: Temple Jr., Davis L.
APPLICANT: McCabe, R. Tyler
APPLICANT: Gones, Robert M.
APPLICANT: Cognetix, Inc.
ITILE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT PLILNG DATE: 2003-07-28
FRIOR APPLICATION NUMBER: US 60/219,438
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/155,135
PRIOR APPLICATION NUMBER: US 60/155,135
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOGTWARR: PARCENTING DATE: 1999-09-22
SOGTWARE: PARCENTING DATE: 1999-09-22
SOGTWARE: PARCENTING DATE: 1999-09-22
SOGTWARE: PARCENTING DATE: 1999-09-22
SOGTWARE: PARCENTING DATE: 1999-09-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 95.0%; Score 153; DB 15; Best Local Similarity 96.3%; Pred. No. 1.1e-11; Matches 26; Conservative 0; Mismatches 1;
                                              CURRENT FILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 1090-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
LENGTH: 27
LENGTH: 27
                         CURRENT APPLICATION NUMBER: US/10/627,685
CURRENT FILING DATE: 2003-07-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CRIXNOKCFOHLADCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CRIXAQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 25, Application US/10627685
Publication No. US20040092447A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                        ORGANISM: Conus purpurascens; FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
OTHER INFORMATION: Xaa is Hyp
US-10-627-685-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: (1)...(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-627-685-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                         Query Match 95.0%; Score 153; DB 15; Length 27; Best Local Similarity 96.3%; Pred. No. 1.1e-11; Matches 26; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: COTNEIL-Bell, Ann H.

APPLICANT: Demberton, Karen E.

APPLICANT: Pemberton, Karen E.

APPLICANT: Temple Jr., Davis L.

APPLICANT: Temple Jr., Davis L.

APPLICANT: McCabe, R. Tyler

APPLICANT: McCabe, R. Tyler

APPLICANT: Cognetix, Inc.

TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA

FILE REFERENCE: Kappa-PVIIA

CURRENT PLING DATE: 2003-07-28

PRIOR APPLICATION NUMBER: US/09/666,837

PRIOR FILING DATE: 2000-09-21

PRIOR PLING DATE: 2000-09-21

PRIOR PLING DATE: 2000-07-20

PRIOR PLING DATE: 1999-09-22

NUMBER OF SEQ ID NOS: 25

SSOFWARE: Patentin Ver. 2.0

SEQ ID NO :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 95.0%; Score 153; DB 15; 1 Similarity 96.3%; Pred. No. 1.1e-11; 26; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Uses of Kappa-Conotoxin PVIIA
                                                                                                                                                                                                                                                                        1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                         1 CRIXNQKCFQHLDDCCSRKCARFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRIXNOKCFOHLDDCCSRKCNRFAKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19, Application US/10627685
Publication No. US20040092447A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 21, Application US/10627685
Publication No. US20040092447A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Pemberton, Karen E.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: MCabe, R. Tyler
APPLICANT: Jones, Robert M.
APPLICANT: Cognetix, Inc.
                                                   ; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-17
ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Uses of
FILE REFERENCE: Kappa-PVIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 26; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                          -10-627-685-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 45
US-10-627-685-21
                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                         a
```

à

ö

Indels

```
5; DB 10; I
0.011;
ches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, Maren
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: University of Utah Research Foundation
       96.3%; Pred. No. 2e-11;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 78.5; DB; Pred. No. 0.0116; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: COGNETIX, INC.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Warkins, Maren
APPLICANT: Warkins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Garrett, James E.
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Garrier, G. Edward
FILE REFERENCE: 2314-241
CURRENT APPLICATION: Omega-Conopeptides
FILE REFERENCE: 2301-07-23
PRIOR PILING DATE: 2001-07-21
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: Patentin version 3.0
SENGTHARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 2314-241
CURRENT APPLICATION NUMBER: US/10/765,926
CURRENT FILING DATE: 2004-01-29
PRIOR APPLICATION NUMBER: US 09/910,082
PRIOR FILING DATE: 2001-07-23
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/265,888
PRIOR APPLICATION NUMBER: US 60/265,888
                                                                                                              1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                1 CRIXNOKCFQALDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CKPKGRKCFPHQKDCCNKTCTR-SKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPLICANT: Shon, Ki-Joon
PPLICANT: Jacobsen, Richard
PPLICANT: Jones, Robert M.
PPLICANT: Cartier, G. Edward
ITLE OF INVENTION: Omega-Conopeptides
                                                                                                                                                                                                                                                                                                                                                     Application US/09910082A
o. US20030119731A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 354, Application US/10765926 Publication No. US20040132663A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 46.2%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Garrett, James E.
       Best Local Similarity 96.3
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Conus ermineus
                                                                                                                                                                                                                                                                                                                           US-09-910-082A-354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-910-082A-354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 50
                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                            APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Demberton-Goodman, Karen
APPLICANT: Temple, Davis
APPLICANT: Temple, Davis
APPLICANT: Mointosh, J. Michael
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 60/352,219
PRIOR APPLICATION NUMBER: US 60/352,219
NUMBER OF SEQ ID NOS: 28
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 15; Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: COGNECT, A. COGNECTAL APPLICANT: COGNECTAL AND APPLICANT: COGNECTAL AND ASSET ASSET ASSET AND ASSET ASSET AND ASSET ASSET AND ASSET ASSET ASSET AND ASSET A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 151; DB 19
Pred. No. 2e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CRIXNQKCFQALDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
US-10-352-254-14,
Sequence 14, Application US/10352254;
Publication No. US20030224343A1;
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/10627685
Publication No. US20040092447A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Pemberton, Karen E.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: Jones, Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LUCCATION: (1)...(27)
; OTHER INFORMATION: Xaa is Hyp. US-10-352-254-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Xaa is Hyp. US-10-627-685-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 93.8
Best Local Similarity 96.3
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               요
```

93.8%; Score 151; DB 15; Length 27;

Query Match

Gapa

ij

Indels

Length 27;

us-10-627-685a-26.rapb

```
ch 46.0%; Score 74; DB 10; Length 26; 1 Similarity 42.3%; Pred. No. 0.037; 11; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                  Query Match
48.8%; Score 78.5; DB 16;
Best Local Similarity 46.2%; Pred. No. 0.025;
Matches 12; Conservative 6; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: University of Utah Research Foundation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 54
US-10-765-926-395
; Sequence 395. Application US/10765926
; Publication No. US20040132663A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation; APPLICANT: Cognetix, Inc.
                             CURRENT PELICATION NUMBER: US/10/765,926
CURRENT FILING DATE: 2004-01-29
PRIOR PELING DATE: 2001-07-23
PRIOR FILING DATE: 2001-07-23
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR PILING DATE: 2000-07-21
PRIOR PILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SEQ ID NO 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Shon, Ki-Joon
APPLICANT: Shon, Ki-Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Cartier, G. Edward
ITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
CURRENT APPLICATION NUMBER: US/09/910,082A
FRIOR APPLICATION NUMBER: US 60/219,616
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: Patentin version 3.0
SEQ ID NO 395
                                                                                                                                                                                                                                                                                                                                                                                                                               1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CKLKGQSCRRIMYDCCSGSCGRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 395, Application US/09910082A Publication No. US20030119731A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cognetix, Inc.
Olivera, Baldomero M.
McIntosh, J. Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   James E.
                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Conus ermineus
US-10-765-926-130
                    FILE REFERENCE: 2314-241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : Conus striatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Garrett,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-910-082A-395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Conu
US-09-910-082A-395
                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                      Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 78.5; DB 10; Length 72;
Pred. No. 0.025;
6; Mismatches 7; Indels
                                                                                                                                                                                                      7; Indels
                                                                                                                                                              5; DB 16;
0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntan, Marchael
APPLICANT: Watkins, Maren
APPLICANT: Garrett, James E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix. Inc.
                                                                                                                                                        Query Match

48.8%; Score 78.5; D
Best Local Similarity 46.2%; Pred. No. 0.01
Matches 12; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 CKPKGRKCFPHQKDCCNKTCTR-SKC 26
                                                                                                                                                                                                                                   1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:::||| | |||::| | :||
47 CKPKGRKCFPHQKDCCNKTCTR-SKC 71
                                                                                                                                                                                                                                                                                                                                                                           Sequence 130, Application US/09910082A Publication No. US20030119731A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cartier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 130, Application US/10765926; Publication No. US20040132663A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cognetix, Inc.
Olivera, Baldomero M.
McIntosh, J. Michael
Warkins, Maren
Garrett, James E.
NUMBER OF SEQ ID NOS: 413
SOFTWARE: PatentIn version 3.0
SEQ ID NO 354
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shon, Ki-Joon
Jacobsen, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 46.2
Matches 12; Conservative
                                                                               ; TYPE: PRT
; ORGANISM: Conus ermineus
US-10-765-926-354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT; ORGANISM: Conus ermineus
US-09-910-082A-130
                                                                                                                                                                                                                                                                                                                                                            US-09-910-082A-130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JS-10-765-926-130
                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

```
APPLICANT: University of Utah Research Foundation
                                                                                  Application US/10765926
                                                                                                                                                                                                                                                                                                 Jacobsen, Richard
Jones, Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JS-09-910-082A-217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-765-926-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
46.0%; Score 74; DB 16; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.037;
Matches 11; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10; Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                University of Utah Research Foundation Cognetix, Inc.
Cognetix, Endowero M.
Olivera, Baldomero M.
McIntosh, J. Michael
Watkins, Maren
Garrett, James B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 74; DB 10
Pred. No. 0.042;
5; Mismatches
                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/765,926
CURRENT FILING DATE: 2004-01-29
PRIOR APPLICATION NUMBER: US 09/910,082
PRIOR PILING DATE: 2001-07-23
PRIOR PILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR PILING DATE: 2000-07-21
PRIOR FILING DATE: 2001-02-05
NUMBER: OF SEQ ID NOS: 413
SEQ ID NO 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/910,082A CURRENT FILING DATE: 2001-07-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CKLKGQSCRRTMYDCCSGSCGRRGKC 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/265,888
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cartier, G. Edward
IITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
                                                                                                                                              CANT: Cartier, G. Edward
OF INVENTION: Omega-Conopeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 257, Application US/09910082A; Publication No. US20030119731A1; GENERAL INFORMATION:
ivera, Baldomero M.
Intosh, J. Michael
tkins, Maren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 42.3%;
Matches 11; Conservative
                                                                                      Shon, Ki-Joon
Jacobsen, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shon, Ki-Joon
Jacobsen, Richard
Jones, Robert M.
                                                                Јатев Е.
                                                                                                                                 Jones, Robert M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Conus striatus
US-10-765-926-395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Conus striatus
US-09-910-082A-257
                                                                                                                                                                                          REFERENCE: 2314-241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
```

```
Ouery Match 46.0%; Score 74; DB 16; Length 30; Best Local Similarity 42.3%; Pred. No. 0.042; Matches 11; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: University of Utah Research Foundation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/910,082A
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2001-02-65
PRIOR APPLICATION NUMBER: US 60/265,888
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: Patentin version 3.0
SEQ ID NO 217
LENGTH: 72
                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2004-01-29
PRIOR APPLICATION NUMBER: US 09/910,082
PRIOR FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR FILING DATE: 2000-07-21
PRIOR PELING DATE: 2000-07-21
PRIOR FILING DATE: 2000-07-80
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
                                                                                                                                                                                                                                  APPLICANT: Carrier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2114-24
CURRENT APPLICATION NUMBER: US/10/765,926
CURRENT FILING DATE: 2004-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Mittosh, J. Michael
APPLICANT: Watkins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Shon, Ki-Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Grees, Robert M.
APPLICANT: Gartier, G. Edward
IITLE OF INVENTION: Omega-Conopeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 ČKLKGÓSCRRTMYDCCSGSCGRRGKC 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 217, Application US/09910082A Publication No. US20030119731A1 GENERAL INFORMATION:
Cognetix, Inc.
Olivera, Baldomero M.
McIntosh, J. Michael
Watkins, Maren
Garrett, James E.
Shon, K.-Joon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.0 SEQ ID NO 257
```

Tue Apr 19 09:12:34 2005

```
60/265,888
                  PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/;
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SCOFTWARE: Patentin version 3.0
SEQ ID NO 384
LENGTH: 27
                                                                                                                                                                                                                                                             th 44.1%;
l Similarity 50.0%;
10; Conservative
                                                                                                                                                                TYPE: PRT ; ORGANISM: Conus purpurascens US-09-910-082A-384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conus purpurascens
                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JS-10-765-926-384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-910-082A-223
                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
0
                                                                                                   Gaps
                                           Query Match 45.3%; Score 73; DB 10; Length 72; Best Local Similarity 50.0%; Pred. No. 0.12; Matches 10; Conservative 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 16; Length 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Indels
                                                                                                                                                                                                                                                                                                                                            APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M. APPLICANT: Michael APPLICANT: Watkins, Maren APPLICANT: Garrett, James E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: University of Utah Research Foundation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 73; DB 16
Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Shon, Ki-Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Gartier, G. Edward
TITLE OF INVENTION: Omega-Conopetides
FILE REFERENCE: 2314-24
CURRENT FILING DATE: 2004-01-29
FRIOR APPLICATION NUMBER: US 09/910,082
FRIOR APPLICATION NUMBER: US 09/910,082
FRIOR APPLICATION NUMBER: US 60/219,616
FRIOR FILING DATE: 2000-07-21
FRIOR FILING DATE: 2000-07-21
FRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: PALENTIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/910,082A CURRENT FILING DATE: 2001-07-23 PRIOR APPLICATION NUMBER: US 60/219,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: MILLOSh, J. Michael
APPLICANT: Watkins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Shon, Ki-Joon
APPLICANT: Jocobsen, Richard
APPLICANT: Jocobsen, Richard
APPLICANT: Cartier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
                                                                                                                                                                                                                                                                                  s Sequence 217, Application US/10765926
publication No. US20040132663A1
general INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 384, Application US/09910082A
; Publication No. US20030119731A1
; GENERAL INFORMATION:
                                                                                                                                 1 CRIXNOKCFOHLDDCCSRKC 20
                                                                                                                                                          1 CRIXNOKCFOHLDDCCSRKC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch
1 Similarity 50.0%;
10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Conus purpurascens
US-10-765-926-217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 10; Conserva
US-09-910-082A-217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-910-082A-384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 217
LENGTH: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
```

```
ö
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                     ;
0
Score 71; DB 10; Length 27; Pred. No. 0.087; 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

44.1%; Score 71; DB 16; Length 27;
Best Local Similarity 50.0%; Pred. No. 0.087;
Matches 10; Conservative 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                           APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Olivers Baddomero M.
APPLICANT: Matkins, Maren
APPLICANT: Watkins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Shon, Ki-Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Jones, Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 223, Application US/09910082A
Publication No. US20030119731A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cartier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2114-241
CURRENT APPLICATION NUMBER: US/10/765,926
CURRENT FILING DATE: 2004-01-29
FRIOR PAPLICATION NUMBER: US 60/910,082
PRIOR FILING DATE: 2001-07-21
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: PatentIn version 3.0
SERVANE: PATENTIN VERSION 3.0
SOFTWARE: PATENTIN VERSION 3.0
                                                                                                                                                                                                                                                                       Sequence 384, Application US/10765926
Publication No. US20040132663A1
GENERAL INFORMATION:
                                                                                        1 CRIXNOKCFOHLDDCCSRKC 20
                                                                                                                           2 CKKTGRKCFPHQKDCCGRAC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CRIXNOKCFOHLDDCCSRKC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 CKKTGRKCFPHQKDCCGRAC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cognetix, Inc.
Olivera, Baldomero M.
McIntosh, J. Michael
Watkins, Maren
Garrett, James E.
```

```
RESULT 64
US-10-765-926-258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                           44.1%; Score 71; DB 10; Length 72; 50.0%; Pred. No. 0.2; tive 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 16; Length 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: University of Utah Research Foundation APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
APPLICANT: Olivers, Baldomero M.
APPLICANT: Matchis, Maren
APPLICANT: Watkins, Maren
APPLICANT: Show, Ki-Joon
APPLICANT: Jocobsen, Richard
APPLICANT: Jones, Robert M.
                                    APPLICANT: Jones, Robert M.
APPLICANT: Cartier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
CURRENT APPLICATION NUMBER: US/09/910,082A
CURRENT APPLICATION NUMBER: US 60/219,616
PRIOR FILING DATE: 2001-07-21
PRIOR FILING DATE: 2001-055
NUMBER OF SEQ ID NOS: 413
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 71; DB 1
Pred. No. 0.2;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAPLICANT: Carrier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
CURRENT APPLICATION NUMBER: US/10/765,926
CURRENT FILING DATE: 2004-01-29
PRIOR APPLICATION NUMBER: US 09/910,082
PRIOR FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2001-07-25
NUMBER OF SEQ ID NOS: 413
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 223, Application US/10765926 Publication No. US20040132663A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CRIXNQKCFQHLDDCCSRKC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CRIXNOKCFQHLDDCCSRKC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 50.0%;
Matches 10; Conservative
.Shon, Ki-Joon
Jacobsen, Richard
                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.0°
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    US-09-910-082A-223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 223
LENGTH: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
```

RESULT 63 US-09-910-082A-258

```
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(26)
OTHER INFORMATION: Xaa at residue 13 is Tyr, 1251-Tyr, mono-iodo-Tyr, di-iodo-Tyr, 0
OTHER INFORMATION: -sulpho-Tyr or O-phospho-Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
41.6%; Score 67; DB 10; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.26;
Matches 11; Conservative 5; Mismatches 10; Indels
                                                              APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: McIntoeh, J. Michael
APPLICANT: McIntoeh, J. Michael
APPLICANT: Garrett, James E.
APPLICANT: Shon, Ki-Joon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Watkins, Maren
                                                                                                                                                                                                                                                   APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jones, Robert M.
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
CURRENT APPLICATION NUMBER: US/09/910,082A
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR APPLICATION NUMBER: US 60/265,888
PRIOR RILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: PatentIn version 3.0
SEQ ID NO 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/765,926
CURRENT FILING DATE: 2004-01-29
PRIOR APPLICATION NUMBER: US 09/910,082
PRIOR FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR PILING DATE: 2000-07-21
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Garrett, James B.
APPLICANT: Shon, Ki-Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Jones, Robert M.
APPLICANT: Carrier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
Application US/09910082A
. US20030119731A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 258, Application US/10765926
Publication No. US20040132663A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Conus striatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Publication No. US20
GENERAL INFORMATION:
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (1)..(26)
. OTHER INFORMATION: Xaa at residue 13 is Tyr, 1251-Tyr, mono-iodo-Tyr,
; OTHER INFORMATION: di-iodo-Tyr, 0 -sulpho-Tyr or O-phospho-Tyr
US-10-765-926-268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa at residue 1, 5, 11 and 27 is Pro or Hyp
US-09-910-082A-218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

39.8%; Score 64; DB 16; Length 26;
Best Local Similarity, 42.3%; Pred. No. 0.59;
Matches 11; Conservative 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 64; DB 10; Length 27; Pred. No. 0.61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: University of Utah Research Foundation
                                                        APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Cartier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
FILE REPERENCE: 214-241
CURRENT APPLICATION NUMBER: US/10/765,926
CURRENT FILING DATE: 2001-01-29
PRIOR PILING DATE: 2001-07-23
PRIOR PILING DATE: 2001-07-23
PRIOR PILING DATE: 2001-07-21
PRIOR PILING DATE: 2001-07-21
PRIOR PILING DATE: 2001-07-21
PRIOR PILING DATE: 2001-05-616
PRIOR FILING DATE: 2001-05-65,888
NUMBER OF SEQ ID NOS: 413
SOFTWARE: PREFILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: PREFILING DATE: 2001-02-05
TYPE: PRT
ORGANISM: Conus striatus
FEATURE: PRT
NAME/KEY: PREFILDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Merincoh, J. Michael
APPLICANT: Watkins, Marchael
APPLICANT: Watkins, March
APPLICANT: Watkins, March
APPLICANT: Shon, Ki-Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Jones, Robert M.
APPLICANT: Jones, Robert M.
APPLICANT: Cartier, G. Edward
APPLICANT: Cartier, G. Edward
APPLICANT: Jones, Robert M.
APPLICANT: Jones M.
AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 218, Application US/09910082A Publication No. US20030119731A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Conus purpurascens
                                       Shon, Ki-Joon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-910-082A-218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (1) . (26)
OTHER INFORMATION: Xaa at residue 13 is Tyr, 1251-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
OTHER INFORMATION: -sulpho-Tyr or O-phospho-Tyr
                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                 . LOCATION: (1)..(26)
. OTHER INFORMATION: Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr,
. OTHER INFORMATION: di-iodo-Tyr, O-sultho-Tyr or O-phospho-Tyr
US-10-765-926-258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                   Query Match
41.6%; Score 67; DB 16; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.26;
Matches 11; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
39.8%; Score 64; DB 10; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.59;
Matches 11; Conservative 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M. APPLICANT: Michael APPLICANT: Watkins, Maren APPLICANT: Garrett, James E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 268, Application US/10765926
Publication No. US20040132663A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cógnetix. Inc.
APPLICANT: Olivera, Baldomero M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: JONES, ROBERT M.
APPLICANT: Cartier, G. Edward
TILE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
CURRENT APPLICATION NUMBER: US/09/910,082A
CURRENT APPLICATION NUMBER: US 60/219,616
PRIOR PILING DATE: 2000-07-21
PRIOR FILING DATE: 2000-07-21
PRIOR PLING DATE: 2000-07-21
PRIOR FILING DATE: 2001-07-65
NUMBER OF SEQ ID NOS: 413
SEQ ID NO 268
                                                                                                                                                                                                                                                                                                                                                                                                      1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 65
US-09-910-082A-268
; Sequence 268, Application US/09910082A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cognetix, Inc.
Cognetix, Inc.
Olivera, Baldomero M.
McIntosh, U. Michael
Warkins, Maren
Garrett, James B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shon, Ki-Joon
: Jacobsen, Richard
ORGANISM: Conus striatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Conus striatus
                                                               NAME/KEY: PEPTIDE LOCATION: (1)..(26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: PEPTIDE LOCATION: (1)..(20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-910-082A-268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-765-926-268
                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

ö

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                               LOCATION: (1)...(27)
CTHER INFORMATION: Xaa at residue 1, 5, 11 and 27 is Pro or Hyp
US-10-765-926-218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 16; Length 27;
                                                                                                                                                                                                                                                                                                                                                           7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Indels
                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Watkins, Maren
APPLICANT: Watkins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Jacobsen, Richard
APPLICANT: Ones, Robert M.
APPLICANT: Jacobsen, Richard
APPLICANTION: Omega-Conopeptides
TILE REFERENCE: 2314-241
CURRENT FILING DATE: 2004-01-29
PRIOR FILING DATE: 2001-07-21
PRIOR FILING DATE: 2001-07-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: PatentIn Version 3.0
SEQ ID NO 382
                                                                                                                                                                                                                                                                                                                  Score 64; DB 16;
Pred. No. 0.61;
                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/265,888
NUMBER OF SEQ ID NOS: 413
SOFTWARE: Patentin version 3.0
SEQ ID NO 218
LENGTH: 27
TYPE: PRT
ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 64;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 71
US-09-910-082A-350
; Sequence 350, Application US/09910082A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 382, Application US/10765926 Publication No. US20040132663A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    1 CRIXNOKCFOHLDDCCSRKC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                           2 CKTYGRKCFXHQKDCCGRAC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CRIXNOKCFQHLDDCCSRKC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CKTXGRKCFXHQKDCCGRAC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-765-926-382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.8%;
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 55.0%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                NAME/KEY: PEPTIDE
                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
        ö
        Gaps
        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10; Length 27;
      7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
APPLICANT: Olivers, Baldomero M.
APPLICANT: Maintosh, J. Michael
APPLICANT: Watkins, Maren
                                                                                                                                                                                                                                                   APPLICANT: University of Utah Research Foundation
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Carrier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
FILE REFREENCE: 2314-241
CURRENT APPLICATION NUMBER: US/09/910,082A
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR APPLICATION NUMBER: US 60/25,888
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: PatentIn version 3.0
SEQ ID NO 382
      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39.8%; Score 64; 55.0%; Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 2314-241
CURRENT APPLICATION NUMBER: US/10/765,926
CURRENT FILING DATE: 2004-01-29
PRIOR APPLICATION NUMBER: US 09/910,082
PRIOR FILING DATE: 2001-07-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/219,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cartier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
                                                                                                                                                                                      Sequence 382, Application US/09910082A; Publication No. US20030119731A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 218, Application US/10765926; Publication No. US20040132663A1; GENERAL INFORMATION:
                                             1 CRIXNQKCFQHLDDCCSRKC 20
                                                                     1 CRIXNOKCFOHLDDCCSRKC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CKTXGRKCFXHQKDCCGRAC 21
                                                                                                                                                                                                                                                                           Cognetix, Inc.
Olivera, Baldomero M.
McIntosh, J. Michael
Watkins, Maren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (1)..(27)
OTHER INFORMATION: Xaa is Hyp
                                                                                                                                                                                                                                                                                                                                                         Garrett, James E.
Shon, Ki-Joon
Jacobsen, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Garrett, James E.
Shon, Ki-Joon
Jacobsen, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                        Jones, Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jones, Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 55.0
les 11; Conservative
    11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-910-082A-382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
    Matches
                                             ઠે
                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
```

ò

ö

Publication No. US20030119731A1

```
Length 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: University Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: McIntosh, J. Michael
APPLICANT: Markins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Garrett, James E.
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Cartier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241-241
FILE REPERENCE: 2314-241-241
FILE REPERENCE: 2314-241-241
FRIOR FILING DATE: 2001-07-23
FRIOR FILING DATE: 2001-07-21
FRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: PatentIn Version 3.0
SEQ ID NO 94
MUNICH 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-765-926-94

Sequence 94, Application US/10765926

Publication No. US20040132663A1

GENERAL INCRMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Ognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Markins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Shon, Ki-Joon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 39.4%; Score 63.5; DB 10; Best Local Similarity 37.0%; Pred. No. 1.7; Matches 10; Conservative 8; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: JORGE, ROBERT M.
APPLICANT: CARTIER, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-24
CURRENT APPLICATION NUMBER: US/10/765,926
CURRENT FILING DATE: 2001-07-23
PRIOR FILING DATE: 2001-07-23
PRIOR PELICATION NUMBER: US 60/219,616
PRIOR FILING DATE: 2001-07-21
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR FILING DATE: 2001-07-21
PRIOR FILING DATE: 2001-07-21
PRIOR FILING DATE: 2001-07-21
PRIOR FILING DATE: 2001-07-21
NUMBER: OF SEQ. ID NOS: 413
           1 CRIXNOKCFQHLDDCCSRKCNRFN-KC 26
                                                                                 1 CRIXNOKCFQHLDDCCSRKCNRFN-KC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 94, Application US/09910082A Publication No. US20030119731A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Conus circumcisus
US-09-910-082A-94
                                                                                                                                                                                                                                                                                                                                      US-09-910-082A-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                       g
                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

39.4%; Score 63.5; DB 10; Length 27;
Best Local Similarity 37.0%; Pred. No. 0.7;
Matches 10; Conservative 8; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.4%; Score 63.5; DB 16; Length 27; 37.0%; Pred. No. 0.7; tive 8; Mismatches 8; Indels 1
APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Watkins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Garrett, James E.
APPLICANT: Garrett, John K.
APPLICANT: Jacobsen, Richard
APPLICANT: Jones, Robert M.
APPLICANT: Jones, Robert M.
APPLICANT: Onnes, Robert M.
APPLICANT: Onnes, Robert M.
APPLICANT: Onnes, Robert M.
APPLICANT: Onnes, Robert M.
APPLICANT: 2314-241
CURRENT PLING DATE: 2001-07-23
PRIOR FILING DATE: 2001-07-21
PRIOR FILING DATE: 2001-07-21
PRIOR FILING DATE: 2001-07-25
NUMBER OF SEQ ID NOS: 413
SOFTWARE: PatentIn version 3.0
SEQ ID NO 350
LENGIN: DATE: 2001-07-05
LENGIN: DATE: 2001-07-05
SEQ ID NO 350
LENGIN: DATE: 2001-07-05
LENGIN: DATE: 2001-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: University of Utah Research Foundation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Unlversity or ucan rescuence APPLICANT: Ognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Watkins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Garcett, James E.
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jones, Robert M.
APPLICANT: Jones, Jones,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CRIXNOKCFQHLDDCCSRKCNRFN-KC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 350, Application US/10765926; Publication No. US20040132663A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Conus circumcisus
US-09-910-082A-350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conus circumcisus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 37.0
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -10-765-926-350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Conu
US-10-765-926-350
```

ò

```
APPLICANT: Marching, Walten, APPLICANT: Shen, Greg S.
TITLE OF INVENTION: 1.2 Superfamily Conotoxins FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTHARE: PATCHIN VERSION 3.0
SEQ ID NO 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
38.8%; Score 62.5; D
Best Local Similarity 40.7%; Pred. No. 2.2;
Matches 11; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39 CLSLGQRCERH-SDCCGYLCCFYDKCV 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Conus purpurascens
PEATURE:
LOCATION: (1)..(27)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Conus betulinus
US-09-894-882-167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JS-09-910-082A-224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                         Query Match

39.4%; Score 63.5; DB 16; Length 73;
Best Local Similarity 37.0%; Pred. No. 1.7;
Matches 10; Conservative 8; Mismatches 8; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 38.8%; Score 62.5; DB 9; Length 36; Best Local Similarity 40.7%; Pred. No. 1.2; Matches 11; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                           Sequence 189, Application US/09894882
Patent No. US20020102607A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Shetty, Reshma
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: Offivera, Baldomero M.
APPLICANT: Olivera, Maichael
APPLICANT: Matkins, Maren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   University of Utah Research Foundation
Cognetix, Inc.
Walker, Craig S.
Shetry, Reshma
Jimenez, Elsie C.
McIncosh, J. Michael
Olivera, Baldomero M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CRIXNOKCFOHLDDCCSRKCNRFN-KC 26
                                                                                                                                                                                                                                            46 CKSKGAKCSRLMYDCCSGSCSRYSGRC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | : |:| :| | | | CLSLGQRCERH-SDCCGYLCCFYDKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 167, Application US/09894882; Patent No. US20020102607A1; GENERAL INFORMATION:
APPLICANT: University of Utah Research applicant: Cognetix, Inc.; APPLICANT: Walker, Craig S.; APPLICANT: Shetty, Reshma
                                       TYPE: PRT CORUS CIrcumcisus US-10-765-926-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Conus betulinus
                                                                                                                                                                                                                                                                                                                                              US-09-894-882-369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-894-882-369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 76
US-09-894-882-167
SEQ ID NO 94
LENGTH: 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

ä

Indels

DB 9; Length 73;

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa at residue 1, 11 and 27 is Pro or Hyp
US-09-910-082A-224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 38.5%; Score 62; DB 10; Length 27; Best Local Similarity 50.0%; Pred. No. 1.1; Matches 10; Conservative 3; Mismatches 7; Indels
Sequence 224, Application US/09910082A

Sequence 224, Application US/09910082A

Publication No. US20030119731A1

GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Matchis, March
APPLICANT: Watkins, March
APPLICANT: Watkins, March
APPLICANT: Garrett, James E.
APPLICANT: Garrett, James E.
APPLICANT: Garrett, Genes E.
APPLICANT: Garrier, G. Edward
APPLICANT: Jacobsen, Richard
APPLICANT: Jones, Robert M.
APPLICANT: Jacobsen, Richard
APPLICANT: Jones, Robert M.
APPLICANT: Jones, Robert M.
APPLICANT: Jones, Robert M.
APPLICANT: Jones, Robert M.
PRING RILING DATE: 2010-07-23
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2001-07-26
PRIOR FILING DATE: 2001-07-26
PRIOR FILING DATE: 2001-07-26
PRIOR PRIOR FILING DATE: 2001-07-26
PRIOR PRIOR FILING DATE: 2001-07-26
PRIOR PLING DATE: 2001-07-27
PRIOR PLING DATE: 2001-07-27
```

'n

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
COTHER INFORMATION: Xaa at residue 1, 4, 11 and 27 is Pro or Hyp
US-09-910-082A-131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.2%; Score 61.5; DB 10; Length 27; 47.8%; Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                DB 9; Length 76; 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                     9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 131, Application US/09910082A

Sequence 131, Application US/09910082A

GENERAL INFORMATION:
APPLICANT: Constix, Inc.
APPLICANT: Constix, Inc.
APPLICANT: Constix, Inc.
APPLICANT: Glover, Baldomero M.
APPLICANT: Matkins, Maren
APPLICANT: Matkins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Shon, Ki-Joon
APPLICANT: Shon, Ki-Joon
APPLICANT: Garrett, James E.
APPLICANT: Garrett, James E.
APPLICANT: Cartier, G. Edward
APPLICANT: Cartier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
CURRENT APPLICATION NUMBER: US 60/219,616
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2001-07-25
PRIOR FILING DATE: 2001-07-25

PRIOR FILING DATE: 2001-07-25

SOFTWARE: PATENTIN NUMBER: US 60/265,888

NUMBER OF SEQ ID NOS: 413

SOFTWARE: PATENTIN VEYSION 3.0

SEQ ID NO 121

LEMETH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 131, Application US/10765926
Publication No. US20040132663A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
                                                                                                                                                                                                                                                                                                                                          Score 62; DB
Pred. No. 2.6;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CRIXNQKCFQHLDDCCSRKCNRF-NKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48 CNEAQEHCTÓN-PÓCCSESCNKFVGRCL 74
                PRIOR APPLICATION NUMBER: US 60/214,263
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/173,754
PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 409
SOFTWARE: PatentIn version 3.0
FORMALL: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S KGRKCFXHQXDCCNKTCTR-SKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 XNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                          Query Match 38.5%;
Best Local Similarity 39.3%;
Matches 11; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 38.2
Best Local Similarity 47.8
Matches 11; Conservative
                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Conus distans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Conus ermineus
                                                                                                                                                                                                                                                                                  US-09-749-637A-207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-910-082A-131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-765-926-131
                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                i LOCATION: (1)..(27)
i OTHER INFORMATION: Xaa at residue 1, 11 and 27 is Pro or Hyp
US-10-765-926-224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 38.5%; Score 62; DB 16; Length 27; Best Local Similarity 50.0%; Pred. No. 1.1; Matches 10; Conservative 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: Clivera, Baldomero M.
APPLICANT: Cartier, G. Edward
APPLICANT: Watkins, Maren
APPLICANT: Watkins, Maren
APPLICANT: Hillyard, David R.
APPLICANT: Hillyard, David R.
APPLICANT: Hillyard, David R.
APPLICANT: Jayer, Richard T.
APPLICANT: Jayer, Richard T.
APPLICANT: Johnsey, Robert M.
TITLE OF INTENTION: O-Superfamily Conotoxin Peptides
FILE REFERENCE: 2314-227
CURRENT APPLICATION NUMBER: US 60/243,412
FRIOR APPLICATION NUMBER: US 60/243,412
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/219,440
FRIOR APPLICATION NUMBER: US 60/219,440
                                                                                                                                                                             Sequence 224, Application US/10765926
Publication No. US20040132663A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
                                                                                                                                                                                                                                                                 APPLICANT: University of Connects.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: Maren
APPLICANT: Garrett, James E.
APPLICANT: Shon, Ki. Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Cartier, G. Edward
ITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
CURRENT APPLICATION NUMBER: US/0/765,926
CURRENT FILING DATE: 2001-07-23
PRIOR FILING DATE: 2001-07-23
PRIOR FILING DATE: 2001-07-21
PRIOR FILING DATE: 2001-07-21
PRIOR FILING DATE: 2001-07-21
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: Patentin version 3.0
ILENGTH. 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 207, Application US/09749637A; Patent No. US20020173449A1; GENERAL INFORMATION:
                              2 CKKTGRKCFXHQKDCCGRAC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CRIXNOKCFOHLDDCCSRKC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CKKTGRKCFXHQKDCCGRAC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Conus purpurascens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-749-637A-207
ò
                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Б
```

ö

Gaps ö

Indels

7:

```
6; Mismatches
                                               1 CRIXNQKCFQHLDDCCSRKCN 21
       8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 2314-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-910-082A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
       Matches
                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa at residue 1, 4, 11 and 27 is Pro or Hyp
US-10-765-926-131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.9%; Score 61; DB 10; Length 27; 38.1%; Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Colivera, Baldomero M.
APPLICANT: Mintosh, J. Michael
APPLICANT: Markins, Maren
APPLICANT: Markins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Shon, Ki-Joon
APPLICANT: Shon, Ki-Joon
APPLICANT: Jones, Robert M.
APPLICANT: Garter, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
FILE REFRENCE: 2314-21
CURRENT APPLICATION NUMBER: US/09/910,082A
CURRENT FILING DATE: 2001-07-23
FRIOR APPLICATION NUMBER: US 60/219,616
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR FILING DATE: 2001-07-21
PRIOR FILING DATE: 2001-07-21
PRIOR FILING DATE: 2001-07-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 38.2%; Score 61.5; E
Best Local Similarity 47.8%; Pred. No. 1.2;
Matches 11; Conservative 5; Mismatches
                                                                                  APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Gartier, G. Edward
TILLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
CURRENT APPLICATION NUMBER: US/10/765,926
FRICH APPLICATION NUMBER: US 60/910,082
PRIOR FILING DATE: 2004-01-29
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: Patentin Version 3.0
SEQ ID NO 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: unknown Conus species US-09-910-082A-359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S KGRKCFXHQKDCCNKTCTR-SKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 359, Application US/09910082A Publication No. US20030119731A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 XNOKCFQHLDDCCSRKCNRFNKC 26
J. Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 413
SOFTWARE: PatentIn version 3.0
                                               James E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Conus ermineus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
DRGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 82
US-09-910-082A-359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBEL
SOFTWARE: Pace
SEQ ID NO 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

```
Query Match 37.9%; Score 61; DB 16; Length 27; Best Local Similarity 38.1%; Pred. No. 1.4; Matches 8; Conservative 6; Mismatches 7; Indels
                                                                                                                                                                                                                                                 APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Cognetix, Inc.
APPLICANT: Mathematical Baldomero M.
APPLICANT: Mathins, Baren
APPLICANT: Mathins, Maren
APPLICANT: Mathins, Maren
APPLICANT: Shon, Ki-Joon
APPLICANT: Shon, Ki-Joon
APPLICANT: Shon, Ki-Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Jones, Robert M.
APPLICANT: Gartier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
CURRENT APPLICATION NUMBER: US/10/765,926
CURRENT APPLICATION NUMBER: US 69/910,082
PRIOR FILING DATE: 2001-07-23
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: University of Utah Research Foundation APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M. APPLICANT: McIncosh, J. Michael APPLICANT: Watkins, Maren APPLICANT: Shon, Ki-Joon APPLICANT: Shon, Ki-Joon APPLICANT: Jacobsen, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/910,082A CURRENT FILING DATE: 2001-07-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: unknown Conus species US-10-765-926-359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/265,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPLICANT: Jones, Robert M.
PPLICANT: Cartier, G. Edward
(TLE OF INVENTION: Omega-Conopeptides
                                                                                                                                        US-10-765-926-359
Sequence 359, Application US/10765926
Publication No. US20040132663A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/09910082A Publication No. US20030119731A1 GENERAL INFORMATION:
1 CKPPGRKCLNRKNECCSKFCN 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CRIXNOKCFQHLDDCCSRKCN 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CKPPGRKCLNRKNECCSKFCN 21
```

```
Watkins, Maren
Garrett, James E.
                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Conus rattus
US-09-910-082A-236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Conus rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-910-082A-390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-910-082A-390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 88
US-10-765-926-236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠ
                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                         Ouery Match
37.9%; Score 61; DB 10; Length 74;
Best Local Similarity 38.1%; Pred. No. 3.4;
Matches 8; Conservative 6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 37.9%; Score 61; DB 16; Length 74; Best Local Similarity 38.1%; Pred. No. 3.4; Matches 8; Conservative 6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M. APPLICANT: Michael APPLICANT: Watkins, Maren APPLICANT: Garrett, James E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEODIL 00.
WS-09-910.002A-236

Sequence 236, Application US/09910082A

Publication No. US20030119731A1

GENERAL INFORMATION: ...

APPLICANT: University of Utah Research Foundation

APPLICANT: Cognetix, Inc.

APPLICANT: Olivera, Baldomero M.

APPLICANT: McIntosh, J. Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US/10/765,926

PRIOR APPLICATION NUMBER: US 09/910,082

PRIOR FILING DATE: 2001-07-23

PRIOR PLILING DATE: 2001-07-21

PRIOR PELICATION NUMBER: US 60/219,616

PRIOR PELING DATE: 2000-07-21

PRIOR PELING DATE: 2001-02-05

NUMBER OF SEQ ID NOS: 413

SOFTWARE: PATENTIN OF 51

LENGTH: 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Shon, Ki-Joan
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Cartier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
CURRENT APPLICATION NUMBER: US/10/765,926
CURRENT FILING DATE: 2004-01-29
                                                                                                                                                                                     ; OTHER INFORMATION: unknown Conus species US-09-910-082A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) OTHER INFORMATION: unknown Conus species US-10-765-926-5
                                                                                                                                                                                                                                                                                                                                                     1 CRIXNOKCFQHLDDCCSRKCN 21
                                                                                                                                                                                                                                                                                                                                                                                  | : : : | | : : | | 47 CKPPGRKCLNRKNECCSKFCN 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CRIXNOKCFOHLDDCCSRKCN 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47 CKPPGRKCLNRKNECCSKFCN 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/10765926; Publication No. US20040132663A1; GENERAL INFORMATION:
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: Patentin version 3.0
SEQ ID NO 5
LENGTH: 74
                                                                                                               TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                    FEATURE
                                                                                            LENGIH:
                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQ
```

```
APPLICANT: Signar M.-Coom
APPLICANT: Signar M.-Coom
APPLICANT: Oscobeen, R.-Coom
APPLICANT: Oscobeen, R
```

ï

```
Gaps
                                                             1;
     Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10; Length 74;
                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Markins, Maren
APPLICANT: Matkins, Maren
APPLICANT: Sancet, James E.
APPLICANT: Shon, Ki-Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Cartier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
Ouery Match
37.0%; Score 59.5; DB 16;
Best Local Similarity 45.5%; Pred. No. 2.1;
Matches 10; Conservative 2; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: University of Utah Research Foundation APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M. APPLICANT: McInael APPLICANT: Watkins, Maren APPLICANT: Garrett, James E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTAGES (100-5)
FILE REPERENCE: 2314-241
CURRENT APPLICATION NUMBER: US/09/910,082A
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR FILING DATE: 2000-07-21
PRIOR PILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SEQ ID NO 235
LENGTH: 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
37.0%; Score 59.5; D
Best Local Similarity 45.5%; Pred. No. 5.1;
Matches 10; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Jacobsen, Richard
APPLICANT: Jones, Robert M.
APPLICANT: Cartier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
CURRENT APPLICATION NUMBER: US/10/765,926
CURRENT FILING DATE: 2004-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2004-01-29
PRIOR APPLICATION NUMBER: US 09/910,082
PRIOR FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/265,888
                                                                                                                                                                                                                                                                                        Sequence 215, Application US/09910082A Publication No. US20030119731A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 235, Application US/10765926 Publication No. US20040132663A1 GENERAL INFORMATION:
                                                                                                                  1 CRIXNOKCFOHLDDCCSRKCNR 22
                                                                                                                                                      1 CNARNDGCSQH-SQCCSGSCNK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48 CNARNDGCSQH-SQCCSGSCNK 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CRIXNQKCFQHLDDCCSRKCNR 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shon, Ki-Joon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Conus rattus
                                                                                                                                                                                                                                                                                US-09-910-082A-235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-910-082A-235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -10-765-926-235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 59.5; DB 16; Length 27;
Pred. No. 2.1;
2; Mismatches 9; Indels 1
                                                                        APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Mointeel
APPLICANT: Mointesh, J. Michael
APPLICANT: Markins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Shon, Ki-Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jacobsen, Richard
APPLICANT: Jones, Robert M.
APPLICANT: Garrier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/765,926
CURRENT FILING DATE: 2004-01-29
PRIOR APPLICATION NUMBER: US 09/910,082
PRIOR FILING DATE: 2001-07-23
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2001-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: Patentin version 3.0
SEQ ID NO 236
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, Jr. Michael
APPLICANT: McIntosh, Jr. Michael
APPLICANT: Garrett, James E.
APPLICANT: Shon, Ki-Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Jones, Robert M.
APPLICANT: Cartier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
TITLE OF INVENTION: 2314-241
CURRENT APPLICATION NUMBER: US/10/765,926
CURRENT FILING DATE: 2004-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 09/910,082
PRIOR FILING DATE: 2004-01-29
PRIOR FILING DATE: 2001-07-23
PRIOR PLICATION NUMBER: US 60/219,616
PRIOR PLILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR PLILING DATE: 2000-07-21
PRIOR PILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: PATENTIN VETSION 3.0
SEQ ID NO 390
LIENGTH. 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 390, Application US/10765926 Publication No. US20040132663A1 GENERAL INFORMATION:
     Application US/10765926
o. US20040132663A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CRIXNQKCFQHLDDCCSRKCNR 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CNARNDGCSQH-SQCCSGSCNK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 45.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Conus rattus
US-10-765-926-390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Conus rattus
US-10-765-926-236
```

원 ò

us-10-627-685a-26.rapb

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 36.3%; Score 58.5; DB 10; Length 27; Best Local Similarity 45.5%; Pred. No. 2.8; Matches 10; Conservative 2; Mismatches 9; Indels
                                                                                                                                       DB 14; Length 735; 43;
                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                             Sequence 321, Application US/09910082A
| Publication No. US20030119731A1
| GENERAL INFORMATION:
| APPLICANT: University of Utah Research Foundation
| APPLICANT: Cognetix, Inc.
| APPLICANT: Cognetix, Inc.
| APPLICANT: McIntosh, J. Michael
| APPLICANT: McIntosh, J. Michael
| APPLICANT: McIntosh, J. Michael
| APPLICANT: Garrett, James E.
| APPLICANT: Garcett, James E.
| APPLICANT: Garcett M. APPLICANT: Cartier, G. Edward
| TITLE OF INVENTION: Omega-Conopeptides
| FILE REPERENCE: 2314-241
| CURRENT FILING DATE: 2001-07-23
| FRIOR FILING DATE: 2000-07-21
| FRIOR FILING DATE: 2001-07-20
| NUMBER OF SEQ ID NOS: 413
| SOFTWARE: PatentIn Version 3.0
| SEQ ID NOS: 413
                                                                                                                                                                                   7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1: University of Utah Research Foundation
1: Cognetix, Inc.
1: Olivera, Baldomero M.
1: McIntosh, J. Michael
1: Matkins, Maren
1: Garrett, James B.
1: Shon, Ki-Joon
1: Jacobsen, Richard
                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Jones, Robert M.
APPLICANT: Cartier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
CURRENT APPLICATION NUMBER: US/09/910,082A
CURRENT FILING DATE: 2001-07-23
                                                                                                                                       Score 59;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 392, Application US/09910082A
Publication No. US20030119731A1
                                                                                                                                                                                                                                                    254 CEKNIDDCVNSKCENGGKCV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CRIXNOKCFOHLDDCCSRKCNR 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CNARNSGCSQH-PQCCSGSCNK 21
                                                                                                                                                                                                                         8 CFQHLDDCCSRKCNRFNKCV 27
                                         ; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-289-776-9
                                                                                                                             Query Match
Best Local Similarity 45.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT; ORGANISM: Conus rattus
US-09-910-082A-391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            US-09-910-082A-391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 95
US-09-910-082A-392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater: Steven C.
APPLICANT: Slater: Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EXPRESSION OF FILE REFERENCE: 38-10 (52052) B.
CURRENT APPLICATION NUMBER: US/10/369, 493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 6999
                                                                                                                                                                                                                                                                     ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                      Query Match
37.0%; Score 59.5; DB 16; Length 74;
Best Local Similarity 45.5%; Pred. No. 5.1;
Matches 10; Conservative 2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
36.6%; Score 59; DB 15; Length 601;
Best Local Similarity 45.0%; Pred. No. 36;
Matches 9; Conservative 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/10289776;
Publication No. US20030170727A1
GENERAL INFORMATION:
APPLICANT: Goodman, Corey
APPLICANT: Rid, Thomas
APPLICANT: Brose, Katja
APPLICANT: Tessier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions;
FILE REFERENCE: B98-031.3
CURRENT APPLICATION NUMBER: US/10/289,776
CURRENT FILING DATE: 2002-11-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATE: 2002-11-06
PRIOR APPLICATION NUMBER: US/09/540,245
PRIOR FILING DATE: 2000-03-31
PRIOR PLING DATE: 1907-11-14
PRIOR PLING DATE: 1997-11-14
PRIOR PLING DATE: 1998-04-07
PRIOR PLING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-369-493-6999
Sequence 6999, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                  1 CRIXNOKCFOHLDDCCSRKCNR 22
                                                                                                                                                                                                                                                                                                                                                48 CNARNDGCSQH-SQCCSGSCNK 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 CEKNIDDCVNSKCENGGKCV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 CFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Caenorhabditis elegans
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: PatentIn version 3.0
SEQ ID NO 235
LENGTH: 74
                                                                                                            TYPE: PRT ORGANISM: Conus rattus US-10-765-926-235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-369-493-6999
                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                              a
```

ò g

```
1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.3%; Score 58.5; DB 10; Length 74; 45.5%; Pred. No. 6.7; tive 2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 238, Application US/09910082A

Sublication No. US20030119731A1

GENERAL INFORMATION:

APPLICANT: University of Utah Research Foundation

APPLICANT: Cognetix, Inc.

APPLICANT: Cognetix, Inc.

APPLICANT: Markins, Maren

APPLICANT: Watkins, Maren

APPLICANT: Watkins, Maren

APPLICANT: Garrett, James E.

APPLICANT: Garrett, James E.

APPLICANT: Jacobsen, Richard

APPLICANT: Jacobsen, Rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 36.3%; Score 58.5; DB 16; Best Local Similarity 45.5%; Pred. No. 2.8; Matches 10; Conservative 2; Mismatches 9;
                                                                                                                      APPLICANT: Jones, Robert M.
APPLICANT: Cartier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
CURRENT FILING DATE: 2004-01-29
PRIOR APPLICATION NUMBER: US 09/910,082
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR APPLICATION NUMBER: US 60/265,888
PRIOR APPLICATION NUMBER: US 60/265,888
PRIOR APPLICATION NUMBER: US 60/265,888
PRIOR FILING DATE: 2000-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: PatentIn version 3.0
SEQ ID NO 392
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CRIXNQKCFQHLDDCCSRKCNR 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CNARNSGCSQH-PQCCSGSCNK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CRIXNOKCFOHLDDCCSRKCNR 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48 CNARNSGCSQH-PQCCSGSCNK 68
                                                       Shon, Ki-Joon
Jacobsen, Richard
            Garrett, James E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 45.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Conus rattus
US-10-765-926-392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Conus rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 98
US-09-910-082A-238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-910-082A-238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36.3%; Score 58.5; DB 10; Length 27; 45.5%; Pred. No. 2.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 16; Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivers, Baldomero M.
APPLICANT: Olivers, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: Garrett, James E.
APPLICANT: Garrett, James E.
APPLICANT: Jacobsen, Richard
APPLICANT: Gartier, G. Edward
TITLE OF INVENTION: Omega-Conopeptides
FILE REFERENCE: 2314-241
CURRENT APPLICATION NUMBER: US 09/910,082
PRIOR FILING DATE: 2000-07-23
PRIOR FILING DATE: 2000-07-21
PRIOR PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 322, Application US/10765926
Sublication No. US20040132663A1
GENERAL INFORMATION:
APPLICANT: University of Utah. Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
36.3%; Score 58.5; E
Best Local Similarity 45.5%; Pred. No. 2.8;
Matches 10; Conservative 2; Mismatches
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/265,888
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SEQ ID NO 392
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 391, Application US/10765926
Publication No. US20040132663A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CRIXNOKCFOHLDDCCSRKCNR 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CRIXNQKCFQHLDDCCSRKCNR 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CNARNSGCSOH-POCCSGSCNK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CNARNSGCSQH-PQCCSGSCNK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 45.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Conus rattus
                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Conus rattus
                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-910-082A-392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 96
US-10-765-926-391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-765-926-391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 97
US-10-765-926-392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 391
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
```

Gaps

ï

Gaps

```
Length 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10;
                                            APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Watkins, Maren
APPLICANT: Garrett, James E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    University of Utah Research Foundation Cognetix, Inc. Olivera, Baldomero M. McIntosh, J. Michael Watkins, Maren
                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/910,082A
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/219,616
PRIOR PILING DATE: 2000-07-21
PRIOR PILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: Patentin version 3.0
LENGTH: 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 36.3%; Score 58.5; D
Best Local Similarity 45.5%; Pred. No. 6.7;
Matches 10; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPLICANT: Jones, Robert M.
PPLICANT: Cartier, G. Edward
TTLE OF INVENTION: Omega-Conopeptides
Sequence 241, Application US/09910082A
Publication No. US20030119731A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CRIXNOKCFOHLDDCCSRKCNR 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48 CNARNSGCSQH-PQCCSGSCNK 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 238, Application US/10765926
Publication No. US20040132663A1
                                                                                                                                           Shon, Ki-Joon
Jacobsen, Richard
                                                                                                                                                                                                                         FILE REFERENCE: 2314-241
                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Conus rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Conus rattus
US-10-765-926-238
                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-910-082A-241
                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
```

DB 16; Length 74;

36.3%; Score 58.5;

Query Match

```
1; Gaps
                         9; Indels
Best Local Similarity 45.5%; Pred. No. 6.7; Matches 10; Conservative 2; Mismatches
                                                    1 CRIXNOKCFQHLDDCCSRKCNR 22
                                                                                  48 CNARNSGCSQH-PQCCSGSCNK 68
                                                                             셤
                                                    ò
```

Search completed: April 18, 2005, 20:43:01 Job time: 92.5 secs

concoxin-like pro acetylcholinestera protein F6N18.15 [EGF repeat transme hypothetical prote conserved hypothet chypothetical prote conserved hypothet concoxin homolog

intrinsic factor-B I-superfamily cono interleukin-1 beta glycoprotein A - m hypothetical prote hypothetical prote

conserved hypothet protein T07E3.4 [i hypothetical prote

integrin beta chai fibropellin Ia - 8 Motch B protein -

hypothetical prote

prote

protein -

prot

transmembrane hypothetical notch 3 prote

hypothetical 14.7K pancreatic ribonuc

protein C24B5.5

hypothetical prote tenascin precursor

hypothetical profe

propionyl acylase probable vitelloge omega-conotoxin GV conotoxin-like pro

notch protein homo notch-1 protein -omega-conotoxin MV crumbs protein - f cell-fate determin

```
Yotch protein - Af
lectin heavy chain
galactose binding
notch protein - fr
omega-conotoxin MV
lectin heavy chain
homeotic protein I
LIM domain transcr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 kappa-conotoxin PV omega-conotoxin SV omega-conotoxin MV hypothetical prote protein F40E10.4 [
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       homeotic protein l
homeotic protein l
homeotic protein l
homeotic protein l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           omega-conotoxin MV
hypothetical prote
glycosyltransferas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical prote
hypothetical prote
hypothetical prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      notch homolog - se
notch protein homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hydroxymethylgluta
170K lectin precur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neurogenic repetit
hypothetical prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                   April 18, 2005, 20:23:04 ; Search time 26.5 Seconds (without alignments) 98.032 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                            283416
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                          US-10-627-685A-26
161
1 CRIXNQKCFQHLDDCCSRKCNRFNKCV
                                                                                                                                                                                                                                                                                                      283416 segs, 96216763 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        summaries
                                                                     model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C44379
JH0699
DB97111
A35844
S2653
T09229
A24420
A24420
JH0701
I58187
I18186
I18637
I18837
I1
                                                                                                                                                                                                                                                  BLOSUM62DX
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A58997
                                                                   protein search, using sw
                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 s
                                                                                                                                                                                                                                                                                                                                                                               seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>B</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *
Query
Match Length D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     601
1924
1924
1927
2703
2703
2703
252
253
1372
253
1372
253
1372
253
1372
253
1372
253
1372
253
1372
253
1372
354
354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161
71
61
59
59
                                                                                                                                                                            Title:
Perfect score:
                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
                                                                                                                                                                                                                                                                                                                                                                              Minimum DB Maximum DB
                                                                   OM protein
                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database
                                                                                                       Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ટ્ર
```

3567 448 448 436 436 436 443 443 443 443 443	1135017 1723017 1723017 1723017 1723017 1723017 173	4400444036841000088888888888888888888888888888888
~~~~~~~~~~~~	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	010010000000000000000000000000000000000
<b>3000000000000000000000000000000000000</b>	1887 3311 3311 1208 1208 403 3623 3623 3623 3623 3623 395 1516 1064 1120 1129 1129 1129 1129 1129 1284 1291 1204 1204 1204 1204 1204 1204 1204 120	NWWO0004404WWB0100440044W008000WR
	, чем	000000000000000000000000000000000000000
52 52 51 51 51 51 51 51 51 51		444444 000000000 444444444444 444444
0 11 2 12 14 14 14 14 14 14 14 14 14 14 14 14 14	4 4 4 4 4 4 4 W W W W W W W W W W W W W	1 4 4 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7

major merozoite su hydroxymethylgluta merozoite surface major merozoite su major merozoite su

protamine I - rabb hypothetical prote hypothetical prote neurogenic protein gene Delta protein neurogenic repetit homeotic protein I

notch3 protein - h variant-specific s alpha-2-macroglobu alpha-2-macroglobu pancreatic ribonuc

finger protein HPF apoptosis inhibito IAP2 orf71 - Bomby repB protein - Cam

transcription repr hypothetical prote transcription regu agpt protein (AF23 rRNA methylase (Sp hypothetical prote

## ALIGNMENTS

```
C;Species: Conus magus (magus cone)
C;Date: 17-Apr-1993 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
C;Accession: JH0699; PC2380
C;Accession: JH0699; PC2380
R;Hillyard, D.R.; Monje, V.D.; Mintz, I.M.; Bean, B.P.; Nadasdi, L.; Ramachandran, J.; Mn. Neuron 9, 69-77, 1992
A;Title: A new conus peptide ligand for mammalian presynaptic Ca2+ channels.
A;Reference number: JH0699; MUID:92337922; PMID:1352986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RiFerral Jones, S.; Basus, V.J.

Submitted to the Brookhaven Protein Data Bank, December 1994

A;Reference number: A6629; PDB:10MM
A;Contents: annotation; conformation by (1)H-NMR, residues 3-28
A;Contents: annotation; conformation by (1)H-NMR, residues 3-28
B;Farr-Jones, S.; Miljanich, G.P.; Nadasdi, L.; Ramachandran, J.; Basus, V.J.
J. Mol. Biol. 248, 106-124, 1995
A;Title: Solution structure of omega-connotxin MVIIC, a high affinity of P-type calcium classification number: A56882; MUID:95248539; PMID:7731037
A;Contents: annotation; conformation by (1)H-NMR
C;Superfamily: omega-connotxin
C;Superfamily: omega-connotxin MVIIC fatatus experimental carboxyl end; calcium channel inhord; R;3-28/Product: omega-connotoxin MVIIC fatatus experimental
F;3-28/Product: amidated carboxyl end (Cys) (amide in mature form following glyc)
                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-29 cHIL>
A; Residues: 1-29 cHIL>
A; Crossidues: 1-29 cHIL>
A; Crossidues: 1-29 cHIL>
B; Nemocro, N.; Kubo, S.; Yoshida, T.; Chino, N.; Kimura, T.; Sakakibara, S.; Kyogoku, Y.;
Biochem. Biophys. Res. Commun. 207, 695-700, 1995
A; Title: Solution structure of omega-conotoxin MVIIC determined by NMR.
A; Reference number: PC2380; MUID:95169113; PMID:7864862
A; Accession: PC2380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-fo1 <WLL>
A;Residues: 1-fo1 <WLL>
A;Cross-references: UNIPROT:Q20204; EMBL:Z69792; PIDN:CAA93668.1; GSPDB:GN00028; CESP:F4(
Experimental source: clone F40E10
C;Genetics:
A;Gene: CESP:F40E10.4
               - cone shell (Conus magus) (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein F40E10.4 - Caenorhabditis elegans (fragment)
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22025
R;Smye, R.
Submitted to the EMBL Data Library, February 1996
A;Reference number: Z19503
A;Reference number: Z19503
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Solecule type: DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.6%; Score 59; DB 2; Length 601;
45.0%; Pred. No. 13;
tive 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.9%; Score 61; DB 2; Length 29; 38.5%; Pred. No. 1.1; Live 4; Mismatches 12; Indels
Omega-conotoxin MVIIC precursor [validated]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 CKGKGAPCRKTMYDCCSGSCGRRGKC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CRIXNQKCFQHLDDCCSRKCNRFNKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 CEKNIDDCVNSKCENGGKCV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 CFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 38.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 45.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein A; Residues: 3-28 <NEM>
                                                                                                                                                                                                                                                                                            A; Accession: JH0699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Map position: X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2

(04379)

(0483-79)

(0483-79)

(0483-79)

(0483-79)

(158-creat count SVIB [validated] - cone shell (Conus striatus)

(158-creat counts striatus (striated cone)

(158-creat counts striatus (striated cone)

(159-creat counts striatus (striated cone)

(159-creat cons striatus (striated cone)

(150-creat cone)
                                                                   Appa-conotoxin PVIIA - cone shell (Conus purpurascens)

NyAlternate names: fin-popping peptide
CySpecies: Conus purpurascens (purple cone,)
CySpecies: Conus purpurascens (purple cone,)
CyAccession: A58997
RyTerlau, H.; Shon, K.J.; Grilley, M.; Stocker, M.; Stuehmer, W.; Olivera, B.M.
Nyture 381, 148-151, 1996
A;Tetle: Strategy for rapid immobilization of prey by a fish-hunting marine snail.
A;Reference number: A58997
A;Reference number: A58997
A;Reference protein
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 1-27 cTER.
A;Residues: 1-27 cTER.
A;Cross-references: UNIPROT: P56633
C;Comment: This conotoxin blocks conductance of the Shaker potassium channel.
C;Keywords: hydroxyproline; neurotoxin; venom
F;4/Modified site: 4-hydroxyproline (Pro) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 161; DB 2; Length 27; 96.3%; Pred. No. 5.2e-12; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 71; DB 2; Length 26;.
Pred. No. 0.074;
4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CRIPNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CHIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch .44.1%;
il Similarity 42.3%;
11; Conservative .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            엄
```

ö

ന

```
Gladicose binding adhesin heavy chain - Entamoeba histolytica
C;Species: Entamoeba histolytica
C;Species: Entamoeba histolytica
C;Accession: T09229
R;Purdy, J.E.; Mann, B.J.; Shugart, E.C.; Petri, W.A.
Mol. Blochem: Parashitol. 62, 53-59; 1993
A;Title: Analysis of the gene family encoding the Entamoeba histolytica galactose-specif;
A;Reference number: 216622; MUID:94158976; PMID:8114826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 1-48,1',50-118,'R',120-230,'I',232-256,'N',258-266,'A',268-872,'R',874-958,'
A;Note: the authors translated the codon ATC for residue 49 as Thr, ATT for residue 2044
R;Tautz, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                notch protein - fruit fly (Drosophila melanogaster)

NyAlternate names: neurogenic repetitive locus protein
Cispecies: Drosophila melanogaster eviain locus protein
Cispecies: Drosophila melanogaster eviain 10-Sep-1999 #text_change 16-Aug-2004
Cist. Britch S.; Kelley, M.R.; Young, M.W.
Rikdid, S.; Kelley, M.R.; Young, M.W.
Mol. Cell. Biol. 6, 3034-3108, 1986
A;Reference number: A24420; MUD:87064624; FMID:3097517
A;Accession: A24420
A;Accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 17, 6463-6471, 1989
A;Title: Hypervariability of simple sequences as a general source for polymorphic DNA mas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q24835; EMBL:L14815; NID:g290648; PID:g290649
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Э.
Э.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 56.5; DB 2; Length 1292;
Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 56.5; DB 2; Length 194;
Pred. No. 12;
3; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A24768; MUID: 86079539; PMID: 3935325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: T09229
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1292 <PUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 CSMGTDNIITYHDDCNSRKSQCGNFNGKCV 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CRIXNOKCFOHLDDCCSRK--CNRFN-KCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CRIXNOKCFQHLDDCCSRK--CNRFN-KCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 35.1%; ll Similarity 43.3%; l3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 35.1%;
Best Local Similarity 43.3%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Gene: hgl3
C,Keywords: lectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠ
                                                                                                     C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: D89711
R;anonymous, The C: elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C: elegans: a platform for investigating biolog A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl:edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: D89711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-601 <STO>
A;Cross-references: UNIPROT:Q20204; GB:chr_X; PIDN:CAA93668.1; PID:g3877014; GSPDB:GN000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession: A35844
Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lectin heavy chain, N-acetylgalactosamine-specific - Entamoeba histolytica (fragment) C;Species: Entamoeba histolytica (c;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A35844
Xotch protein - African clawed frog
C;Species: Kenopus laevis (African clawed frog)
C;Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 16-Aug-2004
C;Accession: A35844
R;Coffman, C.; Harris, W.; Kintner, C.
Science 249; 1438-1441, 1990
A;Title: Xotch, the Xenopus homolog of Drosophila notch.
A;Title: Xotch, the Xenopus homolog of Drosophila notch.
A;Reference number: A35844; MUID:90385285; PMID:2402639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wolecule type: mRNA
Residues: 1-2524 <COF>
Superfamily: Notch protein; ankyrin repeat homology; EGF homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.6%; Score 59; DB 2; Length 601;
45.0%; Pred. No. 13;
tive 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                    protein F40E10.4 [imported] - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 57; DB 2;
Pred. No. 58;
4; Mismatches 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <AN5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F:1991-2023/Domain: ankyrin repeat homology F:2024-2056/Domain: ankyrin repeat homology F:2057-2089/Domain: ankyrin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ankyrin repeat homology
ankyrin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEO SGONCEENIDDCPSNNCRNGGTCV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 XNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1025-1056/Domain: EGF homology <EGX3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 CEKNIDDCVNSKCENGGKCV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;146-177/Domain: EGF homology <EGX1>F;184-215/Domain: EGF homology <EGF>F;225-254/Domain: EGF homology <EGR>F;456-487/Domain: EGF homology <EGX2>F;757-788/Domain: EGF homology <EGX2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 CFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.4%;
ilarity 37.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;1924-1956/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :1957-1989/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: S70663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Genetics:
A;Gene: F40E10.4
A;Map position: X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S70663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
```

1;

Gaps

```
A,Title: Physical mapping and expression of gene families encoding the N-acetyl D-galactor A,Reference number: S70662; MUID:96419166; PMID:8821939
A,Accession: S70664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C,Accession: S23802
R,Taira, M.; Jamrich, M.; Good, P.J.; Dawid, I.B.
Genes Dev. 6, 356-366, 1992
A,Title: The LIM domain-containing homeo box gene Xlim-1 is expressed specifically in the A;Reference number: S23802; MUID:92192449; PMID:1347750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AjGene: lim-1
C;Superfamily: homeotic protein lim-1; homeobox homology; LIM metal-binding repeat homolo
C;Keywords: DNA binding; duplication; embryo; homeobox; nucleus; transcription regulatior
F;4+54/Domain: LIM.metal-binding repeat homology <LIM1>
F;63-117/Domain: LIM metal-binding repeat homology <LIM2>
F;180-236/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-403 <TAL>
A;Cross-references: UNIPROT:P29674; EMBL:X63889; NID:g64829; PIDN:CAA45353.1; PID:g64830
C;Genetics:
                                                                                                                                                                                                                                                                           ectin heavy chain, N-acetylgalactosamine-specific - Entamoeba histolytica (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
G01507
LIM domain transcription factor LIM-1 - human
N/Alternate names: homeotic protein lim-1
C;Species: Homo sapiens (man)
C;Accession: G01507
R;Dong, W.
                                                                                                                                                                                                                                                                                                 C;Species: Entamocba histolytica
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Species: Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: UNIPROT: Q24822; EMBL: U33444; NID: 9993054; PID: 9993055
            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ٠.
۳
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 403; 29;
            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Indels
                                                                                                                                                                                                                                                                                                                                                                                             R;Ramakrishnan, G.; Ragland, B.D.; Purdy, J.E.; Mann, B.J.
Mol. Microbiol. 19, 91-100, 1996
            1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 CSMGTDNVITYHDDCNSRKSQCGNFNGKCI 148
            4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 55.5; |
Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CRIXNOKCFQHLDDCCSRK--CNRFN-KCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translation not shown A;Molecule type: DNA
                                                                   1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                              1 CKGKGASCHRTSYDCCTGSCNR-GKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 55;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 RIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 44.0%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 40.0
Matches 12; Conservative
            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-194 < RAM>
                                                                                                                                                                                                                                                                                                                                                                 C;Accession: S70664
            10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: hgl5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetics
         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
                                                                                                                 g
                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d
                     A;Accession: 809358
A;Molecule type: DNA
A;Residues: 2505-2511, QQQQ, 2552-2576, E', 2578-2604 <TAU>
A;Residues: 2505-2151, QQQQ, 2552-2576, E', 2578-2604 <TAU>
B;Marton, K.A.; Yedvobnick, B.; Finnerty, V.G.; Artavanis-Tsakonas, S.
Cell 40, 55-62, 1985
A;Title: opa: a novel family of transcribed repeats shared by the Notch locus and other A;Title: opa: a novel family of principles repeats shared by the Notch locus and other A;Reference number: A05267; MUID:85099329; PMID:2981631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Mesidues: 1-25 <01.1>
C;Superfamily: omega-conotoxin
C;Keywords: acetylcholine release inhibition; amidated carboxyl end; calcium channel inh
F;1-16,8-20,15-25/Disulfide bonds: #status predicted
F;25/Modified site: amidated carboxyl end (Cys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P05485
R;Olivera, B.M.; Cruz, L.J.; de Santos, V.; LeCheminant, G.W.; Griffin, D.; Zeikus, R.;
Biochemistry 26, 2086-2090, 1987
A;Title: Neuronal calcium channel antagonists. Discrimination between calcium channel su A;Reference number: A34115; MUID:87299637; PMID:2441741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               omega-conotoxin MVIIB - cone shell (Conus magus)
C;Species: Conus magus (magus cone)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: JH0701; B34115
R;H1llyard, D.R.; Monje, V.D.; Mintz, I.M.; Bean, B.P.; Nadasdi, L.; Ramachandran, J.; Neuron 9, 69-77, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title: A new conus peptide ligand for mammalian presynaptic Ca2+ channels. Reference number: JH0699; MUID:9237922; PMID:1352986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;2538-2568/Domain: neurogenic repetitive element #status predicted <OPA>
                                                                                                                                                                                                                                                                                                                                                                              A)Cross-references: FlyBase:FBgn0004647
A;Map position: 8.96-9.36
A;Introns: 53/3; 84/3; 171/3; 240/3; 283/3; 2333/3; 2436/3; 2588/3
C;Superfamily: Notch protein; ankyrin repeat homology; EGF homology
C;Keywords: differentiation; tandem repeat; transmembrane protein
F;27-43/Domain: transmembrane #status predicted <TMM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 56; DB 1; Length 2703;
Pred. No. 79;
5; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transmembrane #status predicted <TMM2>
Reference number: S09358; MUID:89385974; PMID:2780284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;1950-1982/Domain: ankyrin repeat homology <ANI>F;1983-2015/Domain: ankyrin repeat homology <ANI>F;1988-2004/Domain: transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;2017-2049/Domain: ankyrin repeat homology <AN3>F;2050-2082/Domain: ankyrin repeat homology <AN4>F;2083-2115/Domain: ankyrin repeat homology <AN5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 55.5; Di
Pred. No. 4.1;
                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 2504-2576,'E',2578-2611 <WHA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 XNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: JH0701
Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;988-1019/Domain: EGF homology <EGX2>F;1064-1095/Domain: EGF homology <EGF3>F;1187-1218/Domain: EGF homology <EGX3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297-328/Domain: EGF homology <EGX1>
530-561/Domain: EGF homology <EGF1>
568-599/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2538-2568/Region: glutamine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 33.3%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: mRNA
Residues: 1-25 <HIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;1746-1762/Domain:
                                                                                                                                                                                                                                                                                                                                                        A;Gene: notch; opa
```

g ð

.; %

Gaps

;

Gaps

```
C;Superfamily: homeotic protein lim-1; homeobox homology; LIM metal-binding repeat homolc C:Keywords: DNA binding; duplication; embryo; homeobox; nucleus; transcription regulatior F;4-54/Domain: LIM metal-binding repeat homology <LIM1>
F;63-117/Domain: LIM metal-binding repeat homology <LIM2>
F;8181-237/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homeotic protein lim-1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accesion: 146637; 842788
R;Fujil, T.; Pichel, J.G.; Taira, M.; Toyama, R.; Dawid, I.B.; Westphal, H.
Dev. Dyn. 199, 73-83, 1994
A;Fitle: Expression patterns of the murine LIM class homeobox gene lim1 in the developing
A;Reference number: 148637; MUID:94220754; PMID:7909459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Wolecule type: mRNÅ
A;Residues: 1-406 <FUJ>
A;Cross-references: EMBL:Z27410; NID:g425216; PIDN:CAA81797.1; PID:g425217
A;Cross-references: EMBL:Z27410; NID:g425216; PIDN:CAA81797.1; PID:g425217
C;Genetics:
A;Gene: Lhx1
C;Superfamily: homeotic protein lim-1; homeobox homology; LIM metal-binding repeat homology
C;Keywords: DNA binding; duplication; embryo; homeobox; nucleus; transcription regulatior
F;4-54/Domain: LIM metal-binding repeat homology <LIM1>
F;63-117/Domain: LIM metal-binding repeat homology <LIM2>
F;181-237/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P36199; EMBL:Z27410; NID:g425216; PIDN:CAA81797.1; PID:g42521
R;Fujii, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: I50375

R;Tsuchida, T.; Ensini, M.; Morton, S.B.; Baldassare, M.; Edlund, T.; Jessell, T.M.; Pfa:
Cell 79, 957-970, 1994
A;Title: Topographic organization of embryonic motor neurons defined by expression of LII
A;Reference number: A55198; MUID:95094281; PMID:7528105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule_type: mRNA
A;Residues: 1-406 <TSU>
A;Cross-references: UNIPROT:P53411; GB:L35569; NID:g531182; PIDN:AAA62173.1; PID:g531183
C;Genetics:
                                                                                                                                                                                                                                                                                                                                             ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                homeotic protein lim-1 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
                                                                                                                                                                                                                                                                  Match 34.2%; Score 55; DB 1; Length 406; Local Similarity 44.0%; Pred. No. 29; es 11; Conservative 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 55; DB 1; Length 406;
Pred. No. 29;
2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, November 1993
A,Reference number: S42788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.2%; Score 55; 44.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                     2 RIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 RAWHVKCVQ----CCECKCNLTEKC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 RAWHVKCVQ----CCECKCNLTEKC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 RIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 44.0%
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-406 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: I50375
                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: lim-1
                                                                                                                                                                                                                                                                                                            Best Loca
                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
Submitted to the EMBL Data Library, September 1994
A,Reference number: G07570
A,Accession: G01507
A,Crossion: G01507
A,Crossion: G01507
A,Crossion: G01507
A,Crossion: G01507
A,Gene: hLIM-1
C,Superfamily: homeotic protein lim-1; homeobox homology; LIM metal-binding repeat homology
C,Superfamily: Manetal-binding repeat homology <LIMI>F;4-54/Domain: LIM metal-binding repeat homology <LIMI>F;63-117/Domain: LIM metal-binding repeat homology <LIMI>F;63-117/Domain: LIM metal-binding repeat homology <LIMI>F;81-237/Domain: LIM metal-binding repeat homology <LIMI>F;81-237/Domain: LIM metal-binding repeat homology <LIMI>F;81-237/Domain: LIM metal-binding repeat homology <LIMI>F;81-81-237/Domain: LIMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: homeotic protein lim-1; homeobox homology, LIM metal-binding repeat homol C;Keywords: DNA binding; duplication; embryo; homeobox; nucleus; transcription regulatic ep. 45-45-40main: LIM metal-binding repeat homology <LIM1> F;63-117/Domain: LIM metal-binding repeat homology <LIM2> F;81-237/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Crosв-references: UNIPROT:P36199; EMBL:X81407; NID:g587462; PIDN:CAA57164.1; PID:g5874
С;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cispecies: Factus sp. (rat)
Cispecies: Rattus sp. (rat)
Cispecies: Rattus sp. (rat)
Cispecies: Sattus sp. (rat)
Cispecies: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
Cispecession: ISBN 1.
Neurosci. Lett. 170, 266-268, 1994
A;Title: Distribution of Rlim, an LIM homeodomain gene, in the rat brain.
A;Reference number: ISBN 37
A;Accession: ISBN 37
A;Accession: ISBN 37
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: mRNA
A;Residues: 1-406 <RES>
A;Cross-references: GB:S71523; NID:g559635; PIDN:AAC60696.1; PID:g559636
Cigenetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homeotic protein lim-1 - golden hamster
N;Alternate names: homeotic protein lmx2
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I48186
R;Rudnick, A.; Ling, T.Y.; Odagiri, H.; Rutter, W.J.; German, M.S.
Proc. Natl. Acad. Sci. U.S.A. 91, 12203-12207, 1994
A;Title: Pancreatic beta cells express a diverse set of homeobox genes.
A;Reference number: I48185; MuID:95083670; PMID:7991607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 34.2%; Score 55; DB 1; Length 406; Best Local Similarity 44.0%; Pred. No. 29; Matches 11; Conservative 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-406 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 55; DB Pred. No. 29; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | :: || | | || || || || || || || RAWHVKCVQ----CCECKCNLTEKC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 RIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 RAWHVKCVQ----CCECKCNLTEKC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
```

us-10-627-685a-26.rpr

```
A;Accession: T25933
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 33.3
Matches 10; Conservative
                                                                                                                      hypothetical protein T06G6.6
                                                                                                                                                                                                                                                                                                               A; Reference number: Z19913
A; Accession: T24619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
es 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: CESP: T06G6.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: CAC2351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Contents: annotation
R; Mielsen, K.J.; Thomas, L.; Lewis, R.J.; Alewood, P.F.; Craik, D.J.
R; Mielsen, K.J.; Thomas, L.; Lewis, R.J.; Alewood, P.F.; Craik, D.J.
R; Mielsen, K.J.; Thomas, L.; Lewis, R.J.; Alewood, P.F.; Craik, D.J.
A; Reference number: A67648; PDB:1MVI
A; Contents: annotation; conformation by (1)H-NMR, residues 1-25
R; Mielsen, K.J.; Thomas, L.; Lewis, R.J.; Alewood, P.F.; Craik, D.J.
J; Mol. Biol. 263, 297-310, 1996
A; Title: A consensus structure for omega-conotoxins with different selectivities for vol A; Reference number: A58619; MID:9770382; PMED:8913308
A; Contents: annotation; conformation by (1)H-NMR
R; Kohno, T.; Kim, J.I.; Kobayashi, K.; Kodera, Y.; Maeda, T.; Sato, K.
S; Kohno, T.; Kim, J.I.; Kobayashi, K.; Kodera, Y.; Maeda, T.; Sato, K.
B; Contents: annotation; conformation by (1)H-NMR, residues 1-25
B; Contents: annotation; conformation by (1)H-NMR, residues 1-25
B; Contents: annotation; conformation by (1)H-NMR
A; Reference number: A6626; DB:10906
A; Title: Three-dimensional structure in solution of the calcium channel blocker omega-con A; Reference number: A68627; MID:93367555; PMID:7640281
A; Contents: annotation; conformation by (1)H-NMR
C; Superfamily: omega-conotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Accession: JH0700
A, Status: nucleic acid sequence not shown
A, Status: nucleic type: mRNA
A, Residues: 1-25 < HILL>
A, Cross-references: UNIPROT: P05484
S, Colorez 230, 1338-1343, 1985
A, Title: Peptide neurotoxins from fish-hunting cone snails.
A, Reference number: A43620; MUD: 86070213; PMID: 4071055
A, Accession: C60133
A, Molecule type: protein
A, Residues: 1-25 < Color.
A, Residues: 1-25 < Color.
B, Residues: 1-25 < Color.
A, Residues: 1-25 < Color.
B, Residues: 1-25 < Color.
A, Residues: 1-25 < Color.
A, Residues: 1-25 < Color.
B, Accession: Call (1987)
A, Title: Neuronal calcium channel antagonists. Discrimination between calcium channel submitter of the color.
A, Reference number: A34115; MUD: 87299637; PMID: 2441741
C; Superfamily: homeotic protein lim-1; homeobox homology; LIM metal-binding repeat homol C; Keywords: DNA binding; duplication; embryo; homeobox; nucleus; transcription regulatic F; 4-54/Domain: LIM metal-binding repeat homology <LIM1> F; 63-117/Domain: LIM metal-binding repeat homology <LIM2> F; 63-117/Domain: LIM metal-binding repeat homology <LIM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 omega-conotoxin MVIIA [validated] - cone shell (Conus magus)
(;Species: Conus magus cone)
(;Species: Conus magus cone)
(;Accession: JH0700, C66133; A34115
(;H11)yard, D.R.; Monje, V.D.; Mintz, I.M.; Bean, B.P.; Nadasdi, L.; Ramachandran, J.; Neuron 9, 69-77, 1992
A;Title: A new conus peptide ligand for mammalian presynaptic Ca2+ channels.
A;Reference number: JH0699; MUID:92337922; PMID:11552986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: omega-conotoxin
C;Keywords: acetylcholine release inhibition; amidated carboxyl end; calcium channel
F;1-16,8-20,15-25/Disulfide bonds: #status predicted
F;25/Modified site: amidated carboxyl end (Cys) #status experimental
                                                                                                                                                                                                                                                                                 ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ï
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                   DB 1; Length 406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 25;
                                                                                                                                                                                                                                                                          8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.3;
                                                                                                                                                                                                   34.2%; Score 55; DB 44.0%; Pred. No. 29; iive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 54.5;
Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                    2 RIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                         1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
33.9%;
Best Local Similarity 38.5%;
Matches 10, Conservative
                                                                                                                                                                                         Query Match
Best Local Similarity 44.0
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
```

```
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-239 cWIL.
A;Cross-references: UNIRROT:018052; EMBL:Z81587; PIDN:CAB04705.1; GSPDB:GN00019; CESP:TO6.
A;Experimental source: clone T06G6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycosyltransferase [imported] - Clostridium acetobutylicum Cispecies: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004 Cispecies: Orloginal Cispecies: Comelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A.Filte: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clos A.Reference number: A96900; MUID:21359325; PMID:21359325
A.Reference number: A96900; MUID:21359325; PMID:21359325
A.Restuus: preliminary
A.Reference DNA
A.Residues: 1-252 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:097GL5; GB:AE001437; PIDN:AAK80307.1; PID:g15025361; GSPDB:GN
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
       C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein W02C12.1 - Caenorhabditis elegans
CiSpecies: Caenorhabditis elegans
CiSpecies: Caenorhabditis elegans
CiSpate: 15-0Ct-1999 #sequence_revision 15-0ct-1999 #text_change 09-Jul-2004
CiAccession: T25933
R;Murray, J; Wohldmann, P.
Submitted to the EMBL Data Library, December 1996
A;Description: The sequence of C. elegans cosmid W02C12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 1
A;Introns: 20/1; 76/3; 103/3; 148/2; 183/2
C;Superfamily: Caenorhabditis elegans hypothetical protein T06G6.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
- Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
                                                                                                                               R;Kershaw, J.
submitted to the EMBL Data Library, November 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 54.5; DE Pred. No. 24; 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 IXNOKCFOHLD-----DCCSRKCNRFNK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 INDNGCFMHFDSKKLESIELCPLOCORFNE 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.9%; Score 54.5; I larity 37.0%; Pred. No. 24; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :: || :: || :
188 LAEDACF--IEDCCKQGIKIYSCNRFN 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 IXNOKCFOHLDDCCSR----KCNRFN 24
```

ОЪ

ઠે

ô

Gaps

ö

Indela

. 9

Mismatches

ï

10; Conservative

Matches

```
Status: preliminary; nucleic acid sequence not shown; not compared with conceptual trar:
Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                C; Accession: T31070

S; Sherwood, D.R., McClay, D.R.

B; Sherwood, D.R., McClay, D.R.

B; Sherwood, D.R., McClay, D.B.

A; Title: Identification and localization of a sea urchin Notch homologue: insights into A; Reference number: 220966; MUID:97454256; PMID:9310331

A; Accession: T11070

A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Species: J.-Apr.-1992 #sequence_revision 21-Apr-1992 #text_change 16-Aug-2004
C;Accession: A40043
R;Ellisen, L.W.; Bird, J.; West, D.C.; Soreng, A.L.; Reynolds, T.C.; Smith, S.D.; Sklar, Cell 66, 649-661, 1991
A;Title: TAN-1, the human homolog of the Drosophila Notch gene, is broken by chromosomal A;Reference number: A40043; MUID:91347367; PMID:1831692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Cross-references: EMBL:AF000634; NID:g2570350; PID:g2570351; PIDN:AAB82088.1 C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5), ozone-inducible - Scotch pine
                                                                                                                                                                                                                                                                        notch homolog - sea urchin (Lytechinus variegatus)
C;Species: Lytechinus variegatus (variegated urchin)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Superfamily: Notch protein; ankyrin repeat homology; EGF homology 261-292/Domain: EGF homology <EGX1> 494-525/Domain: EGF homology <EGF1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 32.9%; Score 53; DB 2; Length 2531; Best Local Similarity 45.0%; Pred. No. 1.7e+02; Matches 9; Conservative 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <AN4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 notch protein homolog TAN-1 precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;1927-1959/Domain: ankyrin repeat homology F;1960-1992/Domain: ankyrin repeat homology F;1949-42026/Domain: ankyrin repeat homology F;2027-2059/Domain: ankyrin repeat homology F;2060-2092/Domain: ankyrin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 53;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;987-1018/Domain: EGF homology <EGX2>
F;1149-1180/Domain: EGF homology <EGF>
F;1187-1218/Domain: EGF homology <EGF>
F;1233-1264/Domain: EGF homology <EGK3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 XNQKCFQHLDDCCSRKCNRFNKCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         662 CEEDIDDCESRPCHNGGTCV 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 CFQHLDDCCSRKCNRFNKCV 27
                                                                                                   :|||| |||| |
106 EHLDDDCSRKRARTGSC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 32.9%;
Best Local Similarity 33.3%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Residues: 1-2555 <ELL>
Cross-references: GB:M73980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-2531 <SHE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ර. අ
                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           유
                                                                    ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Date: 03-Mug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004
C; Accession: B71406
R; Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk
P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; Giel
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
A; Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech
erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q19345; EMBL:Z54270; PIDN:CAA91028.1; GSPDB:GN00028; CESP:F1
A;Experimental source: clone F11C1
A;Residues: 1-1372 <MUR>
A;Cross-references: UNIPROT:P91526; EMBL:U80815; PIDN:AAB37995.1; GSPDB:GN00022; CESP:WG
A;Experimental source: strain Bristol N2; clone W02C12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal A;Reference number: A71400; MUID:98121113; PMID:9461215
A;Accession: B71406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:023297; GB:Z97336; NID:g2244788; PID:e327451; PID:g2244797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: X
A;Introns: 39/3; 50/3; 87/1; 148/2; 190/1; 286/1; 377/3; 417/2; 499/2
C;Superfamily: steroid hormone receptor Ad4BP; erbA transforming protein homology
                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-277 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein P11C1.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 572;
                                                                                                                                                                                                                                      Score 54; DB 2; Length 1372;
Pred. No. 85;
7; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 53; DB 2; Length 277;
Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                       C;Genetics:
A;Gene: CESP:W02C12.1
A;Map position: 4
A;Introns: 29/1; 66/1; 774/2; 823/2; 1046/1; 1108/2; 1298/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 53.5; DB 2;
Pred. No. 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ripaimer, S. submitted to the EMBL Data Library, September 1995 A; Reference number: 219321 A; Reference number: 219321 A; Accession: T20764 A; Accession: T20764 A; Status: preliminary; translated from GB/EMBL/DDBJA; Molecule type: D.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46 VQNKKQYQCSAEANCHVDRTCRKRCPSCRFQKCL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 IXNOKCFQ-----HLDDCCSRKCN--RFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        4 XNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32.9%;
                                                                                                                                                                                                                                               33.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.2%;
al Similarity 32.4%;
11; Conservative
                                                                                                                                                                                                                Query Match
Best Local Similarity 29.4
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: 4COP9-4G3845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-572 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene: CESP:F11C1.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: T20764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.; Chalwatzis, N.
```

g

ઠે

ö

ö

ö

Gaps

ö

```
A;Residues: 1-354 <WIL>
A;Cross-references: UNIPROT:Q9XV21; EMBL:Z81540; PIDN:CAB04398.1; GSPDB:GN00023; CESP:F46|
A;Experimental source: clone F4683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Molecule type: mRNA
A,Residues: 1-2139 <TEP>
A,Cross-references: UNIPROT:P10040; GB:M33753
A,Note: the authors translated the codon GGC for residue 1928 as Cys, and TAT for residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: A35672
R;Tepass, U.; Theres, C.; Knust, E.
Rell 61, 787-799, 1990
A;Title: crumbs encodes an EGF-like protein expressed on apical membranes of Drosophila A;Teference number: A35672; MUID:90263104; PMID:2344615
                                                                                                                                                                                                                                                                                                                                                                                                                          C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #Bequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C:Species: Drosophila melanogaster
C:Date: 21-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Map position: 5
A;Introns: 23/1; 55/1; 82/1; 112/1; 142/1; 170/1; 193/1; 223/1; 299/1
                                                                                                                                  Length 293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2139;
                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F46B3.9 - Caenorhabditis elegans
                                                                                                                                  2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             crumbs protein - fruit fly (Drosophila melanogaster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: T22274
Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32.3%; Score 52; DB 2;
30.4%; Pred. No. 1.9e+02;
ive 6; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R,Ainscough, R.
Submitted to the EMBL Data Library, November 1996
                                                                                                                                ВВ
                                                                                                                                                     Pred. No. 52;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.3%; Score 52; DB
35.7%; Pred. No. 58;
tive 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158 CKLVNGSPKCVPELDQCSHIKCSIGSHC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CRIXN--OKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                          / Match 32.3%; Score 52; Local Similarity 30.4%; Pred. No. nes 7; Conservative 6; Mismatc
                                                                                                                                                                                                                                                        166 EGQHCEQNIDECADQPCHNGGNC 188
                                                                                                                                                                                                                          4 XNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 XNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Cross-references: FlyBase: FBgn0000368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;1878-1914/Domain: EGF homology <EGX2>
                     F;139-170/Domain: EGF homology <EGX1>
F;177-208/Domain: EGF homology <EGF1>
F;216-252/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F:352-385/Domain: EGF homology <EGX1>
F:392-724/Domain: EGF homology <EGF1>
F:591-722/Domain: EGF homology <EGF2
F:767-799/Domain: EGF homology <EGF3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 35.7
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 30.4 tes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reference number: Z19541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: CESP: F46B3.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: FlyBase:crb
                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 7
                                                                                                                                                     Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 30
                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             임
                                                                  Cyaccession: T05688
R:Wegener, A.; Gimbel, W.; Werner, T.; Hani, J.; Ernst, D.; Sandermann, H. Biophys. Acta 1350, 247-252, 1997
A;Title: Molecular Cloning of Cacone-inducible protein from Pinus sylvertris L. with high A;Reference number: Z16823; MUID:97214637; PMID:9061017
A;Recession: T05688
A;Recession: T05688
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-474 «WEGA
A;Residues: Draininary; translated from GB/EMBL/X96386; NID:g1655678; PIDN:CAA65250.1; PID:g165
A;Experimental source: tissue-type needles
C;Function:
C;Function:
C;Superfamily: hydroxymethylglutaryl-CoA synthase
C;Keywords: carbon-carbon lyase; coenzyme A; oxo-acid-lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C)Accession: A39117
R)Tannich, E.; Ebert, F.; Horstmann, R.D.
Proc. Natl. Acad. Sci. U.S.A. 88, 1849-1853, 1991
A;Title: Primary structure of the 170-kDa surface lectin of pathogenic Entamoeba histoly A;Reference number: A39117; MUID:91156704; PMID:2000392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: EGF homologous sequences encoded in the genome of Drosophila melanogaster, and A;Reference number: A91081; MUID:87218537; PMID:3107986
A;Accession: B26637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecule type: mRNA
Residues: 1-293 «KNU»
Cross-references: UNIPROT:P10040; GB:X05144; NID:g7519; PIDN:CAA28793.1; PID:g929536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2
N;Alternate names: 3-hydroxy-3-methylglutaryl-coenzyme A synthase
C;Species: Pinus sylvestris (Scotch pine)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A39117
170K lectin precursor - Entamoeba histolytica (fragment)
C;Species: Entamoeba histolytica
C;Date: 30-Aug-1991 #sequence_revision 17-Apr-1993 #text_change 09-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-1280 <TAN>
A;Cross-references: GB:M60498; NID:g158958; PID:g158959
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 52.5; DB 2;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
32.6%; Score 52.5; D
Best Local Similarity 43.5%; Pred. No. 62;
Matches 10; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                705 CSMGTDNVITYHDDCDSRKSQCGNFNGKC 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CRIXNOKCFQHLDDCCSRK--CNRFN-KC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211 LSÓTCYLMALDSCYKRFCNKFEK 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 XNOKCF-QHLDDCCSRKCNRFNK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A)Gene: FlyBase:crb
A;Cross-references: FlyBase:FBgn0000368
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 41.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
```

ï

Gaps

5

ö

Gaps

ö

```
250 AGQNCEENVDDCPGNNCKNGGACV 273
                                                                                                                                                                                                                                                                                                   notch-1 protein - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: S25144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        222-254/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            456-487/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           682-713/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   873-904/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: notch-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetics:
                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mammalian development
                                                                                                                                                                                                                                                                                                                                                Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species: Rattus norvegicus (Norway rat)
Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 02-Aug-2002
Accession: S18188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A Molecule type: mRNA
A, Residues: 1-2471 < WEI>
A, Cross-references: UNIPROT: 090W30
A, Experimental source: Schwann cell
A, Experimental source: Schwann cell
A, Note: sequence extracted from NCBI backbone (NCBIP:127811)
C, Superfamily: Notch protein; ankyrin repeat homology; EGF homology
F; 264-295/Domain: EGF homology cEGXI>
F; 799-830/Domain: EGF homology cEGXI>
F; 8777-908/Domain: EGF homology cEGXI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Molecule type: mRNA
A, Residues: 1-2531 «WEI»
A, Cross-references: EMBL: X57405; NID:957634; PID:957635
C; Superfamily: notch protein; ankyrin repeat homology; EGF homology
F;987-1018/Domain: EGF homology «EGF»
F;1025-1056/Domain: EGF homology «EGF»
F;1033-1264/Domain: EGF homology «EGF»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.3%; Score 52; DB 2; Length 2471; ilarity 33.3%; Pred. No. 2.1e+02; Conservative 5; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: A49128 Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 52; DB 2; Length 253
Pred. No. 2.18+02;
4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Riwelnmaster, G.; Roberts, V.J.; Lemke, G.
Development 116, 931-941, 1992
A;Title: Notch2: a second mammalian Notch gene.
A;Reference number: A49128; MUID:93202015; PMID:1295745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RiWeinmaster, G.; Roberts, V.J.; Lemke, G.
Development 113, 199-205, 1991
A;Title: A homolog of Drosophila Notch expressed during
A;Reference number: S18188; MUID:92111383; PMID:1764995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;1876-1908/Domain: ankyrin repeat homology <ANI>F;1909-1941/Domain: ankyrin repeat homology <ANZ>F;1943-1975/Domain: ankyrin repeat homology <ANZ>F;1943-1975/Domain: ankyrin repeat homology <ANZ>F;1206-2008/Domain: ankyrin repeat homology <ANS>F;2009-2041/Domain: ankyrin repeat homology <ANS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;1917-1949/Domain: ankyrin repeat homology <AN1>F;1950-1982/Domain: ankyrin repeat homology <AN2-F;1984-2016/Domain: ankyrin repeat homology <AN3-F;2017-2049/Domain: ankyrin repeat homology <AN3-F;2050-2082/Domain: ankyrin repeat homology <AN5-F;2050-2082/Domain: ankyrin repeat ho
                                                                                                                                                                                                                                                                                                   cell-fate determining gene Notch2 protein - rat
1828 EGQHCEQNIDECADQPCHNGGNC 1850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGSNCERNIDDCPNHKCQNGGVCV 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 XNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;1029-1060/Domain: BGF homology «EGF»
F;1067-1098/Domain: BGF homology «EGK3»
F;1159-1184/Domain: BGF homology «EGF3»
F;1191-1222/Domain: BGF homology «EGF3»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 32.3
Best Local Similarity 33.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              notch protein homolog - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: A49128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: S18188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

4 XNQKCFQHLDDCCSRKCNRFNKCV 27

```
NiAlternate names: motch protein
C;Species: Mus musculus (house mouse)
C;Accession: A46019; S25144; C49175; B46438; A46438; PHI569; S32109
R;del Amo, F.F.; Gendron-Maguire, M.; Swiatek, P.J.; Jenkins, N.A.; Copeland, N.G.; Gridl
Genomics 15, 259-264, 1993
A;Fitle: Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of I
                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-2831 <DEL>
A;Residues: 1-2831 <DEL>
A;Residues: 1-2831 <DEL>
A;Cross-references: UNIPROT:Q01705; GB:Z11886; GB:S47228; NID:g288502; PIDN:CAA77941,1; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Note: sequence extracted from NCBI backbone (NCBIP:127318)
R, Franco del Amo, F.; Smith, D.E.; Swiatek, P.J.; Gendron-Maguire, M.; Greenspan, R.J.; N submitted to the EmBL Data Library, April 1992
A; Description: Expression pattern of Motch, a mouse homolog of Drosophila Notch, suggests A; Reference number: S25144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Rosaidues: 1551-2108; 0, 2110-2114, 'ALP', 2118-2170 <FRA>
A;Cross-references: EMBL:11886
R;Lardelli, M.; Lendahl, U.
Exp. cell Ress. 204, 364-372, 1993
Exp. cell Ress. 204, 364-372, 1993
A;Title: Motch A and Motch B--two mouse Notch homologues coexpressed in a wide variety of
A;Reference number: A49175; MUID:93178563; PMID:8440332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;Kopan, R.; Weintraub, H.
. Cell Biol. 121, 631-641, 1993
. Tritle: Wouse notch: expression in hair follicles correlates with cell fate determinatic
. Reference number: A46438; WUD:93252998; PMID:8486742
. Accession: B46438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: nucleic acid
A;Residues: 1865-1932,'RR',1935-1937,'L',1938-1967,'I',1969-2044,'IE',2047-2052,'S',2054-
A;Experimental source: embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: Sequence extracted from NCBI backbone (NCBIN:131246, NCBIP:131247) (NOTE: Sequence extracted from NCBI backbone (NCBIN:131#1721/Notch repeats.) Comment: This protein has many EGF repeats and lin-12[#11721/Notch repeats.) Comment: This protein is one of the neurogenic proteins controlling the decision between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1161-1547 <LAR>
A; Cross-references: EMBL: X68278; NID: 9287987; PIDN: CAA48339.1; PID: 9287988
A; Experimental source: embryo
A; Experimental source: extracted from NCBI backbone (NCBIP:126159)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          on of chromosome 2
protein; ankyrin repeat homology; EGF homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: C49175; Accession: C49175; Actus: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                     compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: 2
A; Note: proximal region of chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <EGE3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <EG04>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <EG07>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <EG08>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <EG11>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <EG13>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                homology
homology
homology
                                                                                                                                                                                                                                                                                                                                                                              Status: not compared with co
Molecule type: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;911-942/Domain:
F;949-980/Domain:
```

```
probable vitellogenin receptor - fruit fly (Drosophila melanogaster)
(Species: Drosophila melanogaster
(Species: Drosophila melanogaster
(Spate: 13 Aug-1999 #sequence_revision 13 Aug-1999 #text_change 09-Jul-2004
(Scession: T13171
Rischonbaum, C.P.; Lee, S.; Mahowald, A.P.
Rischonbaum, C.P.; Lee, S.; Mahowald, A.P.
Airtle: The Drosophila yolkless gene encodes a vitellogenin receptor belonging to the low A. Rischerence number: 217627; MUID:95183490; PMID:7878005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: mRNA
Residues: 1-1984 <SCH>
Cross-references: UNIPROT:P98163; EMBL:U13637; NID:G535345; PID:G535346; PIDN:AABG0217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J.; Rivier, J.; de Santos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Keywords: acetylcholine release inhibition; calcium channel inhibitor; hydroxyproline; F;1-16,8-19,15-26/Disulfide bonds: #status predicted F;4,7/Modified site: 4-hydroxyproline (Pro) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N;Alternate names: shaker peptide GVIIA
C;Species: Conus geographus (geography cone)
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fil29-166/Domain: LDL receptor ligand-binding repeat homology (LDLB)-
Fil84-220/Domain: LDL receptor ligand-binding repeat homology (LDLD)-
Fil84-220/Domain: LDL receptor ligand-binding repeat homology (LDLD)-
Fil025-1062/Domain: LDL receptor ligand-binding repeat homology (LDL1)-
Fil025-1062/Domain: LDL receptor ligand-binding repeat homology (LDL1)-
Fil18-1152/Domain: LDL receptor ligand-binding repeat homology (LDL2)-
Fil18-1152/Domain: LDL receptor ligand-binding repeat homology (LDL2)-
Fil18-1153/Domain: LDL receptor ligand-binding repeat homology (LDL3)-
Fil18-1279/Domain: LDL receptor ligand-binding repeat homology (LDL5)-
Fil243-1279/Domain: LDL receptor ligand-binding repeat homology (LDL5)-
Fil283-1318/Domain: LDL receptor ligand-binding repeat homology (LDL5)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C,Accession. A43620
R;Ollvera, B.W.; Gray, W.R.; Zeikus, R.; McIntosh, J.M.; Varga,
Science 230, 1338-1343, 1985
A;Title: Peptide neurotoxins from fish-hunting cone snails.
A;Reference number: A43620; MUID:86070213; PMID:4071055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.0%; Score 51.5; DB 2;
llarity 36.7%; Pred. No. 2.1e+02;
Conservative 3; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Conus geographus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31.7%; Score 51; DB 2;
31.0%; Pred. No. 14;
ive 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1336 SSRSCRPHLFDCQDGECVDLSRVCNNFPDC 1365
        27
                                                              44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 XNOKCFQHLDDC-----CSRKCNRFNKC 26
                                   17 CREESRRCMQR--DVCAARCARRRAQQCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----SRKCNRF 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              p position: 1
-124/Domain: LDL receptor ligand-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coss-references: FlyBase: FBgn0004649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: UNIPROT: P05483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: omega-conotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CRIXNOKCFQHLDDCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 31.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein A; Residues: 1-29 <OLI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            omega-conotoxin GVIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A43620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 11
                                                                                                                                         RESULT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 37
                                         g
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Omega-conotoxin MVIID precursor - cone shell (Conus magus) (fragment)
C;Species: Conus magus (magus cone)
C;Species: Conus magus (magus cone)
C;Date: 27-Mar-1997 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
C;Accession: As58537
R;Monje, V.D.; Haack, J.A.; Naisbitt, S.R.; Miljanich, G.; Ramachandran, J.; Nasdasdi, I
Neuropharmacology 32, 1141-1149, 1993
A;Title: A new Conus peptide ligand for Ca channel subtypes.
A;Reference number: A58537; MUID:94150815; PMID:8107968
A;Accession: A58537
A;Molecule type: mRNA
A;Residues: 1-29 <MONS
A;Cross-references: UNIPROT:Q26350; GB:S69322; NID:G545399; PIDN:AAB29902.1; PID:G545406
C;Superfamily: omega-conotoxin
C;Keywords: toxin; venom
F;4-29/Product: omega-conotoxin MVIID #status predicted <MAT>
F;4-19,11-23,18-28/Disulfide bonds: #status predicted
F;4-19,11-23,18-28/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.Molecule type: DNA
A.Residues: 1-113 <CUT>
A.Cross-references: UNIPROT:Q53419; GB:S70840; NID:g546751; PIDN:AAB30769.1; PID:g546752
C;Superfamily: Streptomyces mycarofaciens propionyl acylase
C;Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAccession: JC1088
R/Cui, L.W.; Li, Y.; Liu, B.Y.
Acta Genet. Sin. 20, 551-570, 1993
A;title: Localization and nucleotide sequence of propionyl acylase gene of Streptomyces A;Reference number: JC1088; MUID:94235344; PMID:8179938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ñ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              propionyl acylase (EC 3.5.1.-) - Streptomyces mycarofaciens
C;Species: Streptomyces mycarofaciens
C;Date: 27-Aug-1995 #sequence_revision 19-Cct-1995 #text_change 09-Jul-2004
C;Accession: JC1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                                       Length 2531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                       12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                           Score 52; DB 2;
Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                             F;1917-1948/Domain: ankyrin repeat homology <ANI>F;1949-1981/Domain: ankyrin repeat homology <ANI>F;1943-2015/Domain: ankyrin repeat homology <ANI>F;2016-2048/Domain: ankyrin repeat homology <ANI>F;2016-2048/Domain: ankyrin repeat homology <ANI>F;2049-2081/Domain: ankyrin repeat homology <ANI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 51.5; DE Pred. No. 13; 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 51.5; D
Pred. No. 31;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CQGRGASCRKTMYNCCSGSCNR-GRC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 AGQNCEENVDDCPGNNCKNGGACV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 XNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                            <EG18><EGF4><EG19>
                                                                                                                             homology homology
                                                                                                                                                                                                                                                                                                                                                                              32.3%;
Similarity 33.3%;
8; Conservative
                                                                    homology
homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
32.0%;
Best Local Similarity 34.6%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 32.0
Best Local Similarity 33.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 8; Conserv
                                                                                   F;1187-1218/Domain:
F;1233-1264/Domain:
F;1352-1383/Domain:
                                                                                                                                                                   F;1391-1425/Domain:
F;1917-1948/Domain:
F;1949-1981/Domain:
                                                        :1149-1180/Domain:
                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Б
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
```

us-10-627-685a-26.rpr

```
acetylcholinesterase (EC 3.1.1.7) (clone lambda-AChE8) - marbled electric ray (fragment) C;Species: Torpedo marmorata (marbled electric ray)
C;Species: Torpedo marmorata (marbled electric ray)
C;Date: 01-Dec-1989 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1999
C;Accession: S01348
R;Sikorav, J.L.; Duval, N.; Anselmet, A.; Bon, S.; Krejci, E.; Legay, C.; Osterlund, M.;
BMBO J. 7, 2983-2993, 1988
A;Title: Complex alternative splicing of acetylcholinesterase transcripts in Torpedo electal complex authority (march 1990) (march 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: O-War-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
Cispecies: O-War-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
Cispecies: Ci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: UNIPROT:Q9LPI7; GB:AE005172; NID:g6714280; PIDN:AAF25976.1; GSPDB:GN(
                                                                                                                                                                           ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X13174; NID:g64418; PIDN:CAA31572.1; PID:g64419 A;Note: the authors translated the codon CTT for residue 66 as Leu C;Superfamily: cholinesterase; cholinesterase homology C;Superfamily: cholinesterase; choinesterase; glycoprotein C;Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein
                                                                                                                                                                           Сарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                           5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31.7%; Score 51; DB 2; Length 100;
42.1%; Pred. No. 33;
tive 5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31.7%; Score 51; DB 2; Length 358, 46.7%; Pred. No. 76;
                                                         Length 53;
                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                         31.7%; Score 51; DB 2;
llarity 39.3%; Pred. No. 22;
Conservative 4; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Mismatches
                                                                                                                                                                                                                                                                                        1 CRIXNOKCFOHLDDCCSRKCNR-FNKCV 27
                                                                                                                                                                                                                                                                                                                                                 25 CADTGAVCV-HSDECCSGACSPVFNYCL 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 RIXNQKCFQHLDDCCSRKC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |::: | : | | |||:|
74 RLASSKWWAHSDPLCSRRC 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||:::|:|:||
172 CRVFRKKNYQKIDDC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CRIXNOKCFOHLDDC 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 42.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 46.7
Matches 7; Conservative
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-100 <SIK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-358 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: E86452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene: F6N18.15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
T30176
                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                              NAlternate names: shaker peptide GVIIB
Cispecies: Conus geographus (geography cone)
Cispecies: Conus geographus (geography cone)
Ciscession: B43620
Riolivera, B.M.; Gray, W.R.; Zeikus, R.; McIntosh, J.M.; Varga, J.; Rivier, J.; de Santc Science 230, 1338-1343, 1985
A/Title: Peptide neurotoxins from fish-hunting cone snails.
A/Reference number: A43620; MUD:86070213; PMID:4071055
A/Reference protein
A/Residues: 1-29 <0LI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Condoxin-like protein - Lymantria dispar nuclear polyhedrosis virus
C;Species: Lymantria dispar nuclear polyhedrosis virus, LdWNPV
C;Species: Lymantria dispar nuclear polyhedrosis virus, LdWNPV
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30499
R;Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohr Virology 253, 17-34, 1999
A;Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria d A;Reference number: Z20836; MUID:99124785; PMID:9887315
A;Accession: T30499
A;Accession: T30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RiAhrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F. Virology 229, 381-399, 1997
A;Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis A;Reference number: 217011; MUID:97271300; PMID:9126251
A;Accession: T10405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:P05483
C;Superfamily: omega-conotoxin
C;Keyleds: acetylcholine release inhibition; calcium channel inhibitor; hydroxyproline;
F;1-16,8-19,15-26/Disulfide bonds: #status predicted
F;4,7/Modified site: 4-hydroxyproline (Pro) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OpMNPV
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000
C;Accession: T10405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conotoxin-like protein 1 - Orgyia pseudotsugata nuclear polyhedrosis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.7%; Score 51; DB 2; Length 29;
31.0%; Pred. No. 14;
tive 5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 51; DB 2; Length 53;
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Cross-references: EMBL: U75930; NID: 92934903; PID: 91911382
                                                                                                                                                                                                                                                                            B43620
omega-conotoxin GVIIB - cone shell (Conus geographus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-53 <AHR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CRIXNQKCFQHLDDCC----SRKCNRF 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CRIXNOKCFOHLDDCCSRKCNR-FUKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 CAETGAVCV-HSDECCSGACSPVFNYCL 51
                                                   CKSPGTPCSRGMRDCCTSCLLYSNKCRRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 19.3%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 31.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 39
T10405
                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

1;

Gaps

us-10-627-685a-26.rpr

```
A;Map position: 5
A;Introns: 44/1; 131/3; 167/1; 259/1; 319/1; 355/1; 484/3; 713/3; 765/1; 840/2; 1036/1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-1208 <WIL>
A;Cross-references: UNIPROT:Q23456; EMBL:Z70757; PIDN:CAA94800.1; GSPDB:GN00023; CESP:ZK;
A;Experimental source: clone ZK287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conserved hypothetical protein [imported] - Leishmania major N;Alternate names: probable proline synthetase associated protein C;Species: Leishmania major C;Species: Leishmania major C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #sequence_revi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein ZK287.4 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T27822

R;McMurray, A.

R;McMurray, A.

R;Reference number: Z20425

A;Reference number: Z20425

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Residues: 1-1208 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C72850
Conotoxin homolog - Autographa californica nuclear polyhedrosis virus
C;Species: Autographa californica nuclear polyhedrosis virus, AcMNPV
A;Note: dsDNA virus
C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:09U147; EMBL:AL121861; PIDN:CAB58387.1 A;Experimental source: strain Friedlin
                                                                                                             DB 2; Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31.4%; Score 50.5; DB 2; Length 389; 60.0%; Pred. No. 92; Live 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1208;
                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 31.4%; Score 50.5; DB 2; Local Similarity 47.8%; Pred. No. 1.9e+02; nes 11; Conservative 1; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-389 <VOL>
                                                                                                   Score 50.5; DE Pred. No. 89; 4; Mismatches
                                                                                                                                                                                                                                                                              1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                          31 CRNINQ-CFONYNSPIKCRACRFRKC 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        804 GNONNFOSFDS-CSRACGATIVC 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 XNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                          Query Match
Best Local Similarity 42.3%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | |: |||||| |
84 CLCHV-DCCSRRCFR 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 CFQHLDDCCSRKCNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Genetics:
A;Gene: CESP:ZK287.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Note: L4326.11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 48
                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  원
EGF repeat transmembrane protein - mouse C; Species: Mus musculus (house mouse) C; Date: 32-Oct.1999 #text_change 09-Jul-2004 C; Date: 32-Oct.1999 #text_change 09-Jul-2004 C; Accession: T30176 B; Sell, C.; Hoff III, H.B. submitted to the EMBL Data Library, May 1986 A; Description: Cloning of a novel mRNA regulated by the insulin like growth factor type A; Accession: T30176 A; A; Experimental source: Strain C57BL/6J; clone DBI-1; whole embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A)Status: preliminary, translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Molecule type: DNA
A/Residues: 1-131 cBRA>
A/Cross-references: UNIPROT: Q23053; EMBL: U64837; PIDN: AAB04836.1; GSPDB: GN00023; CESP:TZ
A/Experimental source: strain Bristol N2; clone T2784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-371 (WIL)
A;Cross-references: UNIPROT:017932; EMBL:Z83233; PIDN:CAB05765.1; GSPDB:GN00023; CESP:KG
A;Experimental Bource: çlone K06B4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 44
T25924
hypothetical protein T27E4.5 - Caenorhabditis elegans
CiSpecies: Caenorhabditis elegans
CiSpecies: Caenorhabditis elegans
CiSpecies: T5-0ct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
CiAccession: T25924
Ribradshaw, H.
Ribradsh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 45
T23369
hypothetical protein K06B4.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 115-Oct-11999 #sequence_revision 15-Cct-1999 #text_change 09-Jul-2004
C;Accession: T23369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 31.7%; Score 51; DB 2; Length 1687; Best Local Similarity 40.0%; Pred. No. 2.1e+02; Matches 8; Conservative 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A) Submitted to the EMBL Data Library, December 1996
A) Reference number: 219732
A) Accession: T23369
A) Status: preliminary; translated from GB/EMBL/DDBJ
A) MOlecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h
Similarity 33.3%; Pred. No. 45
9; Conservative 4; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | : : | : : | | 1 | 1 | 1 | 80 CKTDQDCMFSNVQKCCDAGCG-FNVCV 1.05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CRIXNOKCFOHLDDCCSRKCNRFNKCV 2.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                486 CERNIDDCPNHKCQNGGVCV 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 CFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 5
A;Introns: 40/1; 53/2; 98/1; 118/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position: 5
A; Introns: 8/3; 120/3; 242/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: CESP: T27E4.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Gene: CESP: K06B4.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C, Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

1;

13

```
:223-249/Domain: EGF homology <EGF1>:316-342/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                             1449 LNQECKLHLCAQCSKKC 1465
                                                                                                                                                                                                                                                                          4 XNQKCFQHLDDCCSRKC 20
                                                                                                                                                                                                                       9; . Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cenascin precursor - chicken
                                                                                                                                                                                          Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession: B32230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: S01292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Accession: A32230
                                                                                                             A; Introns: 33/2
                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                              셤
C;Accession: C73850; A44003
R;Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
Virology 202, 586-605, 1994
A;Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.
A;Reference number: A72850; MUID:94303173; PMID:8030224
A;Status: preliminary
A;Nolecule type: DNA
A;Residue: 1-53 - AYRA
                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:P41416; GB:L22858; NID:g510708; PIDN:AAA66633.1; PID:g559072
R;Eldridge, R.; Li, Y.; Miller, L.K.
J. Virol. 66, 6563-6571, 1992
                                                                                                                                                                                                                                                                                                                           J. Virol. 66, 6563-6571, 1992
A;Title: Characterization of a baculovirus gene encoding a small conotoxinlike polypepti
A;Reference number: A44003; MUID:93021384; PMID:1404603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Molecule type: DNA.
A,Residues: 1-403 <WLL>
A,Cross-references: UNIPROT:062412; EMBL:AL021479; PIDN:CAA16320.1; GSPDB:GN00023; CESP:
A,Experimental source: clone Y22F5A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: T18281
R;Rieben Jr., W.K.; Gonzales, C.M.; Gonzales, S.T.; Filkington, K.J.; Kiyosawa, H.; Hugh Genetics 148, 1117-1125, 1998
A;Title: Dictyostelium discoideum nuclear plasmid Ddp5 is a chimera related to the Ddp1 A;Reference number: Z14684; MUID:98198836; PMID:9539429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypochetical protein D1 - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Species: Dictyostelium discoideum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: TB1281
R;Rieben Jr., W.K.; Gonzales, C.M.; Gonzales, S.T.; Pilkington, K.J.; Kiyosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Caenorhabditis elegans
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:L22858; NID:g510708; PIDN:AAA66633.1; PID:g559072
C;Genetics:
A;Gene: Ac-ctx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
31.1%; Score 50; DB 2; Length 403;
Best Local Similarity 33.3%; Pred. No. 1.1e+02;
Matches 9; Conservative 8; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              A,Accession: A44003
A,Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Length 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - Caenorhabdítis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R,Gardner, A.
submitted to the EMBL Data Library, January 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 50; DB Pred. No. 28; 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CRIXNOKCFOHLDDCCSRKCNR-FNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 CAETGAVCV-HNDECCSGACSPIFNYCL 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | | : | : | : | : | | | 48 CRQKNEKCTTNNEDRFNCRYCRYQKCL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Introns: 37/2; 84/1; 196/3; 299/2; 339/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein Y22F5A.1
C;Species: Caenorhabditis eleg
C;Date: 15-Oct-1999 #sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reference number: Z20231; Accession: T26551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 11; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetics:
Gene: CESP:Y22F5A.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: T26551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
```

```
A;Residues: 1-1474 <RIE>
A;Cross-references: UNIPROT:Q23870; EMBL:U00796; NID:g2702254; PID:g2702256; PIDN:AAC186:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Status: preliminary
;Molecule type: mRNA
;Residues: 1-1044,1318-1810 <JO2>
;Cross-references: GB:J04519
:Spring, J.; Beck, K.; Chiquet-Ehrismann, R.
Spring, J.; Bock, M.; Obiquet-Ehrismann, R.
:fill 59, 325-334, 1989
:filtle: Two contrary functions of tenascin: dissection of the active sites by recombinar interescence number: A33379; MUID:90030407; PMID:2478295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Residues: 1-204,'G',206-221,'A',223-380,'D',382-386,'H',388-444,'HN',447-450,'V',452-5:
Cross-references: GB:M23121; NID:g212746; PIDN:AAA49086.1; PID:g212749
Accession: B33379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Residues: 1-204,'G',206-221,'A',223-380,'D',382-386,'H',388-444,'HN',447-450,'V',452-55
Cross-references: GB:N23121
Pearson, C.A.; Pearson, D.; Shibahara, S.; Hofsteenge, J.; Chiquet-Ehrismann, R.
100 J. 7, 2977-2982, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecule type: mRNA
Residues: 1-204,'G',206-221,'A',223-380,'D',382-386,'H',388-444,'HN',447-450,'V',452-55
Accession: C33379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecule type: mRNA
Residues: 27-181,'R',183-204,'G',206-221,'A',223-380,'D',382-386,'H',388-444,'HN',447-/
Cross-references: EMBL:X08030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: part of this sequence was confirmed by protein sequencing superfamily: tenascin; EGF homology; fibrinogen beta/gamma homology; fibronectin type 1; Keywords: alternative splicing; calcium binding; cell adhesion; duplication; extracell; 1-22/pomain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Status: preliminary, nucleic acid sequence not shown; not compared with conceptual trar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Status: preliminary; nucleic acid sequence not shown; not compared with conceptual trar
Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N;Alternate names: cytotactin; hexabrachion
N;Contains: tenascin 190K; tenascin 200K
C;Species Gallus gallus (chicken)
C;Species: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004
C;Accession: A32230; B32230; B33379; B33379; C33379; S01292; A30903
C;Accession: A32230; B32230; B33379; B33379; C33379; S01292; A30903
C;Accession: A32230; B32230; B33379; BA; Bdelman, G.M.
Proc. Natl. Acad. Sci. US.A. 86, 1905-1909, 1989
A;Title: A detailed structural model of cytotactin: protein homologies, alternative RNA A;Reference number: A32230; MUID:89184536; PMID:2467292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Molecule type: DNA .
;Residues: 1-1810 <JON>
;Cross-references: UNIPROT:Q90824; GB:J04519; NID:g211717; PIDN:AAA48745.1; PID:g211718
                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                         31.1%; Score 50; DB 2; Length 1474; 52.9%; Pred. No. 2.5e+02;
                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;592-673/Domain: fibronectin type III repeat homology <FN3A>F;681-765/Domain: fibronectin type III repeat homology <FN3B>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title: Tenascin: cDNA cloning and induction by TGF-beta. Reference number: S01292; MUID:89030589; PMID:2460335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-33/Domain: propeptide #status predicted <PRO>34-1810/Product: tenascin 230K #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Accession: A33379
Status: preliminary; nucleic acid sequence not shown; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                 3; Mismatches
```

1;

```
interleukin-1 beta precursor - rabbit
NAlternate names: hematopoietin-1; IL-1 beta; lymphocyte proliferation potentiating fact. C.Specias: Orycolagus cuniculus (domestic rabbit)
C;Date: 25-May-1989 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C;Accession: A27714, A30584; JU0082; A32166
Biochem. Biophys. Res. Commun. 150. 1237-1243, 1988
A;Fitle: Cloning and sequence analysis of a cDNA for lymphocyte proliferation potentiatir: A;Reference number: A27714; MUID:88134238; PMID:2449207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-268 < CAN>
A; Cross-references: GB:M26295; NID:g516632; PIDN:AAA31373.1; PID:g516633
R; Young, P.R.; Sylvester, D.
Protein Eng. 2, 545-551, 1989
A; Title: Cloning of rabbit interleukin-1 beta: differential evolution of IL-1 alpha and 31
A; Reference number: A94230; MUID:89315718; PMID:2787507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Molecule type: mRNA
A;Residues: 1-268 <VOU>
C;Comment: This protein lacks a conventional signal sequence for protein export. Cleavage
C;Comment: This protein-lbeta, unlike interleukin 1-alpha, is inactive.
C;Comment: Interleukin-lbeta precursor is less heavily myristoylated than interleukin-lal
C;Superfamily: interleukin-1
C;Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F;117-268/Product: interleukin-1 beta #status predicted <ILB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein A - mouse
Glycoprotein A - mouse
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: Jun-1998 #sequence_revision 10-Jul-1998 #text_change 15-Jun-2001
C.Accession: JE0120
R.Haidaris, C.G.; Medzihradsky, O.F.; Gigliotti, F.; Simpson-haidaris, P.J.
DNA Res. S., 77-88, 1998
A.Title: Molecular characterization of mouse Pneumocystis carinii surface glycoprotein A. A.Title: Molecular characterization of mouse Pneumocystis carinii surface glycoprotein A. A.Reference number: JE0120; MuID:98344138; PMID:9679195
A.Molecule type: mRNA
A.Molecule type: 
                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                      1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 268;
                                            F;34/Modified site: 6-bromotryptophan (Trp) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Indels
                                                                                                                                    Score 49.5; DE Pred. No. 25; 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 30.7%; Score 49.5; I Similarity 37.0%; Pred. No. 93; 10; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                2 CKTNKMSCSLH-EECCRFRCCFHGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 OKCFOHLDDCCSRK-----CNRFNK 25
                                                                                                                            Query Match
Best Local Similarity 30.8%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: A30584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loc?
Matches
                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           intrinsic factor-B12 receptor CUBILIN precursor - rat Gispedies: Rattus norvegicus (Norway rat)  
Gispedies: Rattus norvegicus (Norway rat)  
Gispedies: Rattus norvegicus (Norway rat)  
Gispedies: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004  
Gispedies: 1708618  
Rimoestrup, S.K.; Kozyraki, R.; Kristiansen, M.; Kaysen, J.H.; Rasmussen, H.H.; Brault, J. Biol. Chem. 273, 5235-5242, 1998  
A;Title: The intrinsic factor-vitemin B12 ::eceptor and target of teratogenic antibodies A;Reference number: 216459; MUID:98148073; PMID:9478979  
A;Accession: T08618  
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: UNIPROT: 070244; EMBL: AF022247; NID: 93834379; PIDN: AAC71661.1; PID: 93
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Status: preliminary
A, Molecule type: protein
A, Molecule type: protein
A, Residues: 1-37 < Cols.
A, Residues: 1-37 < Cols.
A, Rosidues: 1-37 < Cols.
A, Note: Injection of rile in 13- to 15-day-old mice caused hyperactivity, circular motic
Ward swimming or swimming in a vertical direction and death.
F;13/Modified site: gamma-carboxyglutamic acid (Glu) #status predicted
F;14/Modified site: gamma-carboxyglutamic acid (Glu) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology C; Keywords: egg yolk; endocytosis; glycoprotein; intestine; kidney; peripheral membrane F;1-20/Domain: signal sequence #status predicted <SIG> F;21-3623/Product: intrinsic factor-B12 receptor CUBILIN #status predicted <MAT> F;133-164/Domain: EGF homology <EGFP> F;133-164/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Olivera, B. Subatted to the Protein Sequence Database, January 2003
A;Description: Novel Excitatory Conus Peptides Define a New Conotoxin Superfamily.
A;Reference number: A59457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Species: Conus radiatus
;Date: 20-Jan-2003 #sequence_revision 20-Jan-2003 #text_change 09-Jul-2004
;Accession: A59457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
F;773-857/Domain: fibronectin type III repeat homology <FN3C>F;865-949/Domain: fibronectin type III repeat homology <FN3D>F;865-949/Domain: fibronectin type III repeat homology <FN3D>F;1046-1128/Domain: fibronectin type III repeat homology <FN3F>F;1037-1219/Domain: fibronectin type III repeat homology <FN3G>F;1136-1310/Domain: fibronectin type III repeat homology <FN3G>F;1318-1399/Domain: fibronectin type III repeat homology <FN3I>F;1407-1487/Domain: fibronectin type III repeat homology <FN3I>F;1405-1575/Domain: fibronectin type III repeat homology <FN3I>F;1405-1575/Domain: fibronectin type III repeat homology <FN3I>F;1405-1798/Domain: fibronectin type III repeat homology <FN3I>F;1405-1798/Domain: fibronectin type III repeat homology <FN3I>F;1734-1747/Domain: dibrinogen beta/gamma homology <FN3C>F;1734-1747/Domain: calcium binding #status predicted <CAB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.1%; Score 50; DB 1; Length 1810; 35.3%; Pred. No. 2.9e+02; tive 3; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      356 RCENGLCVCHEGFVGDDCSQKRCPKTCNNRGRCV 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
31.1%; Score 50; DB 2; 1
Best Local Similarity 29:2%; Pred. No. 4.66+02;
Matches 7; Conservative 6; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 RIXNOKCFOHL----DDC----CSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I-superfamily conotoxin rile - Conus radiatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 XNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 35.3
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1-3623 <MOE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Accession: A59457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Gene: CUBILIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

```
A;Cross-references: UNIPROT: O9UUM3; EMBL: AL049495; PIDN: CAB39853.1; GSPDB: GN00066; SPDB: & A;Experimental source: strain 972h-; cosmid c2A9_3p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
CiAccession: G88492
Ciance 282, 2012-2018, 1998
Airle: Genome sequence of the nematode C. elegans: a platform for investigating biology
Airle: Genome sequence of the nematode C. elegans: a platform for investigating biology
Airle: Genome sequence of the low for investigating biology
Airle: Genome sequence of the low for investigating biology
Airle: Genome sequence of the low for investigating biology
Airle: genome wustl.edu/gsc/C_elegans/ and www sanger.ac.uk/Projects/C_elegans/ Airle: Genome appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
Airle: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-427 <STO>
A;Cross-references: UNIPROT:Q22310; GB:chr III; PIDN:AAA21083.1; PID:g532471; GSPDB:GN00
A;Note: weak similarity to glycogen branching enzyme
                                                                                conserved hypothetical protein SPBC2A9.11c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypotherical protein F42G2.6 - Caenorhabditis elegans
C;Species: T32289
R;Scheet, P.; Maggi, L.
Submitted to the EMBL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid F42G2.
A;Reference number: Z21146
A;Accession: T32289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                C;Accession: T40102
R;Barrell, B.G.; Rajandream, M.A.; Lyne, M.; Skelton, J.; Churcher, C. submitted to the EMBL Data Library, March 1999
A;Reference number: Z21905
A;Accession: T40102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 49; DB 2; Length 427;
Pred. No. 1.4e+02;
6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    339 LANTLAFEEMEDCVNFFRSCNAVYDSKDPNRILMKESTDRFEKCM 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----RFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 30.4%; Score 49; DB 2; Lei Local Similarity 24.4%; Pred. No. 1.4e+02; les 11; Conservative 7; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -- RKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                              A.Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-395 <BAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 IXNOKCFQHLDDCCS--RKCN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 RIXNOKCFOHLDDCCS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 30.4%;
Best Local Similarity 33.3%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Gene: SPDB:SPBC2A9,11c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Introns: 216/3; 260/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C. Species: Caenorhabditis elegans
C. Species: Caenorhabditis elegans
C. Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000
C. Accession: T16556
R. Pauley, A. Bubmitted to the EMBL Data Library, April 1994
A. Description: The sequence of C. elegans cosmid K04C2.
A. Reference number: 218534
A. Accession: T16556
A. Reference number: 218534
A. Accession: T16556
A. Reference number: 218534
A. Accession: T16556
A. Reference is preliminary; translated from GB/EMBL/DDBJ
A. Residues: 1-194 < PAU>
A. Cession: BMBL: U000044; NID:9470346; PID:9470348; PIDN:AAAS0676.1; CESP: K04C2.1
A. Experimental source: strain Bristol N2
C. Genetios:
A. Gene: CESP: K04C2.1
A. Introns: 26/2; 85/3; 131/3
C. Superfamily: Caenorhabditis elegans hypothetical protein K04C2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein YUPBH12R.38 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: T01055
R;Theologis, A.; Vysotekaia, V.S.; Osborne, B.I.; Schwartz, J.R.; Federspiel, N.A.; Kwan
Submitted to the EMBL Data Library, May 1998
A;Description: Arabidopsis thaliana chromosome 1 YAC YUPBH12R sequence.
A;Accession: T01055
A;Accession: T01055
A;Accession: T01055
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1516 < THE>
A;Conserreferences: UNIPROT:O64548; EMBL:AC002986; NID:g2494106; PID:g3152587; GSPDB:GNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: ATSP:YUP8H12R.38
A;Map position: 1
A;Introns: 59/2; 97/3; 185/1; 319/1; 379/1; 809/3; 908/3; 1001/3; 1044/3; 1111/3; 1159/2
C;Superfamily: Pneumocystis carinii major surface glycoprotein MSG100
C;Keywords: glycoprotein
F;248,612,717,779,1063/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                              Query Match 30.7%; Score 49.5; DB 2; Length 1282; Best Local Similarity 33.3%; Pred. No. 2.6e+02; Matches 9; Conservative 7; Mismatches 10; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 30.7%; Score 49.5; DB 2; Length 1516; Best Local Similarity 28.0%; Pred. No. 2.9e+02; Matches 7; Conservative 11; Mismatches 6; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 30.4%; Score 49; DB 2; Length 194; Best Local Similarity 33.3%; Pred. No. 86; Matches 12; Conservative 6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | | : | : | : | : | : | | RIPNEILFEILENCKSTEPSTVLAARRLSRRFNACM 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 RIXNOKCFOHLDDCCS-----RKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein K04C2.1 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                             366 CQEYLEKCYFYGSSCKDTKCDKVNNKC 392
                                                                                                                                                                                                                                                                                      1 CRIXNOKCFOHLDDCCSRKCNRF-NKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 IXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 56
T01055
hypothetical p
                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

```
F;23-34,28-43,45-54,62-88,180-191,185-200,202-211,218-229,223-238,240-249,256-267,261-276
7,451-466,468-477,464-495/Distilate bonds: #status predicted
F;489-504,506-515,522-533,527-542,544-553,560-571,565-580,589-591,598-609,603-618,620-62;
08,810-819,826-837,831-846,848-857,864-875,869-884,886-895,902-913,907-922,924-933/Distil
                                                                                                                                                                                                                               Ribut, L.T.; Barker, W.C.
FASEB J. 3, 1760-1764, 1989
A;Title: Avidin-11ke domain in an epidermal growth factor homolog from a sea urchin.
A;Reference number: A43131; MUID:89196806; PMID:2784773
A;Contents: annotation
C;Comment: EGF homology repeats 10-17 are spliced out in the short form (fibropellin Ib)
F;1-19/Domain: signal sequence #status predicted <SIG>F;20-1064/Product: fibropellin I #status predicted <FIB>F;20-1064/Promain: CIr/CIs repeat homology <CIR>F;57-175/Domain: CIr/CIs repeat homology <CIR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N;Alternate names: Notch homology
C;Species: Mus musculus (house mouse)
C;Date: 21-Jan-1994 #sequence_revision 05-Jan-1996 #text_change 16-Aug-2004
C;Accession: A49175; PH1570; S32113
R;Lardelli, M.; Lendahl, U.
R;Lardelli, M.; Lendahl, U.
A;Title: Motch A and Motch B--two mouse Notch homologues coexpressed in a wide variety of A;Reference number: A49175; WUID:93178563; PMID:8440332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Residues: 1-1203 <LAR>
A.Residues: 1-1203 <LAR>
A.Cross-references: UNIPROT:035516; EMBL:X68279; NID:g287989; PIDN:CAA48340.1; PID:g28795;
A.Forperimental source: embryo
A.Note: sequence extracted from NCBI backbone (NCBIP:126158)
C.Comment: This protein has many EGF repeats and lin-12/Notch repeats.
C.Comment: This protein is one of the neurogenic proteins controlling the decision betwee C.Superfamily: Notch protein; ankyrin repeat homology; EGF homology
                A;Title: A sea urchin gene encodes a polypeptide homologous to epidermal growth factor. A;Reference number: A29316; MUID:87319677; PMID:3498216 A;Accession: A29316 A;Accession: A29316 A;Status: preliminary
                                                                                                                                           A,Molecule type: mRNA
A,Residues: 'S',280-481,786-1064 <HUR>
A,Cross-references: GB:M17421; NID:g161474; PIDN:AAA30050.1; PID:g552260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.4%; Score 49; DB 2; Length 1064;
40.0%; Pred. No. 2.6e+02;
ive 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               439 CENNIDECASRPCQNGAVCV 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <EG20>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 CFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <EG08>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <EG10>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <EG14>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <EG15>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <EG16>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <EG18>

    mouse (fragment)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    homology
homology
homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               homology
homology
homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :180-211/Domain: EGF homology 218-249/Domain: EGF homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                homology
homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;864-895/Domain:
F;902-933/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94-325/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :936-1064/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -439/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         484-515/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :788-819/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :826-857/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -553/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               598-629/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 636-667/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               674-705/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         712-743/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          750-781/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Motch B protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
A;Residues: 1-833 <SCH>
A;Residues: 1-833 <SCH>
A;Cross-references: UNIPROT:O17102; EMBL:AF024499; PIDN:AAB70358.1; GSPDB:GN00020; CESP:A;Cross-references: UNIPROT:O17102; EMBL:AF024499; PIDN:AAB70358.1; GSPDB:GN00020; CESP:Genetics: Strain Bristol N2; clone F42G2
C;Genetics: Strain Bristol N2; clone F42G2
A;Gene: CESS:F42G2.6
A;Map position: 2
A;Introns: 317/1; 335/1; 362/3; 781/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   integrin beta chain precursor - fruit fly (Drosophila melanogaster)
C.Species: Drosophila melanogaster
C.Species: Drosophila melanogaster
C.Spate: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 16-Aug-2004
C.Accession: A30889
R.MacKrell, A.J.; Blumberg, B.; Haynes, S.R.; Fessler, J.H.
Proc. Natl. Acad. Sci. U.S.A. 85, 2633-2637, 1988
A.Title: The lethal myospheroid gene of Drosophila encodes a membrane protein homologous
A.Reference number: A30889; MUID:88190122; PMID:3128792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fibropellin Ia - sea urchin (Strongylocentrotus purpuratus)
NyAlternate names: epidermal growth factor homolog precursor
NyAlternate names: epidermal growth factor homolog precursor
Scholaria: alternatively spliced fibropellin Ib (EGFI)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 13-May-1992 #sequence revision 17:Sep-1997 #text_change 09-Jul-2004
C;Accession: A40136; B40136; Z40136; A29316; A43131
R;Delgadillo-Reymoso, MG.; Rollo, D.R.; Hursh, D.A.; Raff, R.A.
J. Mol. Evol. 29, 314-327, 1989
A;Title: Structural analysis of the uEGF game in the sea urchin Strongylocentrotus purpu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:P11584; GB:J03251; NID:g157954; PIDN:AAA28714.1; PID:g157955
                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A40136
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-114 < DEL>
A; Cross-references: UNIPROT: P10079; GB:X17530; NID:g10225; PID:g667061
A; Accession: B40136
                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Gene: FlyBase:mys
A;Cross-references: FlyBase:FBgn0004657
C;Superfamily: Integrin beta chain; laminin-type EGF-like homology
C;Keywords: cell adhesion; cytoskeleton; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 30.4%; Score 49; DB 2; Length 846; Best Local Similarity 32.3%; Pred. No. 2.38+02; Matches 10; Conservative 6; Mismatches 11; Indels
                                                                                                                                                                                                                                                         30.4%; Score 49; DB 2; Length 833; ilarity 26.9%; Pred. No. 2.2e+02; Conservative 6; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; not compared with conceptual translation A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 181-251,329-370,'R',372-408,'RA',411-441 <DE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   669 CIVNDQGRFSGRHCEKCPICSGRCQELKDCV 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CRIXNOKCF--OHLDDC--CSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                         87 QVVQNNCFQHLSPLYSKFCEHYGHMI 1.12
                                                                                                                                                                                                                                                                                                                                                                                     2 RIXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 'K',747-821,898-978 <DE3>
R;Hursh, D.A.; Andrews, M.E.; Raff, R.A.
Science 237, 1487-1490, 1987
                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-846 < MAC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Genetics;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 62
A40136
                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                   원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

ö

Gaps

```
C;Accession: S45306
R;Lardelli, M.; Dahlstrand, J.; Lendahl, U.
Mech. 194, 46, 123-136, 195
A;Title: The novel Notch homologue mouse Notch 3 lacks specific epidermal growth factor-1
A;Reference number: S45306; MUD:95001556; PMID:7918097
A;Scaession: S45306
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2318 <LAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:061982; EMBL:X74760; NID:9483580; PIDN:CAA52776.1; PID:948358 C;Superfamily: notch protein; ankyrin repeat homology; EGF homology EGF: 15,163.195/Domain: EGF homology eEGF: 5,163.195/Domain: EGF homology eEGF: 5,854.885/Domain: ankyrin repeat homology eAN1> F;1910-1938/Domain: ankyrin repeat homology eAN3> F;1939-1971/Domain: ankyrin repeat homology eAN4> F;1972-2004/Domain: ankyrin repeat homology eAN4> F;1972-2004/Domain: ankyrin repeat homology eAN5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Riblerkamp, C.; Campos-Ortega, J.A.
Mech. Dev. 43, 87-100, 1993
A;Itle: A zebrafish homologue of the Drosophila neurogenic gene Notch and its pattern of
A;Reference number: S42612; MUID:94128602; PMID:8297791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-2437 <BLE>
A;Residues: 1-2437 <BLE>
A;Cross-references: UNIPROT:P46530; EMBL:X69088; NID:g433866; PIDN:CAA48831.1; PID:g43380
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
F;755-786/Domain: EGF_homology <EGFI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Specie8: Brachydanlo rerio (zebra fish)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S42612
           notch 3 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.4%; Score 43; 25.0%; Pred. No. 4.4e+02; tive 6; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 49; DB 2;
Pred. No. 4.6e+02;
4; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;1915-1947/Domain: ankyrin repeat homology <ANI>F;1948-1980/Domain: ankyrin repeat homology <ANI>F;1948-2014/Domain: ankyrin repeat homology <ANI>F;2018-2014/Domain: ankyrin repeat homology <ANI>F;2018-2047/Domain: ankyrin repeat homology <ANI+F;20180/Domain: ankyrin repeat homology <ANI+F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ransmembrane protein precursor - zebra fish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1116 AGDSCEDNIDECASQPCQNGGSCI 1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 TGQTCEHNVDDCTQHACENGGPCI 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 XNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 XNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1023-1054/Domain: EGF homology <EGF>,1185-1216/Domain: EGF homology <EGF2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 29.2%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 25.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: S42612
A; Status: preliminary
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઢ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein T17F15.240 - Arabidopsis thaliana (5.Species: Arabidopsis thaliana (mouse-ear cress) (5.Species: Arabidopsis thaliana (mouse-ear cress) (5.Date: 23.Apr-1999 #sequence_revision 23.Apr-1999 #text_change 09-Jul-2004 (5.Accession: T06694 (6.C.Accession: T06694 (7.C.Accession: T06694 (7.C.Accession: T06694 (7.C.Accession: T06694 (7.C.Accession: T06694) (7.C.Accession: T06694) (7.C.Accession: T06694)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T06692
hypothetical protein T17F15.220 - Arabidopsis thaliana
c)Species arabidopsis thaliana (mouse-ear cress)
c)Species 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C)Accession: T06692
R;Ouetler, F.; Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artigu abumitted to the Protein Sequence Database, April 1999
A;Reference number: 215793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Introns: 823/3; 866/3; 930/3; 947/2; 1051/3; 1094/1; 1161/1; 1193/1; 1253/3; 1325/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Accession: T06692
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1291 <QUE>
A;Residues: 1-1291 <QUE>
A;Cross-references: UNIPROT:Q9SU54; EMBL.AL049658; GSPDB:GN00061; ATSP:T17F15.220
A;Experimental source: cultivar Columbia; BAC clone T17F15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Reaidues: 1-128 «QUE»
A;Cross-references: UNIPROT:Q9SU52; EMBL:AL049658; GSPDB:GN00061; ATSP:T17F15.240
A;Experimental source: cultivar Columbia; BAC clone T17F15
                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                     Length 1203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.4%; Score 49; DB 2; Length 1291; 42.1%; Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.4%; Score 49; DB 2; Length 1528; 42.1%; Pred. No. 3.4e+02; tive 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Introns: 863/3; 906/3; 970/3; 987/2; 1091/3; 1134/1; 1201/1
                                                                                                                                                                                                                                 30.4%; Score 49; DB 2; I 29.2%; Pred. No. 2.9e+02; Live 6; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               4 XNQKCFQHLDDCCSRKCNRFNKCV 27
           homology <EGF1>
homology <EGF>
homology <EGX2>
homology <EGF3>
homology <EGF3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       679 EKEFYHLQNLCERKCEHLS 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 EKEFYHLQNLCERKCEHLS 737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 QKCFQHLDDCCSRKCNRFN 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 OKCFQHLDDCCSRKCNRFN 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 42.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 42.1
Matches 8; Conservative
                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Gene: ATSP:T17F15.240
A,Map position: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: ATSP:T17F15.220
                                                                               EGF
EGF
F;482-513/Domain: E;560-591/Domain: E;64-705/Domain: E;712-743/Domain: E;836-867/Domain: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               임
                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

ö

ö

RESULT 66

11;

Matches

ò 셤

```
A;Molecule type: DNA
A;Residues: 1-461 <BEV>
A;Cross-references: UNIPROT: PS4873; EMBL: AL078606
A;Experimental source: cultivar Columbia; BAC clone T26M18
R;Montamat, F.; Guilloton, M.; Karst, F.; Delrot, S.
A;Title: Isolation and characterization of a cDNA encoding Arabidopsis thaliana 3-hydrox;
A;Reference number: JC4567; MUID: 96144274; PMID: 8566777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C,Accession: A45545
R;Blackman, M.J.; Ling, I.T.; Nicholls, S.C.; Holder, A.A.
Mol. Biochem. Parasitol. 49, 29-33, 1991
A;Title: Proteolytic processing of the Plasmodium falciparum merozoite surface protein-1 A;Reference number: A45545; MUID:92131048; PMID:1775158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;MOJECTLE type: mRNA
A;Residues: 1-305,'S',307-341,'N',343-461 <MON>
A;Residues: 1-305,'S',307-341,'N',343-461 <MON>
A;Cross-references: EMBL:X83882; NID:g1143389; PIDN:CAA58763.1; PID:g1143390
C;Comment: This enzyme mediates the conversion of three acetyl-CoA molecules to one molecivity, and uptakes amino acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) - Arabidopsis thaliana
N;Alternate names: 3-hydroxy-3-methylglutaryl-coenzyme A synthase; protein T26M18.30
S;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09341; JC4557
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, submitted to the Protein Sequence Database, June 1999
A;Reference number: Z16650
A;Accession: T09341
                                                                                                                                                                                                                                                                                                                                                                                                                                                      major merozoite surface antigen - malaria parasite (Plasmodium falciparum) (fragments)
C:Species: Plasmodium falciparum
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Introns: 21/3; 57/2; 101/3; 149/3; 202/3; 227/2; 252/3; 271/2; 300/3; 347/3; 397/3
C; Superfamily: hydroxymethylglutaryl-CoA synthase
C; Keywords: carbon-carbon lyase; coenzyme A; glycoprotein; oxo-acid-lyase
C; Keywords: carbon-carbon lyase; covalent substrate-binding) #status predicted
F; 269/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                       2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ϊ;
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA,
A;Residues: 1-400 <BLA>,
A;Residues: 1-400 <BLA>
A;Cross-references: UNIPROT:Q03999
A;Note: sequence extracted from NCBI backbone (NCBIN:77612, NCBIP:77621)
C;Superfamily: major merozoite surface antigen
C;Keywords: glycoprotein; merozoite; surface antigen; tandem repeat
                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
30.1%; Score 48.5; DB 2; Length 461;
Best Local Similarity 39.1%; Pred. No. 1.7e+02;
Matches 9; Conservative 4; Mismatches 9; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                              170 CASQNQKTNQCANECNNQCANSCSPSSQTSSYSKCV 205
    Local Similarity 30.6%; Pred. No. 1.4e+02; hes 11; Conservative 7; Mismatches 9;
                                                                                                                                          1 CRIXNQKCFQHLDDC---CSRKC-----NRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300 QNSGCFRHLDERECKCLLNYKQEGDKCV 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 XNOKCFOHLDDCCSRKC----NRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 11; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: ATSP: T26M18.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ', Map position: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
    Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetics:
                                                                                                                                                                                                                                                                                                                                                                 RESULT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72
                                                                                                                                                                                                                 요
                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
Rydan den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
Blochim. Blophys. Acta 453, 400-409, 1976
Blochim. Blophys. Acta 453, 400-409, 1976
A;Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic A;Reference number: A90612; MUID:77065676; PMID:999896
A;Molecule type: protein
A;Molec: a second component of chinchilla ribonuclease has 32-Asp
C;Superfamily: pancreatic ribonuclease
C;Superfamily: pancreatic ribonuclease
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;34/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 69
J01739
hypothetical 14.7K protein - shallot virus X
Nylothetical 14.7K protein - shallot virus X
Nylothetical 14.7K protein
C;Species: shallot virus X
C;Species: shallot virus X
C;Species: shallot virus X
C;Accession: J01739
R;Kanyuka, K.V.; Vishnichenko, V.K.; Levay, K.E.; Kondrikov, D.Y.; Ryabov, E.V.; Zavriev
A;Title: Nucleotide sequence of shallot virus X RNA reveals a 5'-proximal cistron closel
A;Reference number: J01734; MUID:93019008; PMID:1333468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 70

189152

Protein C24B5.5 [imported] - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

R;Annonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog

A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele

A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;Residues: 1-328 <STO>
;Cross-references: UNIPROT:Q9TY01; GB:chr_V; PID:g4883503; GSPDB:GN00023; CESP:C24B5.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ,
,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.1%; Score 48.5; DB 1; Length 124; larity 27.5%; Pred. Nc. 72; Conservative 6; Mismatches 8; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |: : |:| |: | |: || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CRIXNOKCFQ-----HLDDC-----CSRKCNRFNK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.1%; Score 48.5; D
34.6%; Pred. No. 74;
tive 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.1%; Score 48.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | ::: | | | | | | : | :|:| RLLDNKPFQGTSKCAKRRAKRYNRC 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 RIXNQKCFQHLDDCCS-RKCNRFNKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1.128 «KAN»
A;Cross-references: UNIPROT: 004580
A;Experimental source: strain X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
9; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: DNA
```

ઠે g A, Map position: 5

Query Match

A;Cross-referenc C;Genetics: A;Gene: C24B5.5

```
Nucleic Acids Res. 17, 5401, 1989

A; Title: Nucleotide and deduced amino acid sequence of the gpl95 (MSA-1) gene from Plasmc A; Reference number: S04850; MUID:89345116; PMID:2668887

A; Accession: S04850

A; Molecule type: mRNA
A; Residues: 1504-1639 AMIL2>
A; Coss-references: EMBL:XL5063
C; Superfamily: major merozoite surface antigen
C; Superfamily: major merozoite; surface antigen
C; Superfamils: S19ropototal; merozoite; predicted <S1G>
F; 1-19-Domain: s1gnal sequence #status predicted <S1G>
F; 20-1639/Product: major merozoite surface antigen #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                implor metaboute cuttact antiquing precuisor - maidina parabite (riasmodium falciparum) (186 C.Species: Plasmodium falciparum) 26.5pecies: Plasmodium falciparum (c.Species: Plasmodium falciparum) 28-Oct-1994 #text_change 09-Jul-2004 C.Species: Plasmodium A54498 R.P. Coppel, R.L.; McIntyre, P.; Langford, C.J.; Woodrow, G.; Brown, G.V.; P.Mol. Biochem. Parasitol. 27, 291-302, 1988 A;Title: Variation in the precursor to the major merozoite surface antigens of Plasmodium A;Reference number: A54498 MUID:88142999; PMID:2449612 A;Accession: A54498 A;Accession: A54498 A;Accession: A54498 A;Accession: A54498 CB:ACCESSION: A54498 A;Accession: A54498 A;Acc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (8t)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (isc
                                                                                                                                                 A,Molecule type: mRNA
A,Residuss: 1-1639 <MYL>
A,Cross-references: UNIPROT:P04933; EMBL:X1S063; NID:g9896; PIDN:CAA33163.1; PID:g9897
R;Myler, P.J.
Nucleic Acids Res. 17, 5401, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum)
N;Alternate names: 195K glycoprotein
C;Species: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 30-Sep-1987 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004 C;Accession: A23386; S06361 S;Weber, J.L.; Leininger, W.M.; Lyon, J.A. Nucleic Acids Res. 14, 3311-3323, 1986 A;Title: Variation in the gene encoding a major merozoite surface antigen of the A;Reference number: A23386; MUID:86205236; PMID:3517809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .,
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 48.5; DB 2; Length 1639;
Pred. No. 4e+02;
4; Mismatches 9; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ٠.
ت
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 48.5; DB 2;
Pred. No. 4.1e+02;
4; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Accession: A23386
A,Molecule type: DNA
A,Residues: 1-1104. (WEB1>
A,Cross-references: UNIPROT: P04934; EMBL: X03831
R;Weber, J.L.; Sim, B.K.L.; Lyon, J.A.; Wolff, R.
Nucleic Acids Res. 16, 1206, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1539 ONSGCFRHLDEREECKCLLNYKOEGDKCV 1567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Myler, P.J.
submitted to the EMBL Data Library, April 1989
A;Reference number: S05603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 XNOKCFOHLDDCCSRKC----NRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 XNQKCFQHLDDCCSRKC----NRFNKCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y Match
Local Similarity 37.9%;
hes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 30.1%;
Best Local Similarity 37.9%;
Matches 11; Conservative
                                                                                                                     A; Accession: S05603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ठ
                                                                                                                                                                                                                                                                                                           भ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mero
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (st
C;Species: Plasmodium falciparum
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jun-2000
C;Accession: A25120
R;Mackay, M.; Goman, M.; Bone, N.; Hyde, J.E.; Scaife, J.; Certa, U.; Stunnenberg, H.; E
BMBO J. 4, 3823-3829, 1985
A;Title: Polymorphism of the precursor for the major surface antigens of Plasmodium falc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: S47282
A;Aolecule type: DNA
A;Redidues: 1-651 <TOL>
A;Cross-references: UNIPROT:Q25924; EMBL:235329; NID:g535257; PIDN:CAA84558.1; PID:g5352
A;Experimental source: strain R0-71
C;Superfamily: major merozoite surface antigen
C;Keywords: glycoprotein; merozoite; surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A)Residues: 1-1631 <MAC>
C)Comment: The merozoite stages of different strains have strain-specific surface antige
C)Comment: P. falciparum has three stages: sporozoite, merozoite, and gametocyte. The me
C)Comment: P. falciparum has three stages: sporozoite, merozoite, and gametocyte. The me
C)Superfamily: major merozoite surface antigen; tandem repeat; transmembrane prote
F)1-19/Domain: signal sequence #status predicted <SIG>
F)2-1631/Product: major merozoite surface antigen #status predicted <MAT>
F)67-84/Region: 3-residue repeats (S-G-T/P)
F)1614-1631/Domain: membrane anchor #status predicted <MBN>
F)97,259,755,759,835,911,955,1049,1156,1165,1436,1563/Binding site: carbohydrate (Asn) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Bt
                                                                                                                                                                                                                                                                                                       - malaria parasite (Plasmodium falciparum) (strain RO-71)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - malaria parasite (Plasmodium falciparum)
                                                                                                                                                                                                                                                                                                                                                                                   A.Variety: strain RO-71
C;Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: S47282
R;Tolle, R.; Bujard, H.; Cooper, J.A.
RsTolle, R. Bujard, H.; Cooper, J.A.
Submitted to the EMBL Data Library, July 1994
A;Description: Plasmodium falciparum: recombination within the C-terminal region of A;Reference number: 847282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  major merozoite surface antigen precursor - malaria parasite (Plasmodium fa. N.Alternate names: gp195 surface antigen C.Species: Plasmodium falciparum C.Species: Plasmodium falciparum C.Date: 12-Feb-1993 #text_change 09-Jul-2004 C.Bate: 12-Feb-1993 #S04850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.1%; Score 48.5; DB 1; Length 1631; 37.9%; Pred. No. 4e+02; tive 4; Mismatches 9; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48.5; DB 2;
Pred. No. 2.2e+02;
4; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1531 ONSGCFRHLDEREECKCLLNYKOEGSKCV 1559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    551 QNSGCFRHLDEREECKCLLNYKQEGDKCV 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 XNOKCFOHLDDCCSRKC----NRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 XNOKCFOHLDDCCSRKC----NRFNKCV 27
                                                                                208 LSQTCYLMALDSCYKHLCNKFEK 230
                                    XNOKCF-OHLDDCCSRKCNRFNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 37.9%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                           merozoite surface antigen 1 - mal
C;Species: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 37.9'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A25120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 75
S05603
                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
```

Ë

```
1 CRIXNQKCFQHLDDCCSRKCNRFNKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 57.1
nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302 FENLDEICSLICHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
tes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: CESP: Y43F8C.16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: S64135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Si
Matches 9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S:
Matches
                                                                                                                                                              RESULT
                       ò
                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 78

A45948

major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (st C; Species: Plasmodium falciparum
C; Species: Plasmodium falciparum
C; Species: Plasmodium falciparum
C; Species: Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C; Accession: A45948
R; Chang, S.P.; Kramer, K.J.; Yamaga, K.M.; Kato, A.; Case, S.E.; Siddiqui, W.A.
Exp. Parasitol. 67, 1-11, 1988
A; Reference number: A45948; MUID:89005525; PMID:3049134
A; Reference number: A45948; MUID:89005525; PMID:3049134
A; Residues: preliminary
A; Molecule A45948
A; Residues: J-1726 < CHA>
A; Residues: J-1726 < CHA>
A; Cross-references: UNIPROT:Q25922; GB:M37213
C; Superfamily: major merozoite surface antigen
C; Keywords: surface antigen
                                               A; Accession: S06361
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1104-1726 < WEB2>
A; Croment: The merozoite stages of different strains have strain-specific surface antige
C; Comment: The merozoite stages of different strains have strain-specific surface antige
C; Comment: P. falciparum has three stages: sporozoite, merozoite, and gametocyte. The me
C; Keywords: glycoprotein: merozoite surface antigen tandem repeat
C; Keywords: glycoprotein: merozoite surface antigen strains predicted <SIG>
F; 1-19/Domain: signal sequence #status predicted <SIG>
F; 20-1726/Product: major merozoite surface antigen #status predicted <MAT>
F; 20-1726/Product: major merozoite surface antigen #status predicted <MAT>
F; 20-1726/Product: major merozoite surface antigen #status predicted <MAT>
F; 20-1726/Product: major merozoite surface antigen #status predicted <MAT>
F; 57-765/Region: 3-residue repeats (T-E-E)
F; 37-765/Region: 3-residue repeats (T-E-E)
F; 333, 272, 501, 567, 638, 827, 839, 924, 944, 990, 1016, 1114, 1221, 1613, 1658/Binding site: carbohy
                    ра
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3
'Title: Merozoite surface protein sequence from the Camp strain of the human malaria
Reference number: S06361; MUID:88143999; PMID:3278296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 79
S02007
Proctamine I - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C:Accession: S02007
R:Ammer, H.: Henschen, A.
FEBS Lett. 242, 111-116, 1988
A.Title: Primary structure of rabbit sperm protamine, the first protamine of its type v. A;Recession: S02007; MUD:89078594; PMID:3060372
A;Mocession: S02007
A;Molecule type: protein
A;Recialides: 1-49 <Amm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ξ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 30.1%; Score 48.5; DB 1; Length 1726; Best Local Similarity 37.9%; Pred. No. 4.1e+02; Matches 11; Conservative 4; Mismatches 9; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 48.5; DB 2; Length 1
Pred. No. 4.1e+02;
4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48; DB 2;
Pred. No. 45;
5; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :| ||:|||:
1626 ENSGCFRHLDERBECKCLLNYKQEGDKCV 1654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENSGCFRHLDEREECKCLLNYKQEGDKCV 1654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 XNOKCFOHLDDCCSRKC----NRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 XNOKCFOHLDDCCSRKC----NRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:P10119
C;Superfamily: sperm histone
C;Keywords: DNA binding; nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 34.6%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 37.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

```
S64135

hypothetical protein YGL124c - yeast (Saccharomyces cerevisiae)

NyAlternate names: hypothetical protein G2889

NyAlternate names: hypothetical protein G2889

C,Species: Saccharomyces cerevisiae

C,Species: Saccharomyces cerevisiae

C,Accession: S64135; S72027

R;Cerdan, E.; Rodriguez-Torres, A.M.; Rodriguez-Belmonte, E.; Tizon, B.; Cadahia, J.L.; C

A;Reference number: S64134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-644 <CER>
A;Residues: 1-644 <CER>
A;Cross-references: UNIPROT:P53129; EMBL:Z72646; NID:g1322684; FIDN:CAA96832.1; PID:e2433
A;Cross-references: UniproT: P53129; EMBL:Z72646; NID:g1322684; FIDN:CAA96832.1; PID:e2433
A;Tizon, B.; Rodriguez-Torres, A.M.; Rodriguez-Belmonte, E.; Cadahia, J.L.; Cerdan, E.
A;Tile: 1047-1051, 1996
A;Tile: Identification of a putative methyleneterrahydrofolate reductase by sequence ans A;Reference number: S72026; MUID:97051592; PMID:8896269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.Status: mucleic acid sequence not shown, translation not shown
Modecule type: DNA
A.Residues: 1-644 «TILZ»
A.Cross-references: EMBL:X94106, NID:91628448, PIDN:CAA63834.1, PID:e214776, PID:9162845(
A.Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:09XWNS; EMBL:AL032637; PIDN:CAA21616.1; CESP:Y43F8C.16
A;Experimental source: clone Y43F8C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                              hypothetical protein Y43F8C.16 - Caenorhabditis elegans Cipacies: Caenorhabditis elegans Cipacies: Caenorhabditis elegans Cipaces: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 Cipacession: T26875  
RiAinscough, R. submitted to the EMBL Data Library, October 1998  
A;Reference number: 220279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Introns: 31/1; 53/2; 127/2
C;Superfamily: Caenorhabditis elegans hypothetical protein Y43F8C.16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.8%; Score 48; DB 2; Length 296; ilarity 37.5%; Pred. No. 1.5e+02; Conservative 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 48; DB 2; Le
Pred. No. 2.5e+02;
3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-296 <WIL>
56
                                  14 CRRRRRRCRRRRRRCCORR--RVRKC 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 IXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: SGD:MON1
A;Cross-references: SGD:S0003092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 FOHLDDCCSRKCNR 22
```

us-10-627-685a-26.rpr

2

```
A; Molecule type: mRNA
A; Residues: 1-880 eVAE>
A; Residues: 1-880 eVAE>
A; Cross-references: UNIRROT: P10041; EMBL: X06289; NID: 97852; PID: 97853
R; Knust, E.; Dietrich, U.; Tepass, U.; Bremer, K.A.; Weigel, D.; Vaessin, H.; Campos-Orté
EMBO J. 6, 761-766, 1987
A; Title: EGF homologous sequences encoded in the genome of Drosophila melanogaster, and t
A; Reference number: A91081; MUID: 87218537; PMID: 3107986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-1429 <YOC>
A;Cross-references: UNIPROT:P14585; EMBL:M12069; NID:g156357; PIDN:AAA70191.1; PID:g15635
                    Title: The neurogenic gene Delta of Drosophila melanogaster is expressed in neurogenic; Reference number: $00670; Accession: $00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: FlyBase:FBgn0000463
C;Superfamily: neurogenic protein delta; EGF homology
C;Keywords: transmembrane protein
F;1-18/Domain: signal sequence #status predicted <SIG>
F;1-18/Domain: neurogenic repetitive locus delta protein #status predicted <MAT>
F;19-88/Domain: EGF homology <EGFI>
F;533-564/Domain: EGF homology <EGFI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  homeotic protein lin-12 precursor - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Aug-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Introns: 50/2; 90/1; 109/1; 172/3; 545/1; 589/2; 632/2; 1273/3; 1389/3 C;Superfamily: ankyrin repeat homology; EGF homology C;Keywords: glycoprotein; transmembrane protein F;54-4/Domain: EGF homology < EGF1- F;507-540/Domain: EGF homology < EGF2- F;507-540/Domain: EGF homology < EGF2- F;507-578/Domain: EGF2- F;507-578/Domai
                                                                                                                                                                                                                                                                                                                                                                                                                                    ,Accession: A26637
,MOLECULE V.PDE: MRNJ.
,Residues: 422-436, ET', 439-458, 'A',460-489,'T',491-621 <KNU).
,Cross-references: GB:X05140; NID:97851; PIDN:CAA28786.1; PID:9929563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.8%; Score 48; DB 2; Length 1429; 35.0%; Pred. No. 4.2e+02; Live 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 29.8%; Score 48; DB 2; Length 880; Best Local Similarity 28.6%; Pred. No. 3e+02; Matches 6; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Greenwald, I.
Cell 43, 583-590, 1985
A;Reference number: A24769; MUID:86079540; PMID:3000611
A;Accession: A24769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;1093-1125/Domain: ankyrin repeat homology <AN1>F;1206-1238/Domain: ankyrin repeat homology <AN2>F;1240-1272/Domain: ankyrin repeat homology <AN3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       449 RCETNIDDCLGHQCENGGTCI 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 KCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             284 COEGKDNCVNNKCEAGSKCI 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 CFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 35.0
Matches 7; Conservative
6, 3431-3440, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA 'A;Residues: 173-712 <GRE> C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: Delta; Dl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurogenic repetitive locus delta protein precursor - fruit fly (Drosophila melanogastea
                                                              A31246
A31246
A31246
A31246
A31246
A31246
A31246
A31246
A31246
C; Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 02-Aug-2002
C; Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 02-Aug-2002
C; Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 02-Aug-2002
C; Accession: A31246
A; Title: Delta, a Drosophila neurogenic gene, is transcriptionally complex and encodes
A; Accession: A31246
A; MuID: 89196890; PMID: 3149249
A; Residual type: mRNA
A; Residuals: 1-832 < KOP>
A; Cross-references: GB: Y00222
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Drosophila melanogaster
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S19087
R;Muskavitch, M.A.T.
submitted to the EMBL Data Library, June 1991
A;Accession: S19087
A;Accession: S19087
A;Status: preliminary
A;Accession: 1-833 *MUS>
A;Cross-references: UNIPROT:P10041; EMBL:Y00222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NiAlternate names: gene DI protein
C;Species: Drosophila melanogaster
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: S00670; Az6637
R;Vaessin, H.; Bremer, K.A.; Knust, E.; Campos-Ortega, J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene Delta protein precursor – fruit fly (Drosophila melanogaster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29.8%; Score 48; DB 2; Length 833; 28.6%; Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: neurogenic protein delta; EGF homology F;295-328/Domain: EGF homology <EGF1>
F;422-450/Domain: EGF homology <EGF1>
F;457-488/Domain: EGF homology <EGF>
F;533-564/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C,Superfamily: neurogenic protein delta, EGF homology F;335-371/Domain: EGF homology eBGF1>
F;374-415/Domain: EGF homology eBGX1>
F;457-48#/Domain: EGF homology eEGF>
F;533-564/Domain: EGF homology eEGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 2.9e+02;
5; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29.8%; Score 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: FlyBase:Dl
A;Cross-references: FlyBase:FBgn0000463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :| :||| : |||
449 RCETNIDDCLGHQCENGGTCI 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.Gene: FlyBase:Dl
A.Cross-references: FlyBase:FBgn0000463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :| ::||| :|
RCETNIDDCLGHQCENGGTCI 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 KCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 KCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 28.6
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ሯ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
```

```
Accession: A39210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kristensen, T
                                                                                                                      g
Cipace: 34-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
Cipace: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
CiAccession: S78549; S71825
RiJoutel, A.; Tournier-Lasserve, E.
RiJoutel, A.; Tournier-Lasserve, E.
Accession: S78549
Aincelled to the EMBL Data Library, April 1997
Aincession: S78549
Aincelled type: mRNA
Aincelled type: mRNA
Aincelle type: mRNA
Aincelled type: mRNA
Aincelsed to the type: MRNA
Ain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 67-113;138-194;268-333,'G',335-346;536-613;716-765;1240-1279;1815-1888 <JOUZ
A;Cross-references: EMBL:U97669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 87
T28625
Variant-specific surface protein 3 - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Species: Dlasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Cct-1999 #text_change 09-Jul-2004
C;Accession: T28625
R;Su, X.Z.; Heatwole, V.M.; Wertheimer, S.F.; Guinet, F.; Herrfeldt, J.A.; Peterson, D.S.A:Tille: The large diverse gene family var encodes proteins involved in cytoadherence an A;Reference number: Z20487; MUID:95330813; PMID:7606788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a type of stroke and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-3006 <SUX>
A;Cross-references: UNIPROT:Q26032; EMBL:L40609; NID:g886376; PID:g886377; PIDN:AAA75397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description: may be involved in pathogenesis of CADASIL, causing Superfamily: notch protein; ankyrin repeat homology; EGF homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 5.7e+02;
5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Status: preliminary; translated from GB/EMBL/DDBJ:
Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;1871-1903/Domain: ankyrin repeat homology <AN2>F;1905-1937/Domain: ankyrin repeat homology <AN3>F;1998-1970/Domain: ankyrin repeat homology <AN4>F;1971-2003/Domain: ankyrin repeat homology <AN5>F;1971-2003/Domain: ankyrin repeat homology <AN5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A Accession: S71825
A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :| :|:| |: | RCESQVDECRSQPCRHGGKCL 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homology «EGX1»
homology «EGX2»
homology «EGX2»
homology «EGF3»
homology «EGF3»
homology «EGF3»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 KCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;1838-1870/Domain: ankyrin repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1-1903/Domain: ankyrin repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 33.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Gene: notch3
A,Map position: 19p13.1
C,Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1240-271/Domain: EGF
1318-349/Domain: EGF
1473-504/Domain: EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123-155/Domain: EGF
162-194/Domain: EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;853-884/Domain: EGF
F;928-959/Domain: EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Keywords: tandem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: var-3
A;Introns: 2597/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
```

```
alpha-2-macroglobulin receptor precursor - human N.Alternate names: CD91; LDL receptor-related protein 1; low density lipoprotein receptor C; Species: Homo sapiens (man) C;Date: 14-Aug-1998 #sequence revision 14-Aug-1998 #text_change 09-Jul-2004 C;Accession: S02392; S30027; T37998; A39210; S12538 E;Herz, J.; Hamann, U.; Rogne, S.; Myklebost, O.; Gausepohl, H.; Stanley, K.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Title: Surface location and high affinity for calcium of a 500-kd liver membrane protesing Feference number: S02392; MUID:89210795; PMID:3266596
Accession: S02392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A)CONSTRUCT STATE OF THE STATE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: GDB:LRP1; APR; LRP; AZMR
A;Cross-referencés: GDB:119694; OMIM:107770
A;Cross-referencés: GDB:119694; OMIM:107770
A;Cross-referencés: GDB:119694; OMIM:107770
C;Complex: The alpha-2-macroglobulin receptor complex consists of noncovalently-associate C;Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding C;Keywords: beta-hydroxysaparagine; beta-hydroxysaparatic acid; calcium binding; glycoprot F;1-19;Domain: signal sequence #status predicted <SIG>F;20-3943/Product: alpha-2-macroglobulin receptor 515K chain #status predicted <515K>F;27-64/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;72-108/Domain: LDL receptor ligand-binding repeat homology <LDL2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cross-references: EMBL:X15424; NID:g34408; PIDN:CAA33464.1; PID:g34409; Strickland, D.K.; Ashcom, J.D.; Williams, S.; Burgess, W.H.; Migliorini, M.; Argraves, Biol. Chem. 265, 17401-17404, 1990

Fill: Chem. 265, 17401-17404, 1990

Title: Sequence identity between the alpha2-macroglobulin receptor and low density lipcing number: A39210; MUID:91009181; PMID:1698775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Status: preliminary
Molecule type: procein
Residues: 150-166;234-238,'X',240-245,'X',247-252;'G',686-695;902-916;1096-1109;'S',174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Residues: 1-4544 «HER»
Cross-references: UNIPROT:Q07954; EMBL:X13916; NID:G34338; PIDN:CAA32112.1; PID:G34339
                                                                                                                                                                                                 ۲;
                                                                                                                                                                                                 Gaps
                                 Length 3006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       homology
homology
homology
homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat Prepeat Prepeat
                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: 137998
Status: preliminary: translated from GB/EMBL/DDBJ
Molecule type: DNA
Residues: 1-11 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, October 1990 A; Reference number: $30027 A; Accession: $30027
Query Match
29.8%; Score 48; DB
Best Local Similarity 33.3%; Pred. No. 6.8e
Matches 9; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            1052 CKGKAKSCTQKDGCTKCKAACDNYNK 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fil5-148/Domain: Bor homology <EG1-
Fil5-148/Domain: Bor homology <EG2-
198-239/Domain: LDL receptor WTD-containing
Fi240-281/Domain: LDL receptor WTD-containing
Fi22-334/Domain: LDL receptor WTD-containing
Fi335-378/Domain: LDL receptor WTD-containing
Fi379-420/Domain: LDL receptor WTD-containing
                                                                                                                                                                                                                                                                                                                                1 CRIXNOKCFOHLDDC--CSRKCNRFNK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 3275-3864 <KRI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecule type: mRNA
```

us-10-627-685a-26.rpr

```
F;421-468/Domain: LDL receptor YWTD-containing repeat homology <YW06>
F;471-468/Domain: EGF homology <EG3>
F;771-451/Domain: LDL receptor YWTD-containing repeat homology <YW07>
F;614-659/Domain: LDL receptor YWTD-containing repeat homology <YW09>
F;614-659/Domain: LDL receptor YWTD-containing repeat homology <YW10>
F;617-151/Domain: LDL receptor YWTD-containing repeat homology <YW10>
F;731-799/Domain: LDL receptor YWTD-containing repeat homology <YW10>
F;854-890/Domain: LDL receptor Igand-binding repeat homology <LDL3>
F;854-890/Domain: LDL receptor Ilgand-binding repeat homology <LDL3>
F;936-931/Domain: LDL receptor Ilgand-binding repeat homology <LDL5>
F;976-101/Domain: LDL receptor Ilgand-binding repeat homology <LDL5>
F;1062-1097/Domain: LDL receptor Ilgand-binding repeat homology <LDL5>
F;1062-1097/Domain: LDL receptor Ilgand-binding repeat homology <LDL5>
F;1145-1182/Domain: LDL receptor Ilgand-binding repeat homology <LDL5>
F;1163-1221/Domain: LDL receptor Ilgand-binding repeat homology <LDL5>
F;115-1231/Domain: LDL receptor Ilgand-binding repeat homology <LDL5>
F;115-1251/Domain: LDL receptor Ilgand-binding repeat homology <LDL5>
F;115-1251/Domain: LDL receptor YWTD-containing repeat homology <WH13>
F;1259-1386/Domain: LDL receptor YWTD-containing repeat homology <WH15>
F;1356-1398/Domain: LDL receptor YWTD-containing repeat homology <WH15>
F;146-1488/Domain: LDL receptor YWTD-containing repeat homology <WH15>
F;146-1488/Domain: LDL receptor YWTD-containing repeat homology <WH15>
F;146-1488/Domain: LDL receptor YWTD-containing repeat homology <WH15>
F;146-158/Domain: LDL receptor YWTD-containing repeat homology <WH15>
F;1470-158/Domain: LDL receptor YWTD-containing repeat homology <WH15>
F;1470-158/Domain: LDL receptor YWTD-cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g repeat homology <YW24>
g repeat homology <YW25>
g repeat homology <YW26>
g repeat homology <YW26>
g repeat homology <YW27>
g repeat homology <YW27>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homology <YW14>
homology <YW15>
homology <YW16>
homology <YW16>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <YW21><YW22><YW23>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <YW30><YW31><YW32><YW33>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  < YW37>< YW38>< YW39>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       < YW29>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   < XW36 >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <LDLG><LDLG><LDLH><LDLH><
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               < YW34>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <LDLP>
<LDLQ>
<LDLR>
<LDLR>
<LDLS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <LDLD>
<LDLE>
<LDLF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <LDLM>
<LDLN>
<LDLO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homology homology homology homology homology homology homology homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  homology
homology
homology
homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 grepeat homology of repeat homology of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor YWTD-containing repeat homology receptor YWTD-containing repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homology chomology chomology chomology homology chomology chomolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L'ecceptor ligand-binding repeat ho L'ecceptor ligand repeat ho L'ecceptor ligand repeat ho L'ecceptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L receptor ligand-binding repeat ho

L receptor ligand-binding repeat ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat h
repeat h
repeat h
repeat h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat | repeat | repeat |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat |
repeat |
repeat |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F homology <EGB>
L receptor YWTD-containing re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L receptor YWTD-containing re
L receptor YWTD-containing re
L receptor YWTD-containing re
L receptor YWTD-containing re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homology <EG13>
receptor ligand-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <EG10>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               homology <EG9>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homology
receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homology
homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F,1309-1355/Domain: D
F,1356-1398/Domain: D
F,1446-1488/Domain: D
F,1448-1531/Domain: D
F,1540-1578/Domain: D
F,1627-1669/Domain: D
F,1670-1713/Domain: D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;1977-2019/Domain: E;2020-2063/Domain: E;2064-2105/Domain: E;2106-2151/Domain: E;2159-2241/Domain: E;2253-2241/Domain: E;2253-2244/Domain: E;2253-2294/Domain: E;2253-2294/Domain: E;2253-2294/Domain: E;2253-2294/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;2605-2639/Domain:
F;2652-2688/Domain:
F;659-2730/Domain:
F;2734-2769/Domain:
F;2774-2812/Domain:
F;2818-2853/Domain:
F;2658-2897/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;2904-2939/Domain:
F;2944-2980/Domain:
F;2946-3021/Domain:
F;3029-3068/Domain:
F;3069-3113/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;3374-3408/Domain: F;3413-3448/Domain: F;3453-3489/Domain: F;3494-3531/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;2344-2388/Domain:
F;2389-2429/Domain:
F;2430-2473/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;2524-2517/Domain:
F;2524-2561/Domain:
F;2566-2600/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;1797-1846/Domain:
F;1850-1886/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;3157-3200/Domain:
F;3201-3241/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;3242-3284/Domain:
F;3294-3330/Domain:
F;3334-3369/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;3613-3647/Domain:
F;3654-3690/Domain:
F;3695-3731/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;1934-1976/Domain: F;1977-2019/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;3114-3156/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;3536-3570/Domain:
F;3575-3609/Domain:
```

```
in: LDL receptor ....
in: EGF homology <EG14>
ain: EGF homology <EG14>
ain: EGF homology <EG14>
ain: LDL receptor YWTD-containing repeat homology <YW40>
ain: LDL receptor YWTD-containing repeat homology <YW41>
oduct: alpha-2-macroglobulin receptor 85K chain #stetus predicted <85K>
main: LDL receptor YWTD-containing repeat homology <YW42>
omain: LDL receptor YWTD-containing repeat homology <YW43>
omain: LDL receptor YWTD-containing repeat homology <YW45>
omain: LDL receptor YWTD-containing repeat homology <YW45>
omain: LDL receptor YWTD-containing repeat homology <YW45>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N'Alternate names: CD91; LDL receptor-related protein 1; low density lipoprotein receptor C;Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: S22111
A;Molecule type: mRNA
A;Residues: 1-4545 cVANI>
A;Residues: 1-4545 cVANI>
A;Cross-references: 1-4545 cVANI>
A;Cross-references: UNIRROT:061291; EMBD:X67469; NID:949941; PIDN:CAA47817.1; PID:949942
R;van Leuven, F.; Stas, L.; Raymakers, L.; Overbergh, L.; de Strooper, B.; Hilliker, C.;
Biochim. Biophys. Acta 1173, 71-74, 1993
A;Title: Molecular cloning and sequencing of the murine alpha-2-macroglobulin receptor of A;Reference number: S32554; MUID:91250049; PMID:8485155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: 32.534
A; Molecule type: mRNA
A; Mesidues 1.28; 416-4453 < VAN2>
A; Cross = references: EmBit.X67469
C; Complex: The alpha-2-macroglobulin receptor complex consists of noncovalently-associat ciaced protein (see PIR:X70281).
C; Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding C; Keywords: beta-hydroxyasparagine; beta-hydroxyaspartic acid; calcium binding; glycoproficial proper and product: alpha-2-macroglobulin receptor #status predicted <NAT>
F; 20-3944, Domain: alpha-2-macroglobulin receptor fist chain #status predicted <15.5x
F; 20-3944, Domain: alpha-2-macroglobulin receptor fist chain #status predicted <515x>
F; 20-3944/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F; 31-199/Domain: EGF homology <EG3>
F; 31-119/Domain: EGF homology <EG3>
F; 31-139-240/Domain: LDL receptor YWTD-containing repeat homology <YW03>
F; 241-282/Domain: LDL receptor YWTD-containing repeat homology <YW03>
F; 336-335/Domain: LDL receptor YWTD-containing repeat homology <YW04>
F; 336-342/Domain: LDL receptor YWTD-containing repeat homology <YW04>
F; 336-421/Domain: LDL receptor YWTD-containing repeat homology <YW06>
F; 336-421/Domain: LDL receptor YWTD-containing repeat homology <YW06>
F; 324-2-469/Domain: LDL receptor YWTD-containing repeat homology <YW06>
F; 326-421/Domain: LDL receptor YWTD-containing repeat homology <W06>
F; 322-469/Domain: LDL receptor YWTD-containing repeat homology <W06>
F; 326-424/Domain: LDL receptor YWTD-containing repeat homology <W06>
F; 326-424/Do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;445-4544/Domain: intracellular #status predicted <INT>
F;66,2998/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F;2058/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F;4075,4125,4278/Binding site: carbohydrate (Asp) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 29.8%; Score 48; DB 1; Length 4544; Best Local Similarity 44.8%; Pred. No. 9e+02; Matches 13; Conservative 7; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;4421-4444/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - monse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CRIXNQKCFQHLDDCCSRKC--NRFN-KC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;van Leuven, F.
submitted to the EMBL Data Library, July 1992
A;Reference number: $25111
                                                                                                                                                                                                                                                                                                                              LDL receptor YWTD-con
LDL receptor YWTD-con
LDL receptor YWTD-con
LDL receptor YWTD-con
EGF homology eGG17 BGF homology eGG17 BGF homology eGG18 BGF homology eGG18 BGF homology eGG19 BGF homology eGG20 BGF homology eGG20 EGG homology eGG20 BGF homology eGG20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alpha-2-macroglobulin receptor precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C, Accession: $25111; $32554
                                                                  F;3785-3822/Domain: E
F;3828-3860/Domain: E
F;3868-3911/Domain: L
F;3912-3969/Domain: L
                                                                                                                                                                                                                                                  F; 3944-4544/Product:
                                                                                                                                                                                                                                                                                             F;3944-4420/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;4377-4408/Domain:
                                                                                                                                                                                                                                                                                                                                            F;3970-4012/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;4151-4182/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                 F;4013-4056/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                       4057-4099/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;4100-4142/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;4236-4267/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;4272-4303/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;4308-4339/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;4344-4374/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
```

```
F;372-614/Domain: EGF homology <EG3>
F;572-614/Domain: LDL receptor YWTD-containing repeat homology <YW07>
F;572-614/Domain: LDL receptor YWTD-containing repeat homology <YW08>
F;661-711/Domain: LDL receptor YWTD-containing repeat homology <YW09>
F;712-753/Domain: LDL receptor YWTD-containing repeat homology <YW10>
F;712-753/Domain: LDL receptor YWTD-containing repeat homology <WW11>
F;885-891/Domain: EGF homology <EG4>
F;885-891/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F;896-932/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F;977-972/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F;1016-1052/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F;1016-1052/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F;106-1052/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F;106-1052/Domain: LDL receptor ligand-binding repeat homology <LDL9>
F;116-1141/Domain: LDL receptor ligand-binding repeat homology <LDL9>
F;116-1141/Domain: LDL receptor ligand-binding repeat homology <LDL9>
F;116-1135/Domain: LDL receptor ligand-binding repeat homology <WW15>
F;128-1262/Domain: LDL receptor WWTD-containing repeat homology <WW15>
F;137-1399/Domain: LDL receptor WWTD-containing repeat homology <WW15>
F;1447-1489/Domain: LDL receptor WWTD-containing repeat homology <WW15>
F;145-1379/Domain: LDL receptor WWTD-containing repeat homology <WW15>
F;148-1157/Domain: LDL receptor WWTD-containing repeat homology <WW15>
F;148-1157/Domain: LDL receptor WWTD-containing repeat homology <WW15>
F;158-158-159/Domain: LDL receptor WWTD-containing repeat homology <WW15>
F;158-159/Domain: LDL receptor WWTD-containing repeat homology <WW15>
F;158-159/Domain: LDL receptor WWTD-containing repeat homology <WW15>
F;158-168-1670/Domain: LDL receptor WWTD-containing repeat homology <WW15>
F;158-169/Domain: LDL receptor WWTD-containing repeat homology <WW15>
F;158-169/Domain: LDL receptor WWTD-containing repeat homology <WW15>
F;158-169/Domain: LDL receptor WWTD-containing repeat homology <WW1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <YW26><YW27><YW28>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <YW21><YW22>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <YW24><YW25>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <YW35><YW36>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <YW37><YW38><
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           < YW23 >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <YW31>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <YW29>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <LDLH>
<LDLI>
<LDLI>
<LDLJ>
<LDLK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <LDLC>
<LDLD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <LDLF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <LDLS><LDLT><LDLU><LDLU><LDLV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <LDLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homology homology homology homology homology homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          homology chomology homology homology homology homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  homology
homology
homology
homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homology
homology
homology
homology
homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           homology
homology
homology
homology
homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       homology
homology
homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  homology
homology
homology
homology
homology
homology
homology
homology
homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        r YWTD-containing repeat h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C. YWTD-containing repeat he YWTD-containing repeat he
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor ligand-binding repeat ho receptor ligand-binding repeat ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leceptor 199ad-binding repeat ho in receptor 199ad-binding repeat ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat
repeat
repeat
repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat
repeat
repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat
repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                             YWTD-containing r
YWTD-containing r
YWTD-containing r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YWTD-containing r
YWTD-containing r
YWTD-containing r
YWTD-containing r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YWTD-containing
YWTD-containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <EG10>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <EG8>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <EG9>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor.
receptor
receptor
receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               homology
receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;1798-1847/Domain:
F;1851-1887/Domain:
F;1935-1977/Domain:
F;1978-2020/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .5-1754/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1755-1797/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1978-2020/Domain:
2021-2064/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2065-2106/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-2152/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2200-2242/Domain:
2254-2295/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2390-2430/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2431-2474/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2606-2640/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :2735-2770/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2987-3022/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3070-3114/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3295-3331/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;2819-2854/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2859-2898/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3115-3157/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :3454-3490/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;3742-3777/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;3375-3409,
```

```
Pancreatic ribonuclease (EC 3.1.27.5) - reindeer (tentative sequence)
N;Alternate names: RNase 1; RNase A
C;Species: Rangifer tarandus (reindeer)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: B91418; A00812
R;Ledijenaar-van den Berg, G; Beintema, J.J.
R;BES Lett. 56, 101-107, 1975
A;Rtle: The amino acid sequences of reindeer, moose and fallow deer pancreatic ribonucle
A;Reference number: A91418; MUD:76003215; PMID:1157925
A;Accession: B91418
A;Molecule type: protein
A;Residues: 1.124 <LEI>A;Cross references: UNIPROT:P00666
C;Superfamily: pancreatic ribonuclease
C;Superfamily: pancreatic ribonuclease
C;Gywords: hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   finger protein HPF4 - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 08-Dec-2000
C;Accession: A39384
R;Bellefroid, E.J.; Poncelet, D.A.; Lecocq, P.J.; Revelant, O.; Martial, J.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 3608-3612, 1991
A;Title: The evolutionarily conserved Krueppel-associated box domain defines a subfamily A;Reference number: A39384; MUID:91219421; PMID:2023909
A;Status: preliminary
                                                                LDL receptor YWTD-containing repeat homology <YW40>
LDL receptor YWTD-containing repeat homology <YW41>
LDL receptor YWTD-containing repeat homology <YW41>
85K chain extracellular status predicted <85K>
85K chain extracellular status predicted <8XT>
LDL receptor YWTD-containing repeat homology <YW42>
LDL receptor YWTD-containing repeat homology <YW43>
LDL receptor YWTD-containing repeat homology <YW43>
LDL receptor YWTD-containing repeat homology <YW44>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;442-4445/Domain: transmembrane #status predicted <TMM>;4446-4545/Domain: intracellular #status predicted <INT>
;1446-4545/Domain: intracellular #status predicted <INT>
;167,2999/Modified site: erythno-beta-hydroxyasparatic acid (Asp) #status predicted ;2959/Modified site: erythno-beta-hydroxyaspartic acid (Asp) #status predicted ;4076,4126,4279/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ις
·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 4545; 9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1222 CQIQSY-CAKHLK--CSQKCDQNKFSVKC 1247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 29.8%; Score 48; DB Similarity 44.8%; Pred. No. 9e+C 13; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.5%; Score 47.5; I
25.0%; Pred. No. 94;
:ive 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | : : | | : | | CKNGQSNCYQSNSAMHITDCRETGSSKYPNCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CRIXNOKCFQHLDDCCSRKC--NRFN-KC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CRIXNQKCFQ-----HLDDCCSRKCNRFNKCV
                                                                                                                                                                                                            LDL receptor YMTD-con
EGF homology & EG18>
EGF homology & EG18>
EGF homology & EG20>
EGF homology & EG20>
EGF homology & EG20>
EGF homology & EG21>
EGF homology <
EGF homology <
LDL receptor Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 25.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 13; Conserv
                                                                                                                        F;3945-4545/Domain:
F;3945-4421/Domain:
F;3971-4013/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;4345-4375/Domain:
                                                                                                                                                                                                                   ;4014-4057/Domain:
                                                                                                                                                                                                                                                4058-4100/Domain:
                                                                                                                                                                                                                                                                                :4101-4143/Domain:
                                                                                                                                                                                                                                                                                                                 ;4152-4183/Domain:
                                                                                                                                                                                                                                                                                                                                                 ;4201-4232/Domain:
                                                                                                                                                                                                                                                                                                                                                                        4237-4268/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                            ,4273-4304/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                         4309-4340/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 91 A39384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠ
```

ä

셤

ò

```
C;Accession: $49371
Rs:Stonnet, V; Guesdon, J.L.
submitted to the EMBL Data Library, October 1994
A;Description: Nucleotide_sequences and molecular organization of the two small cryptic ;
                                                                                                                                                                                                                                                                A Status: preliminary
Modecule type: DNA
A;Residues: 1-253 < STO>
A;Cross-references: UNIPROT:Q46019; EMBL:X82079; NID:g557228; PIDN:CAA57593.1; PID:g5572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:019120; EMBL:278411; PIDN:CAB01646.1; GSPDB:GN00023; CESP:P07
A;Experimental source: clone F02D8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: UNIPROT: Q03923; EMBL: U35376; NID: g1017721; PIDN: AAA79179.1; PID: g101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GDB:132279
A;Map position: 19p12-19p12
C;Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transcription repressor zinc finger protein 85 - human C;Species: Homo sapiens (man) C;Species: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004 C;Accession: 602075 R;Poncelet, D.A. Submitted to the EMBL Data Library, September 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ).Species: Caenorhabditis elegans
:)Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
:)Accession: T20506
                                    C;Species: Campylobacter coli
C;Date: 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .,
2
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.2%; Score 47; DB 2; Length 285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

29.5%; Score 47.5; DB 2;
Best Local Similarity 34.6%; Pred. No. 1.5e+02;
Matches 9; Conservative 5; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
29.5%; Score 47.5; DB 2;
Best Local Similarity 34.4%; Pred. No. 2.7e+02;
Matches 11; Conservative 7; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: G09169
A;Accession: G02075
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-595 <PON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: T20506
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-285 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 CRHENLPLRKGCESMDECKMHKGGCNGLNQCL 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CRIXN---QKCFQHLDDCCSRK--CNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, August 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CRIXNOK-----CFQHLDDCCSRKCN 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Map position: 5
A;Introns: 27/3; 57/3; 195/3; 235/3
         repB protein - Campylobacter coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lypothetical protein F02D8.2
                                                                                                                                                                                                            A; Reference number: S49367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: Z19284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: CESP: F02D8.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: GDB: ZNF85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . გ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gross-references: UNIPROT:P41454; GB:L22858; NID:g510708; PIDN:AAA66701.1; PID:g559140
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                apoptosis inhibitor - Autographa californica nuclear polyhedrosis virus
CiSpecies: Autographa californica nuclear polyhedrosis virus, AcMNPV
A;Note: abDNA virus
CiAccession: H72858
A;Ayres, MD.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
Virology 202, 586-605, 1994
A;Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.
A;Reference number: A72850; MUD:94303173; PMID:8030224
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                            ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ų,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Variety: isolate T3
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C; Accession: T41814
R; Gomi, S.; Majima, K.; Maeda, S.
J; Gen, Virol. 80, 1323-1337, 1999
A; Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.
A; Reference number: Z22020; MUID:99281911; PMID:10355780
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                           A,Residues: 1-196 <BEL>
A,Cross-references: GB:M61866; NID:g454818; PIDN:AAA52689.1; PID:g184336
C;Keywords: DNA binding; zinc finger
                                                                                                                                                                                                            5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 29.5%; Score 47.5; DB 2; Length 249; Best Local Similarity 34.3%; Pred. No. 1.5e+02; Matches 12; Conservative 6; Mismatches 8; Indels
                                                                                                                                                  Length 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:092435; EMBL:L33180; PIDN:AAC63743.1
A;Experimental source: isolate T3
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IAP2 orf71 - Bombyx mori nuclear polyhedrosis virus (isolate T3)
                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Species: Bombyx mori nuclear polyhedrosis virus, BmSNPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 29.5%; Score 47.5; DB 2;
Best Local Similarity 34.3%; Pred. No. 1.5e+02;
Matches 12; Conservative 6; Mismatches 8;
                                                                                                                                            Query Match 29.5%; Score 47.5; DB 2; Best Local Similarity 34.4%; Pred. No. 1.3e+02; Matches 11; Conservative 7; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202 CKVCFDREKSVCFMPCRHLAVCTECSRRCKRCCVC 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202 CKVCFDREKSVCFMPCRHLAVCTECSRRCKRCCVC 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CRIXNOK----CF---OHLDDC--CSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CRIXNQK----CF---QHLDDC--CSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                  1 CRIXN---QKCFQHLDDCCSRK--CNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-249 <AYR>
A, Molecule type? DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: T41814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: Ac-IAP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 94
S49371
```

요 ð

a

ઠે

7

39.18;

```
4 XNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 29.2%;
Best Local Similarity 37.5%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-365 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                  A, Gene: PFB0855c
                                                                                                                                                                                                                                                                                                                                                                          C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search cor
Job time
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                              transcription regulator, AraC family agpT [imported] - Agrobacterium tumefaciens (strain C;Species Agrobacterium tumefaciens (strain C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004 C;Accession: AG3129 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004 C;Accession: AG3129 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004 E; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Karge, P.; Romero, P.; Zhang, S. Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-295 «KUR»
A;Residues: 1-295 «KUR»
A;Cross-references: UNIPROT:Q8U6Z7; GB:AE008689; PIDN:AAL45453.1; PID:G17743157; GSPDB:C
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 98
B99158
B99158
B99159
B99159
B99159
B99159
B99159
C; Date: 22-Oct-2001 #sequence_revision 22-Cct-2001 #text_change 09-Jul-2004
B; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2322-2328, 2001
Science 294, Z322-2328, Z001
A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tump. Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-295 <KUR>
A,Cross-references: UNIPROT:Q8U6Z7; GB:AE007870; PIDN:AAK88788.1; PID:g15158539; GSPDB:G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 99
B71604
rRNA methylase (SpoU family) (OO, TP) PFB0855c - malaria parasite (Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577, MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                       5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 47, DB 2, Length 295,
Pred. No. 1.9e+02,
3; Mismatches 7; Indels
                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 47; DB 2; Length 232
Pred, No. 1.96+02;
     Pred. No. 1.9e+02;
6; Mismatches 6;
                                                                                                    3 IXNQKCFQHLD--DCCSRKCNRF 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : |: || :||| |
132 LQQETVDHLAECCSRLVN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : |: || :||| |
132 LQQETVDHLAECCSRLVN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 XNOKCFOHLDDCCSRKCN 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Gene: agpT
A, Map position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 44.4%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 XNQKCFQHLDDCCSRKCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 44.4%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Gene: AGR L 448
A,Map position: linear chromosome
                               Conservative
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Accession: AG3129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetics:
                                                                          ò
                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

```
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #text_change 09-Jul-2004
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
C;Datesion: B71604
R;Garcher, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V., Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.; Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:09U202; EMBL:AL110478; NID:e1542139; PIDN:CAB54342.1; CESP:Y; A;Experimental source: clone Y26D4A
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                           A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein Y26D4A.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 47; DB 2; Length 351;
Pred. No. 2.1e+02;
6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29.2%; Score 47; DB 2; Length 365; larity 39.1%; Pred. No. 2.2e+02; Conservative 3; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Introns: 30/1; 126/3; 174/2; 197/2; 223/1; 295/3; 335/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Accession: T26564
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ubmitted to the EMBL Data Library, September 1999; Reference number: Z20234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 CKIKNQSCF--LNPCTHKNNDKRN 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              completed: April 18, 2005, 20:38:46 te : 28.5 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CRIXNOKCFOHLDDCCSRKCNRFN 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    284 SNÓECQÓRNOVVISRRARRINNC 306
```

Q9iat6 brachydanio Q9igmB oryza sativ P07207 drosophila P05482 contamoeba h Q8mxt1 entamoeba h Q8mxt2 entamoeba h P32022 entamoeba h P32022 entamoeba h P60254 scorpio mau	Q7xk99 oryza sativ P37137 xenopus lae Q63x13 xenopus lae Q63x13 xenopus lae P29674 xenopus lae P53411 gallus gall P63006 mesocricetu P63006 mesocricetu P63007 rattus norv Q26107 plasmodium Q80w06 mus musculu Q80w06 mus musculu	088671 rattus norv 088516 mus musculu 09ny17 homo sapien 081286 plasmodium 07rrt3 plasmodium 07rrt3 plasmodium 064644 conus magus 064649 phytophthor 064645 phytophthor 018052 caenorhabdi 099315 clostridium	P58920 conus catus Q801L7 adoxophyss Q801L7 adoxophyss Q60476 brachydanio Q45117 chironomus Q68K8 enorphabdi Q968K8 enorphabdi Q968L9 brachydanio P8183 eledone cir Q633N8 taxus x med Q1934 ceenorhabdi P598G8 pandinus im Q8xk8 clostridium Q8xk8 clostridium Q8xk8 clostridium Q61529 arabidopsis Q8152 dictyosteli Q2329 arabidopsis Q61604 lytechinus P6531 homo sapien Q84615 ceenorhabdi Q74615 caenorhabdi Q74615 caenorhabdi Q74615 caenorhabdi Q74615 caenorhabdi Q646u7 phytophthor Q646u7 phytophthor Q646u7 phytophthor Q658W7 oryza sativ P2530 caenamoeba h Q8xv21 caenorhabdi Q8xv21 caenorhabdi Q8mx5 drosophila Q80xv21 caenorhabdi Q8mx5 drosophila Q80xv21 caenorhabdi Q80xv21 caenorhabdi Q80xv21 caenorhabdi Q8mx5 drosophila Q80xv21 caenorhabdi Q8
34.8 664 2 34.8 708 1 34.8 2703 1 34.5 25 1 34.5 372 2 34.5 372 2 34.5 372 2 34.5 372 2 34.5 1276 1 34.2 133 1	344.2 344.2 344.2 344.2 344.2 344.2 344.2 344.2 344.2 344.2 344.2 344.2 344.2 344.2 344.2 344.2 344.2 344.2 344.2 344.2 344.2 344.2 345.2 346.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2 347.2	34.2 34.2 34.2 34.2 34.2 33.9 33.9 33.9 33.9 33.9 33.9 33.9 33	33.9 1282 2 018720 33.5 73 1 CXOD_CONCT 33.5 405 1 LHXI_BRARE 33.5 405 1 LHXI_BRARE 33.5 911 2 048174 33.5 1372 2 04817 33.1 172 2 091526 33.2 476 2 09336 33.2 476 2 09338 33.2 576 2 06818 33.2 576 2 06818 32.9 234 2 08182 32.9 234 2 08182 32.9 234 2 08182 32.9 234 2 08182 32.9 235 2 078230 32.9 238 2 04467 32.9 238 2 04615 32.9 238 2 04615 32.9 238 2 04615 32.9 283 2 04617 32.9 283 2 04617 32.9 283 2 08187 32.9 283 2 08187 32.9 283 2 08187 32.9 283 2 08187 32.9 283 2 08187 32.9 283 2 08187 32.9 283 2 08187 32.9 283 2 08187 32.9 283 2 08187 32.9 283 2 08187 32.9 283 2 08187 32.9 283 2 08187 32.9 283 2 08187 32.9 283 2 08187 32.9 283 2 08187 32.9 283 2 08187 32.9 283 2 08187 32.9 283 2 08187 32.9 283 2 08187 32.9 283 2 08187 32.9 283 2 08187 32.9 283 2 08187 32.3 354 2 08187 32.3 354 2 08187 32.3 2139 1 CRB_DROME
			66 68 68 70 71 71 71 71 71 72 73 74 74 74 74 74 75 74 74 74 74 74 74 74 74 74 74
n 5.1.6 Compugen Ltd. Search time 117 Seconds (without alignments)	. 1612378	Chance to hav	result being r stribution. Descripti Descripti 071842 c 071842 c 071842 c 071842 c 071849 c 071840
GenCore version 5.1. Copyright (c) 1993 - 2005 Comp protein search, using sw model April 18, 2005, 20:00:51; Search (witho	127-685A-26 TOKCFOHLDDCCSRKCNRFNK 2DX 0.0 , Gapext 0.5 · 1 seqs, 512079187 res tisfying chosen para	th: 2000000000000000000000000000000000000	# SUMMARIES  Query  • Match Length DB ID  1 100.0 72 1 CXK7 CONPU  1 100.0 72 1 CXK7 CONPU  1 100.0 72 1 CXK7 CONPU  1 44.1 67 2 Q71K79  1 31.2 2 Q71K79  2 39.1 2050 2 Q71K70  3 39.1 2050 2 Q71K70  3 39.1 2050 2 Q71K70  3 39.1 2050 2 Q71K79  4 4.1 72 1 CXC CONCT  3 39.1 2050 2 Q71K79  4 4.1 67 2 Q71K79  5 41.3 1125 2 Q97847  9 36.6 1410 2 Q20204  9 36.6 18 2 Q77847  9 36.6 18 2 Q97847  7 35.4 66 1 SCXI_OPICA  7 35.4 65 0 2 Q04081  8 36.0 38.2 1 EFL9_HUMAN  7 35.4 66 1 SCXI_OPICA  7 35.4 65 0 2 Q04081  8 35.1 1292 2 Q24835  8 35.1 372 2 Q88WZT3  8 35.1 3467 2 Q88WZT3  8 35.1 3467 2 Q88WZT3
OM protein - prot Run on:	score: e: table: d: DB seq 1	DB seq 16 ocessing: e : red. No.	Regult Gore greater and is derived Wo. Score Matching Mat

N

```
dependent
                                                                                                                                                                                                                                                                                                                                          Moran 0.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eamily
ö
                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98104087; PubMed=9438859; DOI=10.1016/S0969-2126(97)00307-9; Scanlon M.J., Naranjo D., Thomas L., Alewood P.F., Lewis R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strategy for rapid immobilization of prey by a fish-hunting marine
                                05-UL-2004 (TrEMBLrel. 27, Created)
05-UL-2004 (TrEMBLrel. 27, Last sequence update)
05-UL-2004 (TrEMBLrel. 27, Last sequence update)
05-UL-2004 (TrEMBLrel. 27, Last annotation update)
Four-loop conotoxin preproprocein (Fragment).
Conus purpurascens (Purple cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Canogastropoda; Sorbeconcha; Hypsogastropoda;
NCBI_TaxID=41690;
                                                                                                                                                                                                                                                                                                                             ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                     15-DEC-1998 (Rel. 37, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Kappa-conotoxin PVIIA precursor (Fin-popping peptide).
Conus purpurascens (Purple cone).
Bukaryota; Metazoa; Mollusca; Gastropoda, Orthogastropoda;
Apogastropoda, Caenogastropoda, Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., SYNTHESIS, AND MASS SPECTROMETRY.
MEDLINE=98079023; PubMed=9417043; DOI=10.1074/jbc.273.1.33;
Shon K.-J., Stocker M., Terlau H., Stuehmer W., Jacobsen R.B.,
Walker C.S., Grilley M.M., Watkins M., Hillyard D.R., Gray W.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 46-72, AND SYNTHESIS.
MEDLINE=22068471; PubMed=12074021; DOI=10.1038/381148a0;
Terlau H., Shon K.-J., Grilley M.M., Stocker M., Stuehmer W.,
                                                                                                                                                                                                                                                                                                     ; Score 161; DB 2; Length 67;
Pred. No. 1.4e-12;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Kappa-conotoxin PVIIA is a peptide inhibiting the shaker K+
                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                           Duda T.F. Jr., Palumbi S.R.;
Submitted (FEB-2002) to the EMBL/GenEank/DDBJ databases.
EMBL, AF480312; AAQ05864.1; -...
HSSP; P56633; 1AV3.
                                                                                                                                                                                                    GO, GO:0005576; C:extracellular; IEA.
GO; GO:0008200; F:ion channel inhibitor activity; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR004214; Conotoxin.
                                                                                                                                                                                                                                                                      41 67 four-loop conotoxin.
67 AA; 7712 MW; E7E77CC61873E1DB CRC64;
                          67 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                        72 AA
                                                                                                                                                                                                                                                                                                                                           1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                         41 CRIPNQKCFQHLDDCCSRKCNRFNKCV 67
                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol. Chem. 273:33-38(1998).
                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                            Pfam; PF02950; Conotoxin; 1.
                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                        26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 381:148-151(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=41690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRUCTURE BY NMR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Olivera B.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Olivera B.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                      CONPU
                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              channel.
                      Q71KT2
                                                                                                                                                                                                                                                                                                                                                                                                                      CXK7 CC
P56633
                                                                                                                                                                                                                                                                                                                                                                                                         CXK7_CONPU
 RESULT 1
Q71KT2
                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
                                 ð
                                                                                                                                                                                                                                                                                                                                                                g
```

```
WUTGENESIS OF ARG-47; ILE-48; PRO-49; ASN-50; GLN-51; LVS-52; PHE-54; PHE-54; GLN-55; HIS-56; LEU-57; ASP-58; ASP-59; SER-62; ARG-63; LXS-64; ARG-67; PHE-68; ASN-69 AND LYS-70.

MEDLINE-20387356; PubMed-10818087; DOI=10.1074/jbc.C900990199; Jacobsen R.B., Koch E.D., Lange-Malecki B., Stocker M., Verhey J., Van Wagoner R.M., Vyazovkina A., Olivera B.M., Terlau H.; Single amino acid substitutions in kappa-conotoxin PVIIA disrupt interaction with the shaker K+ channel.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular simulation of the interaction of kappa-conotoxin-PVIIA with the Shaker potassium channel pore.";
Eur. Biophys. J. 30:528-536(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!-SUBCELLUTAR LOCATION: Secreted.
-!-TISSUE SPECIFICITY: Expressed by the venom duct.
-!-MASS SPECIFOMETRY: MW=3268.4; METHOD=FAB; RANGE=46-72; NOTE=Ref.1.
-!-SIMILARITY: Belongs to the conotoxin O-superfamily. Kappa-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAUTION: Because analogs resulting of mutagenesis of Hyp-49, Asn-50, Leu-57 and Asp-59 gave very low yields upon folding, the results of mutagenesis on these residues should be interpreted
                                                                                                                                          MEDLINE=98217295; PubMed=9548922; DOI=10.1021/bi9730341; Savarin P., Guenneugues M., Gilquin B., Lamthanh H., Gasparini S., Zinn-Justin S., Menez A.; "There-dimensional structure of kappa-conctoxin PVIIA, a novel potassium channel-blocking toxin from cone snails."; Blochemistry 37:5407-5416(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BLOCKADE OF SHAKER CHANNEL BY PVIIA.
MEDLINE=99329121; PubMed=10398696;
Terlau H., Boccaccio A., Olivera B.M., Conti F.;
"The block of Shaker K+ channels by kappa-conotoxin PVIIA is state
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single, lethal "fin-pop" in envenomated fish. In mice, induces hyperactivity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           with caution.
PIR; A58997; A58997.
PDB; 1AV3; NMR; @=1-27.
PDB; 1KCP; NMR; @=1-27.
PDB; PF02950; Conctoxin.
Pfam; PF02950; Conctoxin, 1.
3D-structure; Direct protein sequencing; Hydroxylation; Ionic channel inhibitor;
"Solution structure and proposed binding mechanism of a novel potassium channel toxin kappa-conotoxin PVIIA."; Structure 5:1585-1597(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MODEL OF THE SHAKER-PVIIA INTERACTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biol. Chem. 275:24639-24644(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BLOCKADE OF SHAKER CHANNEL BY PVIIA.
MEDLINE=22017751; PubMed=12023223;
Naranjo D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gen. Physiol. 114:125-140(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21678121; PubMed=11820396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22
                                                                                           [4]
STRUCTURE BY NMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal; Toxin.
SIGNAL
```

```
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Consumportaries (Purple cone).

Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Canogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Four-loop contoxin preproprotein (Fragment).
Conus purpurascens (Purple cone).
Eukaryota; Metazza, Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
NCBI_TAXID=41690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 73; DB 2; Length 67;
Pred. No. 0.088;
3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44.1%; Score 71; DB 2; Length 67; 50.0%; Pred. No. 0.15; 7; Indels iive 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                             Duda TF. Jr., Palumbi S.R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; A4480131; A4005865.1; -.
GO, GO:000576; C:extracellular; IEA.
GO, GO:0009200; F:ion channel inhibitor activity; IEA.
GO, GO:0009405; P:pathogenesis; IEA.
InterPro; IFR004214; Conotoxin.
Pfam; PF02950; Conotoxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Duda T.F. Jr., Palumbi S.R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF480315; AA05867.1; -.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR004214; Conotoxin.
PFam; PF02950; Conotoxin; 1.
NOW TER
41 67 four-loop conotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                             41 67 four-loop conotoxin.
67 AA; 7358 MW; E311E06BB6AF702E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 67 four-loop conotoxin.
67 AA; 7488 MW; 1B483B1BB6AF7755 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 AA.
                                                                                                                 67 AA.
                                          99
                                1 CRIXNOKCFOHLDDCCSRKCNRFNKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CRIXNQKCFQHLDDCCSRKC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 50.00,
--hes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 50.0
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                  NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q71KS9
Q71KS9;
                                                                                                              Q71KT1
                                                                                     RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q71KS9
                                                                                                 071KT1
                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4-hydroxyproline.
R-3A,K,Q: 100% reduction of toxicity.
I-3A: 3.fold decrease of toxicity.
P-3A: 100% reduction of toxicity.
N-3A: 100% reduction of toxicity.
Q-3A: 13-fold decrease of toxicity.
K-3A,R: 100% reduction of toxicity.
F-3A,M: 100% reduction of toxicity.
F-3Y: 11-fold decrease of toxicity.
G-3A: 3-fold decrease of toxicity.
H-3A: 3-fold decrease of toxicity.
L-3A: 100% reduction of toxicity.
D-3A: 100% reduction of toxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                        D->A: 100% reduction of toxicity.
S->A: 1.5-fold decrease of toxicity.
R->A: 3.5-fold decrease of toxicity.
K->A: 1.2-fold decrease of toxicity.
                                                                                                                                                                                                                                                                                                              17-fold decrease of toxicity.
                                                                                                                                                                                                                                                                                                                                            117-fold decrease of toxicity
                                                                                                                                                                                                                                                                                                 5-fold decrease of toxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Four-loop conotoxin (Fragment).
Conus ermineus (Atlantic fish-hunting cone).
Bukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Canonqastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 161; DB 1; Length 72; 96.3%; Pred. No. 1.5e-12; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 78.5; DB 2; Length 67;
Pred. No. 0.019;
6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Duda T.F. Dr., Palumbi S.R.; Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases. EMBL; AY236862; AAP75888.1; -.. GO; GO:0005576; C:extracellular; IEA. GO; GO:0009400; F:ion channel inhibitor activity; IEA. GO; GO:0009405; P:pathogenesis; IEA. InterPro; IPR004214; Conotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8317 MW; 53BFAF79EE751C16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 AA; 7575 MW; EBD5557FB2EE9134 CRC64;
  Kappa-conotoxin PVIIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46 CRIPNOKCFQHLDDCCSRKCNRFNKCV 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 96.3%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR004214; Conotox
Pfam; PF02950; Conotoxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 46.2
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. Duda T.F. Jr., Pal
                          DISULFID
DISULFID
MOD_RES
MUTAGEN
MUTAGEN
MUTAGEN
MUTAGEN
MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                  MUTAGEN
MUTAGEN
MUTAGEN
MUTAGEN
                                                                                                                                                                   MUTAGEN
MUTAGEN
MUTAGEN
                                                                                                                                                                                                            MUTAGEN
                                                                                                                                                                                                                                        MUTAGEN
MUTAGEN
                                                                                                                                                                                                                                                                    MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON TER
                                                                                                                                                                                                                                                                                                                                                                                                               STRAND
                                                                                                                                                                                                                                                                                                                                                        STRAND
                                                                                                                                                                                                                                                                                                                                                                                    STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAND
                                                                                                                                                                                                                                                                                                                                                                        I'GRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
```

Gaps

ö

ö

Page

```
11;
                                                                                                                                                                                                                                          family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POI MUSDO
P81765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEPTIDE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
POI_MUSDO
               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Venom duct;
MEDIINE=20037955; PubMed=10573284; DOI=10.1016/S0196-9781(99)00116-3;
Lu B.-S., Yu F., Zhao D., Huang P.-T., Huang C.-F.;
"Conopeptides from Conus striatus and Conus textile by cDNA cloning.";
Peptides 20:1139-1144(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-99003172; PubMed-1390774;
Ramilo C., Zafaralla G.C., Nadasdi L., Hammerland L.G., Yoshikami D.,
Gray W.R., Kristipati R., Ramachandran J., Miljanich G.,,Olivera B.M.
                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2009 conotoxin preproprotein (Fragment).
Conus purpurascens (Purple cone).
Bukaryota, Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Meogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CXOB CONST STANDARD; PRT; 72 AA.
P288B1; 09UB35;
01-DEC-1992 (Rel. 24, Created)
16-OCT-2001 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
Comega-conctoxin SYIB precursor (SNX-183).
Comus striatus (Striated cone).
Bukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbecconcha; Hypsogastropoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Novel alpha" and omega-conotoxins from Conus striatus venom.";
Biochemistry 31:9919:9926 (1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [3]
STRUCTURE BY NWR.
MEDLINE=97070382; PubMed=8913308; DOI=10.1006/jmbi.1996.0576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 71; DB 2; Length 67;
Pred. No. 0.15;
3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Duda T.E. Jr., Palumbi S.R.;

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AF480141, AA005866.1; -..

GO; GO:000576; C:extracellular; IEA.

GO; GO:0008200; F:ion channel inhibitor activity; IEA.

GO; GO:000405; P:ion channel inhibitor activity; IEA.

InterPro; IPR004214; Conotoxin; IEA.

PFam; ---

PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     four-loop conotoxin.
33E83B1BB6AF7435 CRC64;
                                                                                                                                                   67 AA.
      20
                          1 CRIXNOKCFOHLDDCCSRKC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 CKKSGRKCPPHQKDCCGRAC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 46-71, AND SYNTHESIS.
CRIXNOKCFOHLDDCCSRKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 67
67 AA; 7529 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.1%;
50.0%;
                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 50.0
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=41690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=6493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Venom;
                                       42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TER
                                                                                                                                          Q71KT0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONST
                                                                                                 RESULT 6
Q71KT0
                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
MEDLINE=95224066; PubMed=7708756; Daquinag A.C., Nakamura S., Takao T., Shimonishi Y., Tsukamoto T.; Daquinag A.C., Nakamura S., Takao T., Shimonishi Y., Tsukamoto T.; Prinary structure of a potent endogenous dopa-containing inhibitor of phenol oxidase from Musca domestica."; Proc. Natl. Acad. Sci. U.S.A. 92:2964-2968(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Muscoidea;
Muscidae; Musca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cysteine amide (G-72 provides amide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ffam; PF02550; Conforming of the PF02550; Conforming of the PF02550; Conforming of the PF02550; Conforming of the PF02500; Direct protein sequencing; Ionic channel inhibitor; Neurotoxin; Pressynaptic neurotoxin; Signal; Toxin. SIGNAL Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-UTL-2004 (Rel. 44, Last annotation update)
17rospiase inhibitor (Phenol oxidase inhibitor) (Phenoloxidase inhibitor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 6-9, CHARACTERIZATION, AND DEVELOPMENTAL STAGE.
TISSUE=Hemolymph;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 71; DB 1; Length 72;
Pred. No. 0.16;
4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   group).
1F753546AAD39908 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Omega-conotoxin SVIB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE, CHARACTERIZATION, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46 CKLKGOSCRKTSYDCCSGSCGRSGKC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; C44379; C44379.
PDB; 1MVJ; NMR; @=46-72.
InterPro; 1PR004214; Conotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF146346; AAD31906.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7741 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Musca domestica (House fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22
45
71
61
65
71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Hemolymph;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=7370;
```

MEDLINE=92231987; PubMed=1567460;

688 CSMGTDNVIRYHDDCCSRKSQCGNFNGKC 716

```
ñ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7
                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBUNIT: Monomer.
-!- SUBCELULIAR LOCATION: Secreted.
-!- DEVELOPMENTAL STAGE: POI activity increases throughout
pupariation, and is highest in final instar pupae. No activity in
newly emerged adults.
                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                 SYNTHESIS, AND DISULFIDE BONDS.
MEDLINE=99152007; PubMed=10026302; DOI=10.1021/bi9819834;
Daquinag A.C., Sato T., Koda H., Takao T., Fukuda M., Shimonishi Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- MASS SPECTROMETRY: MW-4213.1; MW_ERR=0.2; METHOD=Electrospray; RANGE=1-38; NOTE=Ref.1.
Direct protein sequencing; Hydroxylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dodson J.M., Clark C.G., Lockhart L.A., Leo B.M., Schroeder J.W.,
Mann B.J.;
                         Tsukamoto T., Ichimaru Y., Kanegae N., Watanabe K., Yamaura I.,
Katsura Y., Funatsu M.;
"Identification and isolation of endogenous insect phenoloxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Match 41.3%; Score 66.5; DB 2; Length 1125; Local Similarity 44.8%; Pred. No. 6.7; les 13; Conservative 4; Mismatches 9; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32 32 3',4'-dihydroxyphenylalanine.
38 AA; 4204 MW; E597BE0BFF286792 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 68; DB 1; Length 38;
Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1
1125 1125
1125 AA; 126050 MW; 8DA832DB48A717C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                 Biochem. Biophys. Res. Commun. 184:86-92(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1125 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gal/GalNAc lectin heavy subunit (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CRIXNQKCFQHLDDCCSRK--CNRFN-KC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 CLANGSKCYSH-DVCCTKRCHNYAKKCV 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CRIXNQKCFQHLDDCCSRKCNRF-NKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO, GO:0005529, F:sugar binding; IEA.
InterPro; IPR006209; EGF like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Entamoebidae; Entamoeba.
NCBI_TaxID=46681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR006209; EGF_like.
PROSITE; PS00022; EGF_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U85822; AAB50229.1; -.
HSSP; P60045; IMF4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1997 (TrEMBLrel. 01-JUL-1997 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1997 (TrEMBLrel. 01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=hgl2;
Entamoeba dispar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-SAW 760;
                                                                                                                                                                                                                                                                           reukamoto T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct proposed propo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOD RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P92135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
P92135
쉽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

```
J. Biol. Chem. 275:3535-35344(2000).
-!- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind and block voltage-sensitive calcium channels (VSCC) (By similarity). This toxin blocks N-, P-, and Q-type calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
Carlton J.W., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
Chan M.S., Nene V., Shallom S.J., Suh B., Pererson J., Angiuoli S.,
Pertea M., Allen J., Selengt J., Haft D., Mather M.W., Vaidya A.B.,
Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             Lewis R.J., Nielsen K.J., Craik D.J., Loughnan M.L., Adams D.A., Sharper.I.A., Luchian T., Adams D.J., Bond T., Thomas L., Jones A., Matheson J.-L., Drinkwater R., Andrews P.R., Alewood P.F.; Myeyel omega-conotoxins from Conus catus discriminate among neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; MS484; 1DW4.
Amidation; Calcium channel inhibitor; Direct protein sequencing;
Amidation; Calcium channel inhibitor; Neurotoxin; Presynaptic neurotoxin; Toxin.
DISULEID 1 16 By similarity.
DISULFID 8 20 By similarity.
DISULFID 15 26 By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLUTAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom duct.
-!- SIMILARITY: Belongs to the conotoxin O-superfamily. Omega-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                             Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                TISSUE=Venom;
MEDLINE=20519630; PubMed=10938268; DOI=10.1074/jbc.M002252200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium falciparum (1solate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 66; DB 1; Length 26; Pred. No. 0.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cysteine amide.
56EFC382335C4A8B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Hypothetical protein.
                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 2050 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CKGKGOSCSKLMYDCCTGSCSRRGKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8IKO3;
01-MAR-2003 (TrEMBLrel. 23, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 16
8 20
15 26
26 26
26 AA; 2790 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 41.0%;
Local Similarity 38.5%;
Les 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                calcium channel subtypes."
                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                         SEQUENCE, AND SYNTHESIS.
                                                                                                                                                                  Omega-conotoxin CVIC.
Conus catus (Cat cone)
                                                                                                                                                                                                                                                                                           NCBI_TaxID=101291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORFNames=PF10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            channels.
                                                CONCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
MOD RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8IK03
RESULT 10
CXOC_CONCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q81K03
```

ø

McFadden G.I.,

us-10-627-685a-26.rup

```
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phylogenet. Evol. 22:333-341(2002).

FUNCTION: Protamines substitute for histones in the chromatin of sperm during the haploid phase of spermatogenesis. They compact sperm DNA into a highly condensed, stable and inactive complex (By
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21881971; PubMed=11884158; DOI=10.1006/mpev.2001.1051;
Van Den Bussche R.A., Hoofer S.R., Hansen E.W.;
"Characterization and phylogenetic utility of the mammalian protamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR00021; Protamine Pl.
Pfam; PR00260; Protamine Pl; 1
PROSTIE; PS00048; PROTAMINE Pl; FALSE NEG.
Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein;
Nucleosome core; Spermatogenegis; Testis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Myotis daubentoni (Daubenton's bat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Chiroptera, Microchiroptera, Vespertilionidae,
                                                                                                                                                                                                                      4
 Cummings L.M., Subramanian G.M., Mungall C., Atucci D.J., Hoffman S.L., Newbold C., Davis
                                                                                                                                                                                 Score 63; DB 2; Length 2050;
Pred. No. 30;
                                                "Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                             2050 AA; 243182 MW; 0A0586A5B42A3B8C CRC64;
                                                                                                                                                                                                                    6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0 0 By similarity.
46 AA; 6397 MW; CDBDDD686E6A7BED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE SPECIFICITY: Testis, SIMILARITY: Belongs to the protamine P1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BIMILIARILY/.
SUBCELLULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                      25-OCT-2004 (Rel. 45, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                  46 AA.
                                                                                                                                                                                                                                                               40.0%; Pred. No.
                                                                                                                                                                                                                                            1 CRIXNOKCFOH---LDDCCSRKCNRFN-KC 26
                                                                          Nature 419:498-511(2002).
EMBL; AE014829; AAN35235.1; -.
HSSP; Q931C2; 1MMX.
HYpothetical protein.
SEQUENCE 2050 AA; 243182 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF435946; AAL35580.1; -.
                                                                                                                                                                                39.1%;
                                                                                                                                                           Ouery Match
Best Local Similarity 40.07
                                                                                                                                                                                                                                                                                                                                                           STANDARD;
             Venter J.C., Carucci
Fraser C.M., Barrell
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sperm protamine P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=98922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity)
                                                               falciparum.";
                                                                                                                                                                                                                                                                                                                                                           MYODA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=PRM1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene."
                                                                                                                                                                                                                                                                                                                                                         HSP1 MYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                        RESULT 12
HSP1 MYODA
요
                                                                                                                                                                                                                                            ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND SYNTHESIS.
MEDLINE=92337922; PubMed=1352986; DOI=10.1016/0896-6273(92)90221-X;
MEDLINE=92337922; PubMed=1352986; DOI=10.1016/0896-6273(92)90221-X;
Hillyard D.R., Monje V.D., Mintz I.M., Bean B.P., Nadasdi L.,
Ramachandran J., Miljanich G.P., Azimi-Zoonooz A., McIntosh J.M.,
Cruz L.J., Imperial J.S., Olivera B.M.;
"A new Conus peptide ligand for mammalian presynaptic Ca2+ channels.";
Neuron 9:69-77(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P/Q-type calcium channel.";
Biochem. Biophys. Res. Commun. 214:305-309(1995).
-!- FUNCTION! Omega-contoxins act at presynaptic membranes, they bind and block voltage-sensitive calcium channels (VSCC). This toxin blocks N-type calcium channels as well as types of high-threshold voltage-gated calcium channels resistant to both dihydropyridines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Structure-activity relationships of omega-conotoxins MVIIA, MVIIC and 14 loop splice hybrids at N and P/Q-type calcium channels."; J. Mol. Biol. 289:1405-1421(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nielsen K.J., Adams D., Thomas L., Bond T., Alewood P.F., Craik D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Solution structure of omega-conotoxin MVIIC, a high affinity ligand of P-type calcium channels, using 1H NMR spectroscopy and complete tralaxation matrix analysis.";
J. Mol. Biol. 248:106-124(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Tyri3 is essential for the binding of omega-conotoxin MVIIC to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, S40826; AAB22674.1; -.
PUB; JH0699; MR059; MR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and omega-conotoxin GVIA.
SUBCELLUIAR LOCATION: Secreted.
TISSUE SPECIFICITY: Expressed by the venom duct.
SIMILARITY: Belongs to the conotoxin O-superfamily. Omega-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MUTAGENESIS OF TYR-15.
MEDLINE=95408251; PubMed=7677735;
Kim J.I., Takahashi M., Martin-Moutot N., Seagar M.J., Ohtake A.,
                                                                                                                                                                                                                                                                                                                    Divervices, Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRUCTURE BY NMR.
MEDLINE=99303703; PubMed=10373375; DOI=10.1006/jmbi.1999.2817.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95248539, Pubmed=7731037,
Farr-Jones S., Miljanich G.P., Nadasdi L., Ramachandran J.,
                                                                                                                                   01-OCT-1994 (Rel. 30, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Omega-conotoxin MVIIc precursor (SNX-230) (Fragment).
                    29 AA.
               PRT;
                                                                                                     (Rel. 30, Created)
     STANDARD;
                                                                                                                                                                                                                                                                                      Conus magus (Magus cone)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRUCTURE BY NMR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI TaxID=6492;
                                                                                           01-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Basus V.J.;
CXOC CONMA
P37300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lewis R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       family.
                                             DTTT BEST SEED BY SEED
```

<u>.'</u>

Gaps

. 9

Indels

1 CRIXNOKCFOHLDDCCSRK-----CNRFNKC 26 

à 셤

Score 62; DB 1; Length 46; Pred. No. 1.4;

28.1%; Pred. No.

9; Conservative

Local Similarity

38.5%;

```
MEDLINE=20144115; PubMed=10677532; DOI=10.1073/pnas.040545897; Smith J.D., Graig A.G., Kriek N., Hudson-Taylor D., Kyes S., Fagen T., Pinches R., Baruch D.I., Newbold C.I., Miller L.H.; "Identification of a Plasmodium falciparum intercellular adhesion molecule-1 binding domain: a parasite adhesion trait implicated in
                             Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.3%; Score 60; DB 2; Length 1685; 33.3%; Pred. No. 60; cive 7; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1685 AA; 193671 MW; DIFD42666B0551E CRC64;
                                                                                                                                                                                                                                                                                                                                         Cerebral malaria...; Cerebral Marcad. Sci. U. S. A. 97:1766-1771 (2000). EMBL, AP193424. AAF18980.1; Cerebral C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |::::|| |: |:|: | 1048 CKTKDKKCTNKSDDCNTCTEACTAYNR 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CRIXNQKCFQHLDDC--CSRKCNRFNK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 33.3
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                              NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=PEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQÜENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q7 PM2 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
                                Omega-conotoxin MVIIc.
Essential for calcium channel binding.
                                                                                                                                                                                      Hydroxyproline (Probable).
Cysteine amide (G-29 provides amide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anopheles Genome Sequencing Consortium,
Submitted (ARR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is darvived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                 group).
Y->A: High decrease in binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.9%; Score 61; DB 2; Length 207; 46.4%; Pred. No. 7.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 61; DB 1; Length 29;
Pred. No. 1.2;
4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preliminary data.
L; AAAB01008897; EAA08999.2; -.
G0:0005576, C:extracellular; IEA.
G0:0008200; F:ion channel inhibitor activity; IEA.
G0:0009405; P:pathogenesis; IEA.
erPro; IPR004214; Conotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207 AA; 22432 MW; 2F4552091F91FBE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC7A68948474728A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O9U4A2;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Variant surface protein PfEMP1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1685 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CRIXNQKCFQHLDDCCSRKCNRFN-KCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 CAKNNEYCLTH-RDCCSGSCLSFSYKCV 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 CKGKGAPCRKTMYDCCSGSCGRRGKC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2004 (TrEMBLrel. 26, C. 01-MAR-2004 (TrEMBLrel. 26, L. 01-MAR-2004 (TrEMBLrel. 26, L. ENSANGPO0000015215 (Fragment) Name-ENSANGG0000012726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3071 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 38.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF02950; Conotoxin; 2.
NON TER 207 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=PEST
                                                                                        DISULFID
DISULFID
DISULFID
MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                           MUTAGEN
                                                                 BINDING
                                                                                                                                                                                                                                                                                                                   TURN
STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q7PQD5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9U4A2
                                                                                                                                                                                                                                                                                                                                                                                 HELIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
Q9U4A2
ID Q9U4A,
AC Q9U4A,
DT 01-MA,
DT 01-MA,
DE Varia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
07PQD5
DC 07PQDD
DC 01-MA
DT 
                                                                                                                                                                                                                                                                                                                                                                                                                 TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
```

1;

Gaps

2

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                              Anopheles gambiae etr. PEST.
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                Anopheles Genome Sequencing Consortium,
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 36.6%; Score 59; DB 2; Length 638; Local Similarity 36.0%; Pred. No. 34; les 9; Conservative 5; Mismatches 11; Indels ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  638 638
638 AA; 69390 MW; 026DB44846AB483F CRC64;
                                                                               Last sequence update)
Last annotation update)
638 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 RIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 RLSNHRCIPHCDDCDNGICTKPGYC 54
                                                      Created)
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary data.

EMBL, AARBO1008980; EAA14483.2; -.
HSSP; P19438; IEXT.
InterPro; IPR0063341; DUF139.
InterPro; IPR006209; EGF like.
Pfam; PP02363; C tripleX; 15.
Pfam; PP00008; EGF; 15.
                                             01-MAR-2004 (TrEMBLrel. 26, Cre
01-MAR-2004 (TrEMBLrel. 26, Las
01-MAR-2004 (TrEMBLrel. 26, Las
ENSANGPO0000014402 (Fragment)
Name-ENSANGG00000011913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS01186; EGF 2; 4.
```

```
à
                                                                                                                                                               g
                                              01-NOV-1996 (TrENBLrel. 01, Created)
01-NOV-1996 (TrENBLrel. 24, Last sequence update)
25-OCT-2004 (TrENBLrel. 28, Last annotation update)
Hypothetical protein F40E10.4.
Name=alt-1; ORFManes=F40E10.4;
Caenorhabditis elegans.
Bukaryota; Metazoa; Nematoda; Chromacorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                 "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                        Smye R.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; AL022270; CAB63434.2; --
EMBL; 269792; CAB63443.2; JOINED.
EMBL; AL022270; CAA93668.3; JOINED.
EMBL; ES9792; CAA93668.3; --
PIR; T22025; T22025;
                                                                                                                                                                                                                                                                                                            Smye R.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WormPep; F40EI0.4; CE32412.

GG GG:0005199; F:calcium ion binding; IEA.

GG; GG:0005199; F:calcium ion binding; IEA.

GG; GG:0005195; F:calcium ion binding; IEA.

GG; GG:0005195; F:calcium ion binding; IEA.

GG; GG:0005195; F:calcium ion binding; IEA.

InterPro; IPR00155; F:calcium ion binding; IEA.

InterPro; IPR006207; Gys Knot G.

InterPro; IPR006207; Gys Knot G.

InterPro; IPR00143; EGF Ca.

InterPro; IPR001438; EGF II.

InterPro; IPR001438; EGF II.

InterPro; IPR001519; Laminin G.
                              PRT; 1.410 AA
                                                                                                                                                                                          STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS00010; ASX HYDROXYL; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001611; IRR.
InterPro; IPR000483; IRR Cterm.
InterPro; IPR000372; ILRR Nterm.
InterPro; IPR003591; ILRR Lyp.
InterPro; IPR003129; TSP N.
Pfam; PF00008; EGF; 7.
Pfam; PF02210; Laminin G 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P00740; 1EDM.
WormBase; WBGene00004854; slt-1.
                                                                                                                                                                                                                                                investigating biology.";
Science 282:2012-2018(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR0010; EGFBLOOD.
SMART; PR00019; LEURICHRPT.
SMART; SM00041; CT; 1.
SMART; SM00179; EGF CA; 3.
SMART; SM00282; LAMĞ; 1.
                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYP; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01463; LRRCT; TPfam; PF01462; LRRNT; 4. Pfam; PF00560; LRR 1; 17.
                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                        NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; E
PROSITE; E
PROSITE; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                       020204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART;
SMART;
SMART;
RESULT 17
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESTOURNEE FROM N.A. (ISOFORM 1).

RESTRAIN=FVB/N; TISSUE=Salivary gland;

RESTRAIN=FVB/N; TISSUE=Salivary gland;

RASILINE=2238825; PubMed=12477922; DOI=10.1073/pnas.242603899;

RASILINE=2238825; PubMed=12477922; DOI=10.1073/pnas.242603899;

RASILINE=2238825; PubMed=12477922; DOI=10.1073/pnas.242603899;

RASILINE=2238825; PubMed=12477922; DOI=10.1073/pnas.242603899;

RASILINESPORTER L., Shenmen C.M., Schuler G.D.,

RASILINESPORTER R., Schaefer C.F., Bhat N.K.,

RASILINESPORTER R., Rather R., Rubin G.M., Hong L.,

RASILINESPORTER M.S., Rodin T.B., Tobahyuki S., Carninoi P., Prange C.,

RASILIAN M.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RASILIAN S.S., Workern R.J., Marek J.A., Gunaratne P.H.,

RASILIAN S.S., Workern R.J., Marek J.A., Gunaratne P.H.,

RASILIAN S.S., Workern R.J., Madan A., Gubbs R.A.,

RASILIAN M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RASILIAN M., Krzywinski M.I., Skalska U., Smailus D.E.,

RASILIAN S.C., Grimwood J., Schmutz J., Myers R.M.,

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RASILIAN SERVICESPORTER S.D., Sequences.";

RASILIAN SERVICESPORTER S.D., Marra M.A.;

RASILIAN S.D., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length human process.";

RASILIAN SERVICESPORTER S.D., Sequences.";

R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QBKIE3, QOQYP3, STANDARD, PKI; 382 AA. 25-007-2004 (Rel. 45, Leated) 25-007-2004 (Rel. 45, Last sequence update) 25-007-2004 (Rel. 45, Last annotation update) Multiple EGF-like-domain protein 9 precursor (Endothelial cell Name-EBfily,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fukudome K., Tsuneyoshi N., Kimoto M.;
"Endothelial cell specific protein S-1.";
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLUTAR LOCATION: Type I membrane protein (Potential).
                                                                                                                                                                       36.6%; Score 59; DB 2; Length 1410; 45.0%; Pred. No. 68; 7; Indels ive 4; Mismatches 7; Indels
PROSITE; PS50026; EGF_3; 7.
PROSITE; PS01187; EGF_CA; 2.
PROSITE; PS50025; LAM_G_DOMAIN; 1.
EGF-like domain; Hypothetical protein.
SEQUENCE 1410 AA; 158221 MW; D33716A9C98EBA9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISOId=08KlE3-2; Sequence=VSP_011768;
Note=No experimental confirmation available;
-!- SIMILARITY: Contains 6 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3vent=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   382 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 259-382 FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=Q8K1E3-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                     944 CEKNIDDCVNSKCENGGKCV 963
                                                                                                                                                                                                                                                                                 8 CFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                 Local Similarity 45.0
les 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFL9 MOUSE
                                                                                                                                                                    Query Match
                                                                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EFL9 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 18
```

```
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                             Name=1;
                                                                                                                                                                                                                                                                                                                                                                                                                               Name=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
  entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                   EGF-like 5, calcium-binding (Potential).
EGF-like 6, calcium-binding (Potential).
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                         SHAKKI; SM00179; EGF_CA; 2.
PROSITE; PS00010; ASX HYDROXYL; 2.
PROSITE; PS001010; ASX HYDROXYL; 2.
PROSITE; PS001186; EGF_2; 6.
PROSITE; PS00126; EGF_2; 6.
PROSITE; PS01187; EGF_CA; 2.
Alternative splicing; Calcium; Calcium-binding; EGF-like domain; Repear; Signal 1; Transmembrane...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEL9-HUMAN

BEL9-HUMAN

C GUVII: 098024.

TS-OCT-2004 (Rel. 45, Created)

DT 25-OCT-2004 (Rel. 45, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annocation update)

DF Multiple EGP-like-domain protein 9 precursor (UNQ2903/PRO28633).

GN Name=EGFL9;
                                                                                                                                                                                                                                                                                                                                                                                                                                      N-linked (GlcNAc. . .) (Potential). Missing (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                           Potential.
Multiple EGF-like-domain protein
Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 58; DB 1; Length 382;
Pred. No. 28;
2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                F2C82AD649CA0B3C CRC64;
                                                                                                                                                                                                                         Cytoplasmic (Potential)
EGF-like 1.
                                                                                                                                                                                                                                                                                                                                                                                                                               similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /FTIG=VSP
                                                                                                                                                                                                                      Potential
                        EMBL; BC019431; AAH19431.1; -..
EMBL; AB011019; BAA88686.1; ALT_INIT.
HSSP; P00750; 1TPG.
                                                          InterPro; IPR000152; Aax hydroxyl_S.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001438; EGF_II.
InterPro; IPR006209; EGF_II.
Pf00008; EGF; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              209 CTINLDDCASRPCQRGARC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 CFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 382 AA; 40404 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 52.6'
Matches 10; Conservative
                                         HSSP, P00750, 1TPG.
MGD; MGI:2146838; Egfl9.
                                                                                                                                                                                                                                                                                        DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                    CHAIN
 8
```

```
Observed the mean papers (Human).

Disharyor, Metazan, Chordata, Craniata, Vertebrata, Euceleostomi, Occ. Manamila, Shirthia; Primates, Charathini, Honinidae, Homo.

Manamila, Charage A.L., Abaya E., Baker K., Baldahin D., Bace J.,

Manamila, Charage A.L., Abaya E., Baker K., Baldahin D., Bace J.,

Manamila, Manamila, Charage A.L., Abaya E., Baker K., Baldahin D., Bace J.,

Manamila, Manamila, Charage A.L., Abaya E., Baker K., Baldahin D., Bace J.,

Manamila, Manamila, Charage A.C., Carada, C., Carada B., Dood P.,

Manamila, Manamila, Charage A.C., Manamila, C., Goldon, Hass B.E., Relates S.,

Manamila, Manamila, C., Mishand D., Roods K., Xish M.-H., Yangura D.,

Mila, M., Yann, J., Chang M., Zhang Z., Goddard A., Wood W.I.,

Manamila, M., Manamila, M., Manamila, C., Mishand D., Roods W., Xish M.-H., Yangura B.,

Mila, M., Manamila, M., Manam
```

```
RESULT 21
SCX2_OPICA
ID SCX2_OPICA
AC P60253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                              EGF-like 2.
EGF-like 3.
EGF-like 3.
EGF-like 3.
EGF-like 5. calcium-binding (Potential).
EGF-like 6. calcium-binding (Potential).
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCXI OPICA
AC PG0252;
D SCXI OPICA
AC P60252;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 29-MAR-2004 (Rel. 45, Last annotation update)
DT 29-MAR-2004 (Rel. 45, Last annotation update)
DT 29-MAR-2004 (Rel. 45, Last annotation update)
DT 29-MAR-2004 (Rel. 43, Cast annotation update)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 29-MAR-2004 (Rel. 43, Last s
InterPro; IPR006210; IEGF.

Pfam; PF00008; EGF; S.

PRINTS; PR00101; EGF; G.

SMART; SM0010; EGF; G.

SMART; SM00109; EGF CA; 4.

PROSITE; PS00002; EGF CA; 4.

PROSITE; PS00002; EGF T; G.

PROSITE; PS00002; EGF T; G.

PROSITE; PS01016; EGF T; G.

PROSITE; PS01016; EGF T; G.

PROSITE; PS01187; EGF CA; C.

PROSITE; PS01187; EGF CA; C.
                                                                                                                                                                                                                                                                                         Potential.
Multiple EGF-like-domain protein
Extracellular (Potential),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUBNCE FROM N.A.
TISSUB-Venom gland; '
MEDLINE=22838230; PubMed=12958203; DOI=10.1096/fj.02-1044fje;
Zhu S.-Y., Darbon H., Dyason K., Verdonck F., Tytgat J.;
"Evolutionary origin of inhibitor cystine knot peptides.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    701AC6B043863EA7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                            Cytoplasmic (Potential)
EGF-like 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36.0%; Score 58; DB
52.6%; Pred. No. 28;
tive 2; Mismatiches
                                                                                                                                                                                                                                                                                                                                                              Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            209 CTINLDDCASRPCQRGARC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 CFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                     Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       383 AA; 40547 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 52.6
nes 10; Conservative
                                                                                                                                                                                                                                                                   Repeat; Signal;
SIGNAL
                                                                                                                                                                                                                                                                                                                              DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
      셤
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its web by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ï
FASEB J. 17:1765-1767(2003).
-1- FUNCTION: Potently and reversibly modifies channel gating behavior of the type 1 ryanodine receptor (RyR1) by inducing prominent subconductance behavior. Binds a different site as ryanodine (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Venom gland;

TISSUE-Venom gland;

MEDLINE-22893203; PubMed=12958203; DOI=10.1096/fj.02-1044fje;

MEDLINE-22893203; PubMed=12958203; DOI=10.1096/fj.02-1044fje;

Zhu S.-Y., Darbon H., Dyason K., Verdonck F., Tyrgat J.;

"EVOILTION: POTEDIN of inhibitor cystine knot peptides.";

FASEB J. 17:1765-1767(2003).

-!- FUNCTION: Potently and reversibly modifies channel gating behavior of the type I ryanodine receptor (RyR1) by inducing prominent subconductance behavior. Binds a different site as ryanodine (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
05-oct-2014 (Rel. 45, Last annotation update)
Opicalcine 2 precursor.
Opisalcine 2 precursor.
Opisalcine 3 precupitus (African yellow leg scorpion)
Eukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Scorpiones, Iurida, Scorpionidea, Scorpionidae, Scorpionidae, Opistophthalmus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AY225784; AAP7322.1; -.
Calcium channel inhibitor; Cleavage on pair of basic residues;
Ionic channel inhibitor; Neurotoxin; Signal; Toxin.
SIGNAL
1 22 PROPEP 23 33 By similarity.
CHAIN 34 66 Opicalcine 1.
DISULED 36 50 By similarity.
DISULED 43 54 By similarity.
DISULED 49 65 By similarity.

**ANTENTIAL STATE OF STATE O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity).
--- SUBCELLULAR LOCATION: Secreted.
--- TISSUE SPECIFFICITY: Expressed by the venom gland.
--- SIMILARITY: Belongs to the scorpion calcine family.
--- Calcium channel inhibitor; Cleavage on pair of basic residues;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                       similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom gland.
-!- SIMILARITY: Belongs to the scorpion calcine family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6DC7632E9F205F5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | Control of the cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 57; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 CFQHL-----DDCCSRKCNR 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 CLPHLKRCKENNDCCSKKCKR 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 47.6
les 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=190115;
```

```
Bukaryota, hetazoa; Chordata, craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae, Danio.
NCBI_TaxID=7955;
                                                                                                     SEQUENCE FROM N.A.
Westin J., Lardelli M.;
Whree novel Notch genes in zebrafish: implications for vertebrate
Notch gene evolution and function.";
Dev. Genes Evol. 207:51-63(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordara; Craniara; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
35.4%; Score 57; DB 2; Length 752;
Best Local Similarity 37.5%; Pred. No. 68;
Matches 9; Conservative 2; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cobbe N.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ534332; CAD58847.2; -.
HSSP; Q9XOR4; 1E69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fugu rubripes (Japanese pufferfish) (Takifugu rubripes)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82103 MW; 30939E16E0327F8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q802S2;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                         GO; GO: 00160020; C: Grambrane; IEA.
GO; GO: 0016020; C: Grambrane; IEA.
GO; GO: 0005509; F: Galcium ion binding; IEA.
GO; GO: 0004612; F: receptor activity; IEA.
GO; GO: 00030154; F: receptor activity; IEA.
GO; GO: 00030154; F: receptor activity; IEA.
InterPro; IPR00152; Asx hydroxyl_S.
InterPro; IPR00181; EGF_2.
InterPro; IPR00181; EGF_II.
InterPro; IPR006209; EGF_II.
InterPro; IPR006000; Notch_region.
Pfam; PF00608; EGF_CA; I.
Pfam; PF00606; Notch; 2.
PRINTS; PR00100; EGFBLOOD.
PRINTS; PR00109; EGF_CA; I.
SMART; SM00109; EGF_CA; I.
SMART; SM00109; EGF_CA; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1245 AA
   Brachydanio rerio (Zebrafish) (Danio rerio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 SGDNCQTHIDDCSSNPCRNGGTCV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 XNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00010; ASX HYDROXYL, 9. PROSITE; PS000022; EGF 1; 17. PROSITE; PS01186; EGF 2; 15. PROSITE; PS50026; EGF 3; 17.
                                                                                                                                                                                                                              ZFIN; ZDB-GENE-000329-4; notch2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0016020; C:membrane; IEA. GO; GO:0005634; C:nucleus; IEA.
                                                                                                                                                                                           EMBL; Y10354; CAA71380.1; -. HSSP; P00740; IEDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS01187; EGF_CA; 7
EGF-like domain; Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        752 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMC1 beta protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=smclb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      080252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 24
Q802S2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                           Name=ebiG2886; ORFNames=ENSANGG0000002379;
Anopheles gambiae str. PEST.
Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterrygota; Diptera; Nematocera; Culicoidea; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.4%; Score 57; DB 2; Length 650; 33.3%; Pred. No. 60;
Query Match " 35.4%; Score 57; DB 1; Length 66; Best Local Similarity 47.6%; Pred. No: 8;
                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71172 MW; 19C43512C5B5FCC8 CRC64;
                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05, Last sequence update)
26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO: GO:0016020; C:membrane; IEA.
GO: GO:0016020; C:membrane; IEA.
GO: GO:0007150; F:calcium ion binding; IEA.
GO: GO:0007154; P:cell communication; IEA.
InterPro; IPR001774; DSL.
InterPro; IPR001774; DSL.
InterPro; IPR001431; EGF_Ca.
InterPro; IPR001431; EGF_Ca.
InterPro; IPR001431; EGF_II.
FEAM: PF00414; DSL; 1.
PFGm; PF000008; EGF; 7.
                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 XNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     042374;
01-3AN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preliminary data.
EMBL; AAAB01008980; EAA14361.1; -.
                                                                                         36 CLPHLKRCKENNDCCSKKCKR 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00010; ASX HYDROXYL; 3.
PROSITE; PS00022; EGF_1; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Notch receptor protein (Fragment). Name=notch2; Synonyms=Notch6;
                                                                     8 CFQHL-----DDCCSRKCNR 22
                                                                                                                                                                                                                        01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PSO1186; EGF 1; 9.
PROSITE; PSS01186; EGF 2; 9.
PROSITE; PSS01187; EGF 3; 7.
PROSITE; PS01187; EGF CA; 2.
EGF Like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF07645; EGF CA; 1.
PRINTS; PR00010; EGFBLOOD
                                  10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Conservative
                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      650 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                          Q7Q0M5;
01-MAR-2004 (
01-MAR-2004 (
                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=PEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                         Q7Q0M5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      042374
                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 23
042374
                                                                                                                                                          RESULT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Separa
```

**Gaps** 

SORREDER

ò 셤

```
PRINTS; PRO1415; ANKTRIN.

RR PRINTS; PRO1415; ANKTRIN.

RR PRINTS; PRO1415; ANKTRIN.

RR PRINTS; PRO1425; NOTCH.

SWART; SW00248; ANK; G.

SWART; SW00179; EGF CA; 24.

SWART; SW00179; EGF CA; 24.

RR SWART; SW00179; EGF CA; 24.

RR PROSITE; PS00088; ANK REPER REGION; 1.

RR PROSITE; PS00010; ASX_HYDROXYL; 23.

RR PROSITE; PS001186; EGF 3; 34.

RR PROSITE; PS01187; EGF CA; 21.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  calcium-binding (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neurogenic locus notch protein homolog.
Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       calcium-binding (calcium-binding (calcium-binding (calcium-binding (calcium-binding) (calcium-binding)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           calcium-binding (calcium-binding (calcium-binding (calcium-binding (calcium-binding (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     calcium-binding (calcium-binding (calcium-binding (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 calcium-binding calcium-binding calcium-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  calcium-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              calcium-binding
calcium-binding
calcium-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytoplasmic (Potential).
EGF-like 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGF-like 28, EGF-like 29, EGF-like 31, C EGF-like 31, C EGF-like 31, C EGF-like 33, EGF-like 35, EGF-like 35, EGF-like 35, EGF-like 35, EGF-like 36, EGF-like 37, ANK 2, ANK 6, ANK 6, ANK 6, EGF-like 36, EGF-like 38, EGF-like 37, ANK 6, EGF-like 38, EGF-like 31, EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGF-like 2.
EGF-like 3.
EGF-like 4.
EGF-like 5.
EGF-like 6.
EGF-like 9.
EGF-like 9.
EGF-like 10.
EGF-like 11.
EGF-like 11.
EGF-like 12.
EGF-like 13.
EGF-like 14.
EGF-like 14.
EGF-like 14.
EGF-like 14.
EGF-like 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGF-like 18, c EGF-like 19, c EGF-like 21, c EGF-like 22, c EGF-like 22, c EGF-like 24, c EGF-like 25, c EGF-like 25, c
                       Pfam; PF00008; EGF; 36.
Pfam; PF06816; NOD; 1.
Pfam; PF00066; Notch; 3.
PIRSF; PIRSF002279; Notch; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2524
1728
1750
2524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 942
980
1018
1056
1094
1142
11180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1264
1304
1346
1383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1144
1182
1220
1266
1306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
DOMAIN
BOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial or send an email to license@isenent (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kintner C., Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

-- Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

-- In SUBLIARITY BUTCH (STATE): Expressed almost uniformly in early embryos.

-- SIMILARITY: Belongs to the NOTCH family.

-- SIMILARITY: Contains 6 ANK repeats.

-- SIMILARITY: Contains 3 EGF-like comains.

-- SIMILARITY: Contains 3 Lin/Notch repeats.
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0042626; F:ATPase activity, ccupled to transmembrane m. ..;
GO; GO:0042626; F:Chromosome segregation; IEA.

R GO; GO:0006810; P:transport; IEA.

R InterPro; IPR003439; ABC_transporter.

R InterPro; IPR003405; SMC_C.

R InterPro; IPR003405; SMC_C.

R InterPro; IPR003405; SMC_N.

R Pfam; PF06440; SMC_Minge; 1.

R Pfam; PF06470; SMC_Minge; 1.

R Pfam; PF06470; SMC_Ninge; 1.

R Pfam; PF06470; SMC_Ninge; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa; Chordata; Craniata; Vertebrata, Euteleostomi,
Amphibia; Batrachia, Anura, Mesobatrachia, Pipoidea; Pipidae;
Xenopodinae; Xenopus.
NCBI_TaxID=8155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MXY-1991 (Rel. 18, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Newrogenic locus notch protein homolog precursor (XOTCH protein)
Name=XOTCH;
                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                          35.4%; Score 57; DB 2; Length 1245; 42.9%; Pred. No. 1.1e+02; 1ve 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE=90385285; PubMed=2402639;

Coffman C., Harris W., Kintner C.;

"Xocch, the Xenopus homolog of Drosophila notch.";

Science 249:1438-1441(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 2524 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002110; ANK.
InterPro; IPR00152; Ask hydroxyl_S.
InterPro; IPR001742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001488; EGF_II.
InterPro; IPR006209; EGF_II.e.
InterPro; IPR006609; NOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1056 RKCSQEFEQVKFQRCQRFNKC 1076
                                                                                                                                                                                                                                                                                                                                                                                                                         6 OKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR008297; Notch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M33874; AAB02039.1; -.
HSSP; P46531; 1PB5.
                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 42.9#
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REVISIONS TO 1759-1782.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000800; N
Pfam; PF00023; Ank; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 25
NOTC_XENLA
ID NOTC_XENLA
AC P21783;
```

(Potential).
(Potential).
(Potential).
(Potential).
(Potential).

(Potential)

(Potential)

(Potential)

(Potential)

(Potential)

(Potential)

(Potential)

(Potential). (Potential). (Potential).

```
similarity.
similarity.
similarity.
similarity.
similarity.
                  similarity,
similarity,
similarity,
similarity,
similarity,
similarity,
similarity,
                                                                   similarity.
similarity.
similarity.
                                                                                                                                                                                             similarity.
similarity.
                                                                                                        similarity.
similarity.
similarity.
similarity.
                                                                                                                                         similarity.
similarity.
                                                                                                                                                    similarity.
similarity.
                                                                                                                                                            similarity.
similarity.
                                                                                                                                                                   similaritý.
similarity.
                                                                                                                                                                           similarity.
similarity.
                                                                                                                                                                                  similarity.
similarity.
                                                        similarity.
similarity.
            similarity
similarity
                                                    similarity
                                                               similarity
                                                                                                                       similarity
                                                                                                                          similarity.
Similarity.
                                                                                                                                  similarity.
similarity.
                                                                                                                                                                                                            similarity.
Similarity.
                                                                                                                                                                                                                           similarity.
Similarity.
                                                                                                                                                                                                                                      similarity
Similarity
                                                                                                                                                                                                                                             similarity
                                                                                                                                                 similarity
                                                                                                                                                                                          similarity
                                                                                                                                                                                                     Bimilarity
                                                                                                                                                                                                         similarity
                                                                                                                                                                                                                    similarity
                                                                                                                                                                                                                       Bimilarity
                                                                                                                                                                                                                                                  similarity
                                                                                                                                                                                                                                                                       similarity
                                                                                                                                                                                                                                                                           similarity
 941
997
1006
1017
1035
DISULPID
                                                                                                                                                                                                                              DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
                                                                                                   DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                               DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                   DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                           DISULFID
DISULFID
DISULFID
                                                                                                                                                                                     DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                    DISULFID
DISULFID
DISULFID
                                                                                                                                                    DISULFID
                                                                                                                                                            DISULFID
DISULFID
                                                                                                                                                                   DISULFID
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                               Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The genome sequence of Clostridium tetani, the causative agent of tetanus disease.";
Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).
EMBL; AE015944; AA036841.1; -.
Complete protecome.
SEQUENCE 153 AA; 17382 MW; 6334C88F39A8E189 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=Massachusetts / E88;
STRAIN=Massachusetts / E88;
MEDLINE=22457253; PubMed=12552129; DOI=10.1073/pnas.0335853100;
Brueggemann H., Baeumer S., Fricke W.F., Wiezer A., Liesegang H.,
Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,
Gottschalk G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clostridium tetani.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
NCBI_TaxID=1513;
                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Length 153;
                                                                                                                                                 Score 57; DB 1; Length 2524;
Pred. No. 2e+02;
4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PERUNCE FROM N.A.
STRAIN=HM1:IMSS;
STRAIN=HM1:IMSS;
STRAIN=HM1:IMSS;
Samakrishan G., Furdy J.E., Mann B.J.;
Submitted (40C-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U33443; AAA75551.1; -.
EMBL; U33443; AAA75551.1; -.
GO; GO:0005259; F:sugar binding; IEA.
InterPro; IPR006209; EGF_like.
PROSITE; PS00022; EGF_Like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Membrane-associated protein.
OrderedLocusNames=CTC02367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B
                          similarity.
similarity.
similarity.
similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 35.1%; Score 56.5; 1
Best Local Similarity 38.5%; Pred. No. 19;
Matches 10; Conservative 3; Mismatches
  similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CSGKDDKCHHHDNCCHHHGGCNNF 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CRIXNOKCFQHLDDCCSRK---CNRF 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Fragment)
                                                                                                                                                                                                                                                                                                249 SGONCEENIDDCPSNNCRNGGTCV 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last seq.
01-MAR-2004 (TrEMBLrel. 26, Last anno
GalNAc lectin heavy subunit (Fragment Name-h914;
Entamoeba histolytica.
Eukaryota; Entamoebidae; Entamoeba.
                                                                                                                                                                                                                                                             4 XNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
     7 Match 35.4%;
Local Similarity 37.5%;
les 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
  1055
1073
1082
1083
1121
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                               Q891K4
Q891K4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              024821
                                                                                                                                                                                       Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 27
Q24821
                                                                                                                                                                                                                                                                                                                                                                                              56
                                                                                                                                                                                                                                                                                                                                                                                         RESULT :
Q891K4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DACO
DOTT
DOTT
DOTT
SERVINE SE
  FI
                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
```

DB 2; Length 372;

```
1 1
372 372
372 AA; 41994 MW; 3812E4DC7B310B13 CRC64;
                         NON TER
NON TER
SEQUENCE
                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       024835
                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDR RET RESERVED BY SECTION OF SE
                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Entamoeba histolytica: sequence conservation of the Gal/GalNAc lectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINES-22314996; PubMed=12427470; DOI=10.1016/S0014-4894(02)00113-3;
Beck D.L., Tanyuksel M., Mackey A.J., Haque R., Trapaidze N.,
Pearson W.R., Loftus B., Petri W.A. Jr.;
"Entanoba histolytics: sequence conservation of the Gal/GalNAc lectin
from clinical isolates.";
Exp. Parasicol. 101:157-163(2002).
Exp. Parasicol. 101:157-163(2002).
EMBL, AFS01276; RAM22197.1;
-.
GO; GO:005529; F:sugar binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=22314996; PubMed=12427470; DOI=10.1016/S0014-4884(02)00113-3;
Beck D.L., Tanyuksel M., Mackey A.J., Haque R., Trapaidze N.,
Pearson W.R., Loftus B., Petri W.A. Jr.;
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                      3;
                                                                                                                                                                                                                 DB 2; Length 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 372;
                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Indels
                                                                            194 194
194 AA, 21501 MW; BD0C3HD9406AAB58 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      372 372
372 AA; 41984 MW; 5BE2A013D596D124 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Gal/GalNAc lectin heavy subunit region D (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Gal/GalNAc lectin heavy subunit region D (Fragment)
                                                                                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                                                                                                                                                                                                                     372 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 56.5; DE; Pred. No. 42; 3; Mismatches
                                                                                                                                                                                           Query Match 35.1%; Score 56.5; Dest Local Similarity 43.3%; Pred. No. 24; Matches 13; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                              1 CRIXNOKCFOHLDDCCSRK--CNRFN-KCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 CSMGTDNIITYHDDCNSRKSQCGNFNGKCV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CRIXNOKCFQHLDDCCSRK--CNRFN-KCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from clinical isolates.";
Exp. Parasitol. 101:157-163(2002).
EMBL; AF533541; AAM97358.1; -.
GO; GO:0005529; F:sugar binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Entamoebidae, Entamoeba.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Entamocba histolytica.
Eukaryota, Entamocbidae; Entamocba.
NCBI_TaxID=5759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 43.34
Best Local 3 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Entamoeba histolytica
Lectin.
NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8MUB9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8MU89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8MZT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 28
Q8MU89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 29
10 80 MZT3
AC Q8MZT3
AC Q8MZT
DT 01-0C
S FT SO
                                                                                                                                                                                                                                                                                                                                                                                                                                               යු
                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A PAC 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
```

```
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=HM-1:IMSS;
MEDLINE=91195330; PubMed=2014248;
Mann B.J., Torian B.E., Vedvick T.S., Petri W.A.Jr. .;
"Sequence of a cysteine-rich galactose-specific lectin of Entamoeba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-HM-1:IMSS;
MEDLINE=94158976; PubMed=8114826; DOI=10.1016/0166-6851(93)90177-Y;
Purdy J.E., Mann BJ., Shugart B.C., Petri W.A.;
"Analysis of the gene family encoding the Entamoeba histolytica
galactose-specific adhesin 170-kDa subunit.";
Mol. Blochem. Parasitol. 62:53-59(1993).
                                                          3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1292;
                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 Potential.
145176 MW; E3123F4C7B6FDB98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=HM-1:IMSS;
Purdy J.E., Mann B.J., Petri W.A.Jr.;
Submitted (OCT-1993) to the EMBL/GenBank/DDBJ databases.
EMBL; L14815; AAA18828.1; -.
                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Galactose-specific adhesin 170kD subunit precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             081218 PRELIMINARY; PRT; 3467 AA.
081218;
01-MAR-2003 (TrEWBLrel. 23, Created)
01-MAR-2004 (TrEWBLrel. 23, Last sequence update)
01-MAR-2004 (TrEWBLrel. 26, Last annotation update)
Erythrocyte membrane protein 1 (PfEMP1).
Name=VAR; Synonyms=PFD0020c;
                                                       11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          histolytica.";
Proc. Natl. Acad. Sci. U.S.A. 88:3248-3252(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 35.1%; Score 56.5; DB 2; Similarity 43.3%; Pred. No. 1.3e+02; 13; Conservative 3; Mismatches 11;
                                                                                                                           / Match 35.1%; Score 56.5; D Local Similarity 43.3%; Pred. No. 42; nes 13; Conservative 3; Mismatches
                                                                                                                                                                                                                                                             PRT; 1292 AA
                                                                                           1 CRIXNOKCFOHLDDCCSRK--CNRFN-KCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 CSMGTDNIITYHDDCNSRKSQCGNFNGKCV 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CRIXNOKCFQHLDDCCSRK--CNRFN-KCV 27
                                                                                                                                                                                                                                                                                                                                                                                              Name-hgl3;
Bratamoeba histolytica.
Eukaryota; Entamoebidae; Entamoeba.
NCBI_TaxID=5759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR006209; EGF like.
PROSITE; PS00022; EGF_1; UNKNOWN_1.
                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A31435; A31435.
PIR; T09229; T09229.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 1292 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 31
Q81218
ID Q8121
AC Q8121
AC Q8121
DT 01-MA
DT 01-MA
DE EFYTH
GN NAME=
```

```
InterPro; IPR001841; Znf_ring
    Pfam; PF01414; DSL; 1.
                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gramene;
                                                                                                                                                                                                                                                                                                                                          O9LGMB
                                                                                                                                                                                                    Best Loca
Matches
                                                                                                                                                                                                                                                                                                              RESULT 33
Q9LGM8
    ò
                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                       ~
                                                 MEDLINE-22255708; PubMed=12368867; DOI=10.1038/nature01095;
MEDLINE-22255708; PubMed=12368867; DOI=10.1038/nature01095;
MIDGALL N. Beriman M., Churcher C., Harris B., Hall N., Pain A., Beriman M., Churcher C., Harris B., Brooks K., Mungall K., Bowman S., Aktin R., Baker S., Barron A., Brooks K., Buckee C.O., Burrows C., Cherevach I., Chillingworth C., Corton C., Croin A., Davis R., Davis P., Dearden F., Corton C., Reltwell T., Goble A., Goodhead I., Gwilliam R., Hamilin N., Hance Z., Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P., Hamper D., Hanser H., Hornsby T., Holroyd S., Morrocks P., Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A., Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lawmard N., Line A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L., Oliver K., Ormond D., Perice C., Quall M.A., Rabbinowitsch B., Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M., Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K., Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J., Stevens K., Sulston J.E., Craig A., Newbold C., Barrell B.G;
Wature 499:527-531(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20054100; PubMed=10585570; DOI=10.1016/S0925-4773(99)00231-2; Smithors L.E., Haddon C., Jiang Y.-J., Lewis J.; Squence and embryonic expression of deltaC in the zebrafish."; Mech. Dev. 90:119-123(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brachydanio rezio (Zebrafish) (Danio rezio).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii; Teleostei; Ostariophysi, Cypriniformes,
Cyprinidae, Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.1%; Score 56.5; DB 2; Length 3467; 31.9%; Pred. No. 3e+02; ive 3; Mismatches 8; Indels 21;
Plasmodium,falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        318 CRIRNHKLRKIKDACRNDKERLYCSONGYDCTKRIEKGSSCSRENKC 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRIXNOK-----KCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF03011; PFEMP; 2.
PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
SEQUENCE 3467 AA; 398216 WW; E8FCBA37025989D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                         EMBL; AL034557; CAD49096.1; -.
GO; GO:0005539; F:glycosaminoglycan binding; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR00345; CytC, heme_BS.
InterPro; IPR004258; PEEMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               664 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mech. Dev. 90:119-123(2000).

EMBL; AF146429; AAF27299.1; -.
HSSP; P00740; 1EDM.
ZFIN; ZDB-GENE-000125-4; dlc.
GO; GO:001620; C:membrane; IEA,
GO; GO:0005509;-F:calcium ion binding; IEA,
GO; GO:00071254; P:cell communication; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000152; Aax hydroxyl_S.
InterPro; IPR001774; DSL.
InterPro; IPR00742; EGF 2.
InterPro; IPR001881; EGF II.
InterPro; IPR001881; EGF II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 31.9
Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=dlc; Synonyms=delC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 32
Q91AT6
 ઠે
```

```
Problecal FROM N.A.

PubMed=1244438; DOI=10.1038/nature01184;

PubMed=12444438; DOI=10.1038/nature01184;

A Sasaki T., Matsumcto T., Yamamoto K., Sakata K., Baba T., Katayose Y., Rasaki T., Matsumcoto T., Yamamoto K., Antonio B.A., Kanamori H., An Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M., Ando T., Aoki H., Arita K., Hamada M., Harada C., Reno M., Itoh S., Honda M., Ichikawa Y., Idonuma A., Ilijima M., Ikeda M., Rasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I., Ramiya K., Maranara T., Mizuno H., Mizubayashi N., Mukai Y., Nakahima M., Nakashima M., Nakama Y., Nakamichi Y., Nakahima M., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M., Sang J., Takazaki Y., Terasawa K., Tsuji K., Amiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai, K, Shibata M., Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K., Waki K., Yamagata H., Yamaga H., Yoshiki S., Yoshihara R., Yukawa K., Yano M., Jiang J., Golobori T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0000151; C:ubiquitin ligase complex; IEA.
GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
GO; GO:0006355; P:regulation of transcription, IRA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000567; Znf. NFX1.
InterPro; IPR001965; Znf. NFX1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OJ-OGT-2000 (TrEMBLrel. 15, Created)
OJ-OGT-2001 (TrEMBLrel. 17, Last sequence update)
25-OGT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to Arabidopsis thaliana chromosome V P1 MJJ3 (Similar to Arabidopsis thaliana chromosome V P1 MJJ3.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7
                                                                                                                                                                                                                                                                                                                                                                                                     34.8%; Score 56; DB 2; Length 664; 34.5%; Pred. No. 81; ive 4; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The genome sequence and structure of rice chromosome 1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sasaki T., Matsumoto T., Yamamoto K.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; APO02521; BAA85756.2; -.
EMBL; APO02539; BAB08195.2; -.
                                                                                                                                                                                                                                                                                                                         664 AA; 72547 MW; 0AD6C34C8579116B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      708 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CR--IXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                              ď.
                              SWART; SM00051; DSL; 1.

SWART; SM00179; EGF CA; 4.

PROSITE; PS00010; ASX HYDROXYI

PROSITE; PS00022; EGF 1; 8.

PROSITE; PS01186; EGF 2; 8.

PROSITE; PS01187; EGF CA; 2.

EGF-11xe domain.

SEQUENCE 664 AA; 72547 MW;
PRINTS; PRO0010; EGFBLOOD
                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 34.5 tes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 420:312-316(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=39947;
```

```
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGENTALIANEER STATE OF THE R. S. TOTAL SCIENCE 287.5461.2185;

AGENTALIANEER S. S. Holt R. N. Evans C. A. Gocayne J. D.,

AGENTAL Scherer S. L. Li P. W. Hoskins R. A. Galle R. F.,

Annantides P. G., Scherer S. E., Li P. W. Hoskins R. A., Galle R. F.,

B. Annantides P. G., Scherer S. E., Li P. W. Hoskins R. A., Galle R. F.,

B. George R. A. Lewis S. E., Richards S., Ashburner M., Henderson S. N.,

B. Erandon R. C., Rogers Y. H. C., Blazej R. G., Champe M., Pfeiffer B. D.,

R. Abril J. F., Agbayani A., An H. J., Andrews-Ffannkoch C., Baldwin D.,

R. Ballew R. M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E. M.,

R. Ballew R. M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E. M.,

R. Ballew R. M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E. M.,

R. Borkova D., Botcham M.R., Bouck J., Brokstein P., Brottier P.,

R. Burtis K. C., Busam D. A., Butler H., Cadiou E., Center A., Chandra I.,

R. Ablos B., Delcham M.R., Deng Z., Mays A.D., Dew I. District S., Pleischmann W.,

R. Dodson K., Doup L. E., Downes M., Dugan-Rocha S., Dunkov B. C., Dunn P.,

R. Abrill M., Sanielian A.E., Garg N.S., Gelbart W. M., Glasser K.,

R. Aleris N. C., Harrey, D. A., Heiman T. J., Hernandez J. R., Houck J.,

R. Alali M., Kalush F., Karpen G. H., Ke Z., Kennison J. A., Ketchum K. A.,

Lasko P., Lei Y., Levitsky A.A., Li J. H., Li Z., Liang Y., Lin X.,
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=Canton-S, and Oregon-R; TISSUE=Embryo;
MEDLINEE=8704664; PubMed=3097517;
Kidd S., Kelley M.K., Young M.W.;
Kidd S., Kelley m.K., Young M.W.;
Sequence of the notch locus of Drosophila melanogaster: relationship of the encoded protein to mammalian clotting and growth factors.";
Mol. Cell. Biol. 6:3094-3108(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAINS-CREADORARY TISSUB-Embryo;
STRAINS-CREADORARY TISSUB-Embryo;
MEDLINE-86079539; PubMed=3935325; DOI=10.1016/0092-8674(85)90229-6;
Wharton K.A., Johansen K.M., Xu T., Arravanis-Tsakonas S.;
"Nucleotide sequence from the neurogenic locus norch implies a gene product that shares homology with proteins containing EGF-like
                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTC DROWE STANDARD; PRT; 2703 AA.
P07207; 097458; P04154; 09W4T8;
P07207; 097458; P04154; 09W4T8;
O1-NOV-1986 (Rel. 03, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Neurogenic locus Notch protein precursor.
Name-N; ORFNames-GC3396;
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Endoptery; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                  34.8%; Score 56; DB 2; Length 708; 40.0%; Pred. No. 86;
                                                                                                                                                                                                                                                                                                                                                              10; Indels
Pfam; PF01422; zf-NF-X1; 5.

SWART; SW00438; ZnF NFX; 7.

PROSITE; PS00197; ZFE2S FERREDOXIN; UNKNOWN_1.

PROSITE; PS01359; ZF_PHD 1; UNKNOWN_1.

PROSITE; PS50089; ZF_RING 2; 1.

SEQUENCE 708 AA; 77563 MW; C886Di.2B927FC928 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            395 CRCGGLKKEVPCYQEL--TCERKCQRLRNC 422
                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      1 CRIXNOK----CFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                     Local Similarity 40.09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeats.";
Cell 43:567-581(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTC_DROME

ID NOTC_DROME

ID NOTC_DROME

DT 28-FEB.
DE Nome=NA.
DE Nome=NA.
DE NOTO_DE NA.
DE 
                                                                                                                                                                                                                                                                                                                 Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 34
                          ò
```

```
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mourt S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Relazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas K. Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Wang Z.-Y., Wascarman D.T., Weinstock G.W. D., Yang S., Yao Q.A.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
A. The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22426669; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.B., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stappeton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-20166011; PubMed=10731137; DOI=10.1126/science.287.5461.2220; MEDLINE-20166011; PubMed=10731137; DOI=10.1126/science.287.5461.2220; Benos P.V. Gatt M.K., Ashburner M., Murphy L., Harris D., Barrell B.G., Ferrac C., Vidal S., Brun C., Demailles J., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D., Minnan B., Rafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S., Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B., Modolell J., Peter A., Schoettler P., Werner M., Mourkiotis F., Callister D., Werner M., Mourkiotis F., Callister D., Callister D., Merner M., Mourkiotis F., Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S., Galloser D.M., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEOURINCE OF 2505-2611 FROM N.A.
MEDLINE-85099129; PubMed-2981631; DOI=10.1016/0092-8674(85)90308-3;
Wharton K.A., Yedvobnick B., Finnerty V.G., Artavanis-Tsakonas S.;
"Opa: a novel family of transcribed repeats shared by the Notch locus and other developmentally regulated loci in D. melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-8 FROM N.A.
MEDLINE-87257846; PubMed=3037327;
Kelley M.R., Kidd S., Berg R.L., Young M.W.;
"Restriction of P-element insertions at the Notch locus of Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S.;
repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=55401878; PubMed=7671825;
Matsuno K., Diederich R.J., Go M.J., Blaumueller C.M.,
Artavanis-Tsakonas S.;
"Deltex acts as a positive regulator of Notch signaling through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "From sequence to chromosome: the tip of the X chromosome of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERACTION WITH DX, AND MUTANT SU42C.
MEDLINE=94215489; PubMed=8162848;
Diederich R.J., Mateuno K., Hing H., Artavanis-Tsakonas "Cytosolic interaction between deltex and Notch ankyrin implicates deltex in the Notch signaling pathway.";
Development 120:473-481(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mol. Cell. Biol. 7:1545-1548(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 287:2220-2222 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          systematic review.";
                                                                                                                                                                                                                                                                                                                                                                                                      GENOME REANNOTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERACTION WITH DX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lewis S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      melanogaster
```

```
Length 2703;
   Score 56; DB 1; 1
Pred. No. 2.8e+02;
                                                                                                                                                                                          25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                     5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                          : ||| ::||| : ||| 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Fragment)
                                                                       4 XNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CKGKGASCHRISYDCCTGSCNR-GKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Entamoebidae; Entamoeba
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=87299637; PubMed=2441741;
                                                                                                                                                                                                                          01-NOV-1988 (Rel. 09, Created)
 34.8%;
ilarity 33.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 38.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 AA; 2626 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GalNAc lectin heavy subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 01, (TrEMBLrel. 26,
                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=hgl5;
Entamoeba histolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             family.
PIR; JH0701; JH0701.
     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=6492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=5759;
                                     8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rivier J.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2004
                                                                                                                                                                                            CONMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
MOD RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          024822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        024822
                     Best Loc
Matches
                                                                                                                                                                            CONMA
                                                                                                                                                          RESULT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224822
                                                                                                       셤
                                                                        à
                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Via its ANK repeats.
SUBCELLULAR LOCATION: Type I membrane protein. Upon activation and 33 cleavage, it is released from the cell membrane and enters into the nucleus in conjunction with Su(H).
FTM: Upon binding its ligands such as Delta or Serrate, it is cleaved (S2 cleavage) in its extracellular domain, close to the transmembrane domain. S2 cleavage is probably mediated by Kuz. It is then cleaved (S3 cleavage) downstream of its transmembrane domain, releasing it from the cell membrane. S3 cleavage requires
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21575956; PubMed=11719214; DOI=10.1016/S0960-9822(01)00562-0;
                                                                   MEDLINE=99221487; PubMed=10206646; DOI=10.1038/19091;
Struhl G., Greenwald I.;
"Presenilin is required for activity and nuclear access of Notch in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'General outlines of the molecular genetics of the Notch signalling
                                                                                                                                                                        S3 CLEAVAGE BY PSN.
MEDLINE=99221488; PubMed=10206647; DOI=10.1038/19096;
Ye Y., Lukinova N., Fortini M.E.;
"Neurogenic phenerypes and altered Notch processing in Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Notch alleles reveal a Deltex-dependent pathway repressing
                                                                                                                                                                                                                                                                                                                                                                                                                                     Ramain P., Khechumian K., Seugnet L., Arbogast N., Ackermann C.,
                                                                                                                                                                                                                                                                                                            MEDLINE=21657146; PubMed=11799064; DOI=10.1101/gad.942302; Liebbr T., Kidd S., Young M.W.; "kuzbanian-mediated cleavage of Drosophila Notch."; Genes Dev. 16:209-221(2002).
interactions with the Notch ankyrin repeats."; Development 121:2633-2644(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Belongs to the NOTCH family. SIMILARITY: Conteains 6 ANK repeats. SIMILARITY: Contains 36 EGF-like domains. SIMILARITY: Contains 3 Lin/Notch repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22256570; PubMed=12369105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Curr. Biol. 11:1729-1738(2001).
                                                                                                                                                                                                                                                              Nature 398:525-529(1999).
                                                                                                                                       Nature 398:522-525(1999).
                                                                                                                                                                                                                                                                                              CLEAVAGE BY KUZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fate."
                                                                                                                       Drosophila.",
                                                       CLEAVAGE
                                                                                                                                                                                                                                                                                                                                                                                                   MUTANT MCD5
```

Portin P.; REVIEW.

++++

<u>:</u>

"Novel neural

```
-1- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind and block voltage-sensitive calcium channels (VSCC).
-1- SUBCELLULAR LOCATION: Secreted.
-1- TISSUB SPECIFICITY: Expressed by the venom duct.
-1- SIMILARITY: Belongs to the conotoxin O-superfamily. Omega-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              calcium channel antagonists. Discrimination between calcium
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP, P05484; 1DW4.
Amidation; Calcium channel inhibitor; Direct protein sequencing;
Ionic channel inhibitor; Neurotoxin; Presynaptic neurotoxin; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Olivera B.M., Cruz L.J., de Santos V., Lecheminant G.W., Griffin
Zelkus R.D., McIntosh J.M., Galyean R., Varga J., Gray W.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    channel subtypes using omega-conotoxin from Conus magus venom.";
Biochemistry 26:2086-2090(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
;
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1988 (Rel. 09, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
065-JUL-2004 (Rel. 44, Last annotation update)
0mega-conotoxin MVID (SNX-159).
Conus magus (Magus cone).
Eukaryota, Metazoa, Mollusca, Gastropoda, Orthogastropoda,
Apogastropoda, Caenogastropoda, Sorbeoconcha, Hypsogastropoda,
Neogastropoda, Conoidea, Conidae, Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 55.5; DB 1; Length 25; Pred. No. 5.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=HM1:IMSS;
Ramakrishnan G., Ragland B.D., Purdy J.E., Mann B.J.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cysteine amide.
E4B9CESEFAA3734D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
```

;

```
RT KW DR DR FT SO 
                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                           7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1] -
SEQUENCE FROM N.A.
MEDLINE-22314996; PubMed=12427470; DOI=10.1016/S0014-4894(02)00113-3;
Beck D.L., Tanyuksel M., Mackey A.J., Haque R., Trapaidze N.,
Pearson W.R., Loffus B., Petri W.A. Jr.;
"Entamoeba histolytica: sequence conservation of the Gal/GalNAC lectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Entamoeba histolytica: sequence conservation of the Gal/GalNAc lectin
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22314996; PubMed=12427470; DOI=10.1016/S0014-4894(02)00113-3; Beck D.L., Tanyuksel M., Mackey A.J., Haque R., Trapaidze N., Pearson W.R., Loftus B., Petri W.A. Jr.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                       3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              т
т
                                                                                                                                                                                              DB 2; Length 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 372;
                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Indels
                                                                                                                                                    21438 MW; 8A9DF5FC481C671D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1
372 372
372 AA; 41994 MW; 49AA800CGECE259F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Gal/GalNAc lectin heavy subunit region D (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-001-2003 (TrEMBLrel. 22, Last sequence update) Gal/GalNac lectin heavy subunit region D (Fragment) Name-bol.
                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.5%; Score 55.5; DB 2;
40.0%; Pred. No. 56;
tive 4; Mismatches 11;
                                                                                                                                                                                                                                                                                         372 AA
                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 372 AA.
                                                                                                                                                                                            Score 55.5; |
Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 CSMGTDNIITYHDDCNSRKSQCGNFNGKCI 109
                                                                                                                                                                                                                                                                   1 CRIXNOKCFOHLDDCCSRK--CNRFN-KCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CRIXNOKCFOHLDDCCSRK--CNRFN-KCV 27
            PIR; S70664; S70664.

GO; GO:0005529; F:sugar binding; IEA.
InterPro; IPR006209; EGF like.
PROSITE; PS00022; EGF_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from clinical isolates.",
Exp. Parasitol. 101.157-163 (2002).
EMBL, AF501278, AAM2199.1;
GO; GO:0005529; F:sugar binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Entamoeba histolytica.
Eukaryota, Entamoebidae, Entamoeba.
NCBI_TaxID=5759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Entamoebidae, Entamoeba
NCBI_TaxID=5759;
                                                                                                                                                                                          Match 34.5%;
Local Similarity 40.0%;
les 12; Conservative 4
EMBL; U33444; AAA75552.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Entamoeba histolytica
                                                                                                                                      194 J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                            NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON TER
NON TER
SEQUENCE
                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                 Q8MZT1
                                                                                                                                                                                                             Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8MZT2
                                                                                                                                                                                                                                                                                                                                                           RESULT 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O8MZT:
S FFF S S S FFF S
                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                   .
연
```

```
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buxopean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 88:3248-3251(1991).
-!- FUNCTION: Lectin that binds galactose.
-!- SUBUNIT: Heterodimer of a heavy (170 kDa) and a light subunit (35 kDa) linked by disulfide bonds.
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=91195330; PubMed=2014248;
Mann B.J., Torian B.E., Vedvick T.S., Petri W.A. Jr.;
"Sequence of a cysteine-rich galactose-specific lectin of Entamoeba
                                                                                                                                                                                                                   Э;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Potential)
                                                                                                                                                                         Score 55.5; DB 2; Length 372;
Pred. No. 56;
4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143239 MW; A6B903F11DC2D5B4 CRC64;
                                                                                                                                   41961 MW; 1FF00CE22FBF5100 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, M59850; -; NOT ANNOTATED CDS.
Direct protein sequencing; Glycoprotein; Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 55.5; DB 1;
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Galactose-inhibitable lectin 170 kDa subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GlcNAc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GlcNAc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GlcNAc.
(GlcNAc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1cNAc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GlcNAc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNAC
                                                                                                                                                                                                                                                                               80 CSMGTDNIITYHDDCNSRKSQCGNFNGKCI 109
                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1276 AA.
                                                                                                                                                                                                                                             1 CRIXNOKCFOHLDDCCSRK--CNRFN-KCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from clinical isolates.";
Exp. Parasitol. 101:157-163(2002).
EMBL; AF501277; AAM22198.1; -.
GO; GO:0005529; F:sugar binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Entamoeba histolytica.
Eukaryota, Entamoebidae; Entamoeba.
NCBI_TaxID=5759;
                                                                                                                                                                         34.58;
                                                                                                                                                                                         40.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34.5%;
                                                                                                                                                                 Query Match
Best Local Similarity 40.09
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       kDa) linked by disur-
-!- PTM: N-glycosylated.
                                                                                                                 372
                                                                                                                                   372 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1276 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 histolytica."
                                                                                                                                                                                                                                                                                                                                                                                 GIL1 ENTHI P32022;
                                                                         Lectin.
NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT
                                                                                                                                                                                                                                                                                                                                           RESULT 39
```

Matches

ઠે

```
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:000156; F:two-component response regulator activity; IEA.
GO; GO:0000160; P:sensory perception; IEA.
GO; GO:000160; P:two-component signal transduction system (p. . .; IEA.
InterPro; IPR01006; Chey like.
InterPro; IPR009057; Homeodomain_like.
InterPro; IPR006447; Myb_SHAQKYF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Han B., Feng Q., Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X., Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L., Liu Y.C., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L., Liu Y.O., Yu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y., Li C., Li T., Zhang Y., Hu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H., Hao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Fu G., Wang S.Y., Zhang L., Wu M., Chen J., Kang H., Chen J.P., Fu G., Wang S.Y., Au Q.P., Zhang X.L., Zhang H., Chen X.Y., Shao C.Y., Sun Y., Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H., Gu J.L., Chen S.T., Ni L., Zhu F.H., Hong G.F.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
HSSP, 049397; IIRZ.
                                                                                                                                                                                                                                                           MEDLINE=97420748; PubMed=9275190; DOI=10.1073/pnas.94.18.9717; Rebbert M.L., Dawid I.B.; Paris I.B.; Dawid I.B.; D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eppermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
    Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoldea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 112; 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 AA; 12975 MW; F491D6CCF80D882F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO: 0005534; C:nucleus; IEA.
InterPro; IPR001781; LIM.
Pfam; PF00412; LIM; 2.
Promon; PD000094; LIM; 2.
PROSITE; PS00478; LIM DOMAIN 1; 2.
PROSITE; PS0023; LIM DOMAIN 2; 2.
LIM domain; Metal-binding; Nuclear protein; Zinc.
NON TER 112 112
SEQÜENCE 112 AA; 12975 MW; F491D6CCF80D882F CRC6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-077-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     380 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.2%; Score 55; 44.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 RIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 RAWHVKCVQ----CCECKCNLTEKC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001789; Response_reg.
Pfam; PF00072; Response_reg; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 44.09
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OSJNBa0038P21.2 protein.
Name=OSJNBa0038P21.2;
                                                                                                                           Xenopodinae; Xenopus
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gramene; Q7XKS9; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q7XKS9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q7XKS9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   임
        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DDT TOO COCCOOC OOL TO THE COCCO
            'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRUCTURE BY NMR.

MEDLINE=20321140; PubMed=10861934;

MEDLINE=20321140; PubMed=10861934;

MOSDAN A., Kharrat R., Fajloun Z., Renisio J.-G., Blanc E.,

Sabatier J.-M., El Ayeb M., Darbon H.;

A new fold in the scorpion toxin family, associated with an activity
on a ryanodine-sensitive calcium channel.";

Proteins 40:436-442(2000)

-I-FUNCTION: Pocently and reversibly modifies channel gating behavior
of the type I ryanodine receptor (RYR1) by inducing prominent
subconductance behavior. Binds a different site as ryanodine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
PubMed=10713267; DOI=10.1016/S0014-5793 (00) 01239-4;
Fajloun Z., Kharrat R., Chen L., Lecomte C., Di Luccio E., Bichet D.,
El Ayeb M., Rochat H., Allen P.D., Pessah I.N., De Waard M.,
Sabatier J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Chemical synthesis and characterization of maurocalcine, a scorpion toxin that activates Ca(2+) release channel/ryanodine receptors."; FBBS Lett. 469:179-185(2000).
            Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scorpio maurus palmatus (Chactoid scorpion).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Iurida; Scorpionoidea; Scorpionidae; Scorpioninae; Scorpio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDB; 1C6W; NWR; -. 3D-structure; Calcium channel inhibitor; Direct protein sequencing; Ionic channel inhibitor; Neurotoxin; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- TOXIC DOSE: LD(50) is 20 ug/mice by intracerebroventricular injection.
            .,
m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom gland.
-!- MASS SPECTROMETRY: WW=3858.2; METHOD=MALDI; RANGE=1-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 55; DB 1; Length 33; Pred. No. 7.6; 1; Mismatches 4; Indels
        11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Belongs to the scorpion calcine family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 32
33 AA; 3865 MW; ASFE70F945FEC8E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
11-MAY-2003 (TrEMBLrel. 23, Last annotation update)
Homeobox protein Lim-1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                    29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 AA.
                                                                                                                                                                                                                                                                                                                                                              33 AA
                                                                                                                               4; Mismatches
                                                                                  1 CRIXNQKCFQHLDDCCSRK--CNRFN-KCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 CFQHL-----DDCCSRKCNR 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    з спрнікискемкресіжене 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 34.2%;
Best Local Similarity 47.6%;
Matches 10; Conservative :
12; Conservative
                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maurocalcine (MCa).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=53957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE=Ref.1.
                                                                                                                                                                                                                                                                                                                                                              SCOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                          P60254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9PSU2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9PSU2
```

RESULT 41
Q9PSU2
ID Q9PSU
AC Q9PSU
DT 01-MA
DT 01-MA
DE HOMEO
GN NAME

셤

ઠે

Gaps

4 ;

```
ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its web by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1994 (Rel. 30, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last sequence update)
05-JUJ-2004 (Rel. 44, Last annotation update)
LIM/homeobox protein Linx5 (Homeobox protein Linx-5) (XLIM-5) (XLIM-2A).
Name-LHX5; Synonymes-LHAZ4, LIMS2,
Xenopus laevis (African clawed frog)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=95377545; PubMed=7649385; DOI=10.1006/dbio.1995.1238;
Toyama R., Curtiss P.E., Otani H., Kimura M., Dawid I.B., Taira M.;
"The LIM class homeobox gene lim5: implied role in CNS patterning in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 188-225 FROM N.A.

MEDLINE=92192449; PubMed=1347750;

Taira M., Jamrich M., Good P.J., Dawid I.B.;

Taira M., Jamrich M., Good P.J., Dawid I.B.;

The LIM domain-containing homeo box gene Xiim-1 is expressed specifically in the organizer region of Xenopus gastrula embryos.";

Genes Dev. 6:356-366(1992)

-I- FUNCTION: Probably involved in the patterning of the nervous system, in particular in the early specification of the diencephalon.
                                                                                                                                                                                                                                                                                                  5
                                                                                                                                                                                                                                DB 2; Length 380;
66;
                                                                                                                                                                                                                                                                                               10; Indels
                          SWART; SW00446; REC; 1. TGREAMS; TIGREAMS; TIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Nuclear (Probable).
SIMILARITY: Contains 1 homeobox domain.
SIMILARITY: Contains 2 LIM zinc-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 402 AA.
                                                                                                                                                                                                                             Query Match
34.2%; Score 55; DB
Best Local Similarity 44.0%; Pred. No. 66;
Matches 11; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                3 IXNOKCFOHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                               17 IDEDKC--HADSTCSMICTQLNFCV 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001356; Homeobox.
InterPro; IPR09057; Homeodomain_like.
InterPro; IPR001781; LIM.
InterPro; IPR007107; LIM_homeo.
Pfan; PF00046; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
ProDom; PD000039; Response_reg; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS, PRO0024; HOMEOBOX.
ProDom; PD000010; Homeobox; 1.
ProDom; PD000094; LIM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus and zebrafish.";
Dev. Biol. 170:583-593(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L42546; AAA99464.1; -.
EMBL; Z11587; CAA77672.1; -.
HSSP; P06601; 1FJL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T04209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LHX5 XENLA
P37137;
                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRANSFAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 43
LHX5_XENLA
   SKRRRRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                            g
```

```
1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=1247932; DOI=10.1073/pnas.242603899;
RX PubMed=1247932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Warusina K., Farmer A.A., Rubin G.M., Hong L.,
Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Raponstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Robards S.W., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahay J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Willalon D.K., Muzny D.M., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Richards N.M., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
T. "Generation and initial analysis of more than 15,000 full-length human and mouse conna sequences."
                                                                                                                                                                                                                                                                                           Gaps
                                   PROSITE; PSS0071; HOMEOBOX-2; 1.
PROSITE; PSS00478; LIM DOMAIN 1; 2.
PROSITE; PSS0023; LIM DOMAIN-2; 2.
Developmental protein; DNA-binding; Homeobox; LIM domain;
Metal-binding; Nuclear protein; Repeat; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                           4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.

Kenopus laevis (African clawed frog)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost

Eukaryota; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Kenopodinae; Kenopus.
                                                                                                                                                                                                                                              Query Match
34.2%; Score 55; DB 1; Length 402;
Best Local Similarity 44.0%; Pred. No. 69;
Matches 11; Conservative 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Embryo;
Klein S., Gerhard D.S.;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                   3 61 LIM 1.
62 125 LIM 2.
180 239 Homeobox.
402 AA; 44959 MW; AS852B94747E09F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ź
                                                                                                                                                                                                                                                                                                                      2 RIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                          23 RAWHVKCVQ----CCECKCNLTEKC 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
SMART; SM00132; LIM; 2.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 28, (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dev. Dyn. 225:384-391(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           initiative.
                                                                                                                                                                                        DNA BIND
SEQUENCE
                                                                                                                                                   DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q63ZR3
                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 44
Q63ZR3
     ð
```

44934 MW; 4147EB3A2774C110 CRC64;

```
403 AA;
                                                                                                                                                                                                                                                                                                                                                                                    LHX1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA BIND
SEQUENCE
         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                               P48742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                           RESULT 46
LHX1 HUMAN
                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-92122449; PubMed=1347750;
MEDLINE-92122449; PubMed=1347750;
MEDLINE-92122449; PubMed=1347750;
Taira M., Jamrich M., Good P.J., Dawid I.B.;
Genea Dev. 6.356-366(1992);
Genea Dev. 6.356(1992);
Gene
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=LHXI; Synonyms=LIM-1, LIM1;
Renopus laevis (African clawed frog).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobarrachia; Pipoidea; Pipidae;
                                                                                                                                                                                    4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
LIM/homeobox protein Lhx1 (Homeobox protein LIM-1) (XLIM-1).
                                                                                                                     34.2%; Score 55; DB 2; Length 402; 44.0%; Pred. No. 69; ive 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS: PRODO24; HOMEOBOX.

ProDom; PD000010; Homeobox; 1.

ProDom; PD000094; LIM; 2.

PROSITE; PS00027; HOMEOBOX 1; 1.

PROSITE; PS0001; HOMEOBOX 2; 1.

PROSITE; PS0001; HOMEOBOX 2; 1.

PROSITE; PS0001; LIM DOWAIN 1; 2.

PROSITE; PS0001; LIM DOWAIN 2; 2.

Developmental protein; DNA-binding; Homeobox; LIM domain; Metal-binding; Nuclear protein; Repeat; Zinc.
EMBL; BC082847; AAH82847.1; -.
Hypothetical protein.
SEQUENCE 402 AA; 44898 MW; 1928D588311BDA5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             403 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSFAC, T01962; -.
InterPro; IPR001356; Homeobox.
InterPro; IPR001356; Homeodomain_like.
InterPro; IPR001761; LIM.
InterPro; IPR001781; LIM.
Pfam; PF000146; Homeobox; 1.
                                                                                                                                                                                                                                       2 RIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                     ношеорох.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIM 1.
LIM 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X63889; CAA45353.1; -.
                                                                                          Query Match
Best Local Similarity 44.01
Best Local Similarity 14.01
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S23802; S23802.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P06601; 1FJL.
                                                                                                                                                                                                                                                                                                                                                                                                                                       LHX1 XENLA
P29674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA BIND
                                                                                                                                                                                                                                                                                                                                                                                 RESULT 45
LHX1_XENLA
LHX1_XENLA
AC P29674;
DT 01-APR:
DT 01-APR:
DT 01-APR:
DT 01-APR:
DT 01-APR:
DE LIM/hon
DE LIM/hon
DE C Amphilbio
CC Amphilbio

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
      SXX
                                                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                       ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                       1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genew; HGNC:6593; LHX1.
MIM; 601999; -.
GO; GO:0003702; F:RNA polymerase II transcription factor acti. . .; TAS.
GO; GO:0007399; P:neurogeneeis; TAS.
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50071; HOMBOBOX-2; 1.
PROSITE; PS500418; LIM DOWAIN 1; 2.
PROSITE; PS50043; LIM DOWAIN 1; 2; 2.
DNA-Dinding; Homeobox; LIM domain; Metal-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                       4
                       Length 403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homeobox.
; CAF2847A340B393F CRC64;
                                                                                                                                                                                                                                                                                                                      01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
LIM/Anomeobox protein Lhx1 (Homeobox protein Lim-1).
Name=LHX1; Synonyms=LIM1;
                          DB 1;
69;
                                                                                                                                                                                                                                                                                404 AA
                                                                     2; Mismatches
                          34.2%; Score 55; 44.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001356; Homeobox.
InterPro; IPR009057; Homeodomain_like.
InterPro; IPR001781; LIM.
InterPro; IPR07107; LIM.homeo.
Pfam; PF00046; Homeobox; 1.
Pfam; PF00412; LIM; 2.
                                                                                                                2 RIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                        22 RAWHVKCVQ----CCECKCNLTEKC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIM 1.
LIM 2.
                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00027; HOMEOBOX_1; 1
PROSITE; PS50071; HOMEOBOX_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00024; HOMECBOX.
ProDom; PD000010; Homeobox; 1.
ProDom; PD000094; LIM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44482 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U14755; AAA21644.1; -. PIR; G01507; G01507.
Query Match
Best Local Similarity 44.0%;
                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P06601; 1FJL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRANSFAC; T01960; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             404 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Repeat; Zinc.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Brain;
```

```
ò
                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bicinformatics and the EMBL outstation. The European Bicinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial or send an email to license@isb-sib.ch).
                                                                                                                                                            01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
LIM/homeobox protein Lhx! (Homeobox protein LIM-1).
Name-LIMX!, Synonyms-LIM-1, LIM1;
Gallus gallus (Chicken).
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                             MEDLINE=95094281, PubMed=7528105; DOI=10.1016/0092-8674(94)90027-2; Tsuchida T., Ensini M., Morton S.B., Baldassare M., Edlund T., Jessell T.M., Pfaff S.L., "Topographic organization of embryonic motor neurons defined by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA-binding; Homeobox; LIM domain; Metal-binding; Nuclear protein;
                                4;
 Score 55; DB 1; Length 404;
Pred. No. 70;
2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIM 1.
LIM 2.
Homeobox.
DF1B7BF1F32B9056 CRC64;
                                                                                                                                           406 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L35569; AAA62173.1; -. PIR; 150375; 150375. HSSP; p66601; 1FUL. InterPro; 1PR001356; Homeobox. InterPro; 1PR001356; Homeodomain_like. InterPro; 1PR001781; LiM. InterPro; 1PR007107; LiM. PF00412; Homeobox; 1. PF00412; LiM. PF00412; LiM. 2. PF00412; LiM. 2. PF00412; LiM. 2.
                                                2 RIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                LIM DOMAIN 1, 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HOMEOBOX 1; 1.
HOMEOBOX 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD000010; Homeobox; 1.
  34.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44845 MW;
            Best Local Similarity 44.0
Matches 11; Conservative
                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00024; HOMEOBOX,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom; PD000094; LIM; 2.
PROSITE; PS00027; HOMEOBC
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       406 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS50071;
                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat; Zinc,
                                                                                                                                       CHICK
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DNA BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                       83777¥¥¥¥¥¥¥¥¥¥¥¥¥¥¥¥
                                                 ò
```

```
ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                         Gaps
                                                                                                                                                                               LHX1 MESAU STANDARD, rki, rv. ....
P63008; P36199;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
LIM/homeobox protein Lhx1 (Homeobox protein LIM-1) (Homeobox protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0024; HOMEOBOX.
SWART; SW00389; HOX; 1.
SWART; SW00132; HOX; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS00478; LIM DOWALIN 1; 2.
PROSITE; PS00478; LIM DOWALIN 1; 2.
PROSITE; PS00478; LIM DOWALIN 2; 2.
DNA-binding; Homeobox; LIM domain; Metal-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95083670; PubMed=7991607;
Rudnick A., Ling T.Y., Odagiri H., Rutter W.J., German M.S.;
Pancreatic beta cells express a diverse set of homeobox genes.";
Proc. Natl. Acad. Sci. U.S.A. 91:12203-12207(1994).
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- SIMILARITY: Contains 1 homeobox domain.
-!- SIMILARITY: Contains 2 LIM zinc-binding domains.
                                                                                                                                                                                                                                                                                            Name-Lhx1; Synonyms-Lim-1, Lim1, Lmx2;
Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                           4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 ;
     Score 55, DB 1; Length 406;
Pred. No. 70;
2; Mismatches 8; Indels
                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.2%; Score 55; DB 1; Length 406; 44.0%; Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            406 AA; 44780 MW; CC8637984998ADAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                       56
                                                                                                  22 RAWHVKCVQ----CCECKCNLTEKC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSFAC; T04264; -.
InterPro; IPR001356; Homeobox.
InterPro; IPR009057; Homeodomain_like.
InterPro; IPR001781; LIM.
InterPro; IPR001781; LIM.
Pfam; PF00046; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ношеорож
                                                                   2 RIXNOKCFQHLDDCCSRKCNRFNKC
   ch 34.2%;
l Similarity 44.0%;
ll; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X81407; CAA57164.1; -.
PIR; I48186; I48186.
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE=Pancreatic islets;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Conservative
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRANSFAC; T04264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat; Zinc.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQÜENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                               LHX1_MESAU
                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
                                                                                                                                                                                 ò
                                                                                             셤
```

2 RIXNQKCFQHLDDCCSRKCNRFNKC 26

ä

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                      STRAIN=BALB/C; TISSUE=Brain; MEDLINE=94220754; PubMed=7909459; Pujii T., Pichel J.G., Taira M., Toyama R., Dawid I.B., Westphal H.; "Expression patterns of the murine LIM class homeobox gene liml in the developing brain and excretory system."; Dev. Dyn. 199:73-83(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDINE=94123856; PubMed=7904966; DOI=10.1006/dbio.1994.1018; Barnes J.D., Crosby J.L., Jones C.M., Wright C.V., Hogan B.L.; Embryonic expression of Lim-1, the mouse homolog of Kenopus Xlim-1, suggests a role in lateral mesoderm differentiation and
                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LHX1_MOUSE STANDARD; PRT; 406 AA. P63066; P36199; Created) 01-JUN-1994 (Rel. 29, Created) 01-JUN-1994 (Rel. 29, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) LIM/homeobox protein LHX1 (Homeobox protein LHX1 (Homeobox protein LHX1) Name=LhX1; Synonyms=Lim-1, Liml; Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF039706; AAD02169.1; --
EMBL; AF039705; AAD02169.1; --
EMBL; AF039705; AAD02169.1; JOINED.
PIR; 148637; 148637.
HSSP; P06601; 1FJL.
TRANSPAC; T01961; --
MGD; MGI:99783; Lhx1.
InterPro; IPR0010136; Homeodomain_like.
InterPro; IPR009057; Homeodomain_like.
InterPro; IPR001781; LIM.
InterPro; IRR007107; LIM.
| 3: || | || || || || RAWHVKCVQ----CCECKCNLTEKC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00024; HOMEGBOX.
SMART; SM00139; HOX; 1.
PROSITE; PS00027; HOMEGBOX 1; 1.
PROSITE; PS00017; HOMEGBOX 2; 1.
PROSITE; PS00478; LIM DOMAÏN 1; 2.
PROSITE; PS50023; LIM DOMAÏN 1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neurogenesis.";
Dev. Biol. 161:168-178(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z27410; CAA81797.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00046; Homeobox; 1. Pfam; PF00412; LIM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                  22
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94336075; PubMed=7914684; DOI=10.1016/0304-3940(94)90334-4; FurryAma T., Inagaki S., Iwahashi Y., Takagi H.; FurryAma T., Inagaki S., Iwahashi Y., Takagi H.; Instribution of Rlim, an LIM homeodomain gene, in the rat brain."; Neurosci. Lett. 170:266-268(1994).
-!- SUBCELLUARA LOGATION: Nuclear (Probable).
-!- SIMILARITY: Contains 1 homeobox domain.
-!- SIMILARITY: Contains 2 LIM zinc-binding domains.
DNA-binding; Homeobox; LIM domain; Metal-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIM domain; Metal-binding; Nuclear protein;
                                                                                                                                                                                      4
                                                                                                                                                       DB 1; Length 406; 70;
                                                                                                                                                                                                                                                                                                                          P63007; P36199;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
LIM/homeobox protein Lhx1 (Homeobox protein LIM-1) (Rlim).
Name=Lhx1; Synonyms=Lin-1, Lim1;
                         LIM 1.
LIM 2.
LIM 2.
LA 2.
L -> LARQVRPVL (in Ref. 2).
Missing (in Ref. 2).
R -> A (in Ref. 2).
R -> H (in Ref. 2).
W, CC8637984998ADAF CRC64;
                                                                                                                                                                                   8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC8637984998ADAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 55; DB 1; Pred. No. 70; 2; Mismatches
                                                                                                                                                                                                                                                                                                                 406 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro; IPR001356; Homeobox.
Interpro; IPR009057; Homeodomain_like.
Interpro; IPR001701; LIM.
InterPro; IPR007107; LIM.homeo.
Pfam; PF00046; Homeobox; 1.
                                                                                                                                                                                                               2 RIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                               22 RAWHVKCVO----CCECKCNLTEKC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIM 1.
LIM 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
PROSITE; PS00478; LIM DOMAIN 1; 2.
PROSITE; PS50023; LIM DOMAIN 2; 2.
DNA-binding; Homeobox; LIM domain;
                                                                                                                            44780 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44780 MW;
                                                                                                                                                        34.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; S71523; AAC60696.1; -.
HSSP; P06601; 1FJL.
                                                                                                                                        PRINTS; PR00024; HOMEOBOX.
SMART; SM00389; HOX; 1.
SMART; SM00132; LIM; 2.
                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
                          54
1117
239
12
31
236
335
                                                                                 24
236
335
406 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 1
180 2
406 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RGD; 71074; Lhx1
              Repeat; Zinc.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Repeat; Zinc.
                                       DOMAIN
DNA BIND
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA BIND
SEQUENCE
                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
 STTTTTTS
                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                        셤
```

```
1 CRIXNOKCFQHLDDCCSRKCNRF 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00008; EGF; 5.7-PRINTS; PR00010; EGFBLOOD. SMART; SM00181; EGF; 6.
                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                        NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGF-like domain.
SEQUENCE 585 A.
                                                                                                                                                                                                                                                                           Name=D113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                          Q80W06
                                                                                                                     RESULT
                                                                                                                                        90M080
                                                       g
                                                                                                                                                                             à
                                                         ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Plasmodium reichenowi: deduced amino acid sequence of sexual stage-specific surface antigen Prs48/45 and comparison with its homologue in Plasmodium falciparum.";
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22925870; PubMed=14563886;
MEDLINE=22925870; PubMed=14563886;
DOI=10.1128/JB.15.21.6481.6485.2003;
Molawa P.T., Schmieger H., Heuzenceder M.W.;
"Bacteriophage ST648, a genetic mosaic of genes from diverse sources isolated from Salmonella enterica serovar typhimurium DT 64.";
J. Bacteriol. 185:6481.6485(2003).
BNBL; AY055382; AAL25881.1; -
InterPro; IPR005021; Phage_termin.
Pfam; PP03334; Terminase 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella typhimurium phage ST64B.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae.
NCBI_TaxID=175950;
                                                         4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=97467681; PubMed=9326890; DOI=10.1006/expr.1997.4204;
Milek R.L., Kocken C.H., Kaan A.M., Jansen J., Meijers H.,
Konings R.N.;
                                                                                                                                                                                                                                                                                                                                                                  Plasmodium reichenowi.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5854;
                DB.1; Length 406; 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.2%; Score 55; DB 2; Length 448; 40.9%; Pred. No. 76; Live 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 34.2%; Score 55; DB 2; Length 577; Best Local Similarity 39.1%; Pred. No. 95; Mismatches 9; Indels
                                                       8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Exp. Parasitol. 87:150-152(1997).
EMBL: L33882; AAA91881.1; -.
InterPro; IPR010884; 548-45.
Pfam; PF07422; 848-45; 1.
SEQUENCE 448 AA; 51563 MW; D2ED630F439D3757 CRC64;
                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
34.2%; Scor.
44.0%; Pred. No. /v,
                                                                                                               22 RAWHVKCVQ----CCECKCNLTEKC 42
                                                                                        2 RIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227 CELINKKCFQETNDKALYKSNK 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CRIXNOKCFOHLDDCCSRKCNR 22
                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 40.5.
Best Local Similarity 40.5.
                                                   11; Conservative
                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                               Surface antigen.
                                                                                                                                                                                                                                                                                                                                                    Name=Prs48/45
            Query Match
                                                                                                                                                                                                                              026107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QBHAD6
                                                                                                                                                                                       RESULT 51
Q26107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 52
08HAD6
1D 08HADD
AC 08HADD
DT 01-MP
DT
                                                 Matches
                                                                                                                           g
                                                                                          ò
                                                                                                                                                                                                                                                 요
```

```
STRAIN=C57BL/6; TISSUE=Brain;

STRAIN=C57BL/6; TISSUE=Brain;

MEDLINE=223825; PubMed=1247932; DOI=10.1073/pnas.242603899;

MEDLINE=223825; PubMed=1247932; DOI=10.1073/pnas.242603899;

A straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A strauberg R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A stachen R.E., Jozdan H., Moore T., Max S. I., Wang J., Hsieh F.,

A physins R.F., Jozdan H., Moore T., Max S. I., Wang J., Hsieh F.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,

Brownstein M.J., Wackernan K.J., Malek J.A., Gunaratne P.H.,

Rachards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffaud G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Nodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

M. Marra M.J.,

Jones S.J., Marra M.A.,

""Green Extion and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34.2%; Score 55; DB 2; Length 585; 37.9%; Pred. No. 97; ive 2; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
strausberg R.;
submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: Contains 6 EGF-like domains.
EMBL; BC052002; AAH52002.1;
-.. BKDF; P00740; IEDM.
MGD; MGI:1096877; D113.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:007386; P:compartment specification; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          585 AA; 61125 MW; EB276F608998D4E9 CRC64;
                                                                                                                                                                                                                                                                                                                01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Delta-like 3, isoform 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                           585 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000742; EGF 2.
InterPro; IPR001438; EGF II.
InterPro; IPR006209; EGF IIke.
InterPro; IPR006210; IEGF.
InterPro; IPR001005; Myb_DNA_binding.
27 CQYVIQACQRHIDDMAAEKSKRF 49
                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00022; EGF_1; 6.
PROSITE; PS00186; EGF_2; 6.
PROSITE; PS0036; EGF 3; 5.
PROSITE; PS00334; MYB_2; UNKNOWN_1.
```

```
formation of somite boundaries during segmentation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        440
457
589 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
  Boulter J., Greenfield A., Weinmaster G., Boulter J., Greenfield A., Weinmaster G., Rattus norvegicus mRNA for Delta 3: a putative ligand for Notch."; Submitted (AuG-1998) to the EMBL/GenBank/DDBJ databases.
-:- FUNCTION: Inhibits primary neurogenesis. May be required to divert neurons along a specific differentiation pathway. Play a role in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                             Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T., Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K., Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N., Hattori A., Okumura K., Iwayanagi T., Ninomiya K.; Subahited (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AKO75302; BAC11535.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Delta-like protein 3 precursor (brosophila Delta homolog 3).
Name-Dll3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Match 34.2%; Score 55; DB 2; Length 587; Local Similarity 37.9%; Pred. No. 97; Losservative 2; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               587 AA; 61144 MW; 2FF5E3EA66789B1B CRC64;
                                                                                                                                                                                                    01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            589 AA
                                                          377 CRAGFAGPRCEHDLDDCAGRACANGGTCV 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       379 CRAGFAGPRCEHDLDDCAGRACANGGTCV 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CR--IXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INCEPPO: 1 PR00143; EGF 2.
INCEPPO: 1 PR00143; EGF 2.
INCEPPO: 1 PR001438; EGF II.
INCEPPO: 1 PR0016209; EGF II.
INCEPPO: 1 PR001005; Myb_DNa_binding.
FEAM; PR001001; EGF 5.
PRINTS; PR001018; EGF 6.
PROSITE; PS00122; EGF 1.
PROSITE; PS00122; EGF 1.
PROSITE; PS01186; EGF 2; 6.
PROSITE; PS00126; EGF 2; 6.
PROSITE; PS00126; EGF 2; 6.
PROSITE; PS00134; MYB_2; UNKNOWN_1.
                   CR--IXNOKCFOHLDDCCSRKCNRFNKCV
                                                                                                                                                                                                                                                                 Hypothetical protein FLJ90821.
Homo sapiens (Human).
                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P00740; 1EDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGF-like domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLL3 RAT
ID DLL3 RAT
AC 088671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                     QBNBS4;
                                                                                                                         RESULT 54
QBNBS4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                    HERE TO THE PROPERTY OF THE PR
                     ઠે
                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ï
paraxial mesoderm (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                        (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
-!- DOMAIN: The DSL domain is required for binding to the Notch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R GO; GO: 0005112; F: Notch binding; ISS.

R GO; GO: 0001709; P: cell fate determination; ISS.

R GO; GO: 0001709; P: cell fate determination; ISS.

R GO; GO: 0007219; P: nembryonic development (sensu Mammalia); ISS.

R GO; GO: 0007219; P: newtergenesis; ISS.

R GO; GO: 0007219; P: nekeletal development; ISS.

R GO; GO: 0007219; P: nekeletal development; ISS.

R InterPro; IPR000142; EGF_II.

R InterPro; IPR000142; EGF_II.

R InterPro; IPR00016; EGF_II.

R PROSITE; PS00022; EGF_II.

R PROSITE; PS00025; EGF_II.

R PROSITE; PS0026; EGF_II.

R PROSITE; PS0026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 34.2%; Score 55; DB 1; Length 589; l Similarity 37.9%; Pred. No. 97; ll; Conservative 2; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A17B3BF9B9SEC17F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                    -!- SIMITARITY: Contains 1 DSL domain.
-!- SIMILARITY: Contains 6 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Poly-Ala.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGF-like 1.
EGF-like 2.
EGF-like 3.
EGF-like 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGF-like 5.
EGF-like 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF084576; AAC33303.1; -. HSSP; P00740; 1EDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61424 MW;
```

```
modified and this statement is not removed. entities requires a license agreement (See hor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                              Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62069 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.2%;
                                                                                                                                                                                                                                                            Pfam; PF00008; EGF; 5. PRINTS; PR00010; EGFBLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94
401
592 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                         ransmembrane.
                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the BMBL outstation Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=129/SvJ;
WBDLIRB=98324780; PubMed=9662403; DOI=10.1038/961;
Kusumi K., Sun E.S., Kerrebrock A.W., Bronson R.T., Chi D.-C.,
Bulotsky M.S., Spencer J.B., Birren B.W., Frankel W.N., Lander E.S.;
"The mouse pudgy mutation disrupts Delta homologue Dll3 and initiation of early somite boundaries."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nakayama K., Nakayama N., Tomooka Y., Hayashi Y., Takahashi M.;
"Specific expression of a divergent type of Delta in a set of earliest generated neurons including the prospective subplate neurons.";
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Inhibits primary neurogenesis. May be required to divert neurons along a specific differentiation pathway. Play a role in the formation of somite boundaries during segmentation of the
                                                                                             DLL3_MOUSE STANDARD; PRT; 592 AA.
088516; 031675; 090WL9; 090WZ7;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Delta-like protein 3 precursor (Drosophila Delta homolog 3) (M-Delta-
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN=CS7BL/6 X DBA; TISSUE=Embryo;
MEDLINE=97417575; PubMed=9272948;
Dunwoodie S.L., Henrique D.M.P., Harrison S.M., Beddington R.S.P.;
"Mouse Dll3: a novel divergent Delta gene which may complement the function of other Delta homologues during early pattern formation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISEASE: A truncating mutation in D113 is the cause of the pudgy (pu) phenotype. Pudgy mice exhibit patterning defects at the earliest stages of somitogenesis. Adult pudgy mice present severe vertebral and rib deformities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           paraxial mesoderm.
SUBUNIT: Can bind and activate Notch-1 or another Notch receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=O88516-2; Sequence=VSP 001376;
TISSUE SPECIFICITY: Predominantly expressed in the neuroectoderm
and paraxial mesoderm during embryogenesis.
DOMAIN: The DSL domain is required for binding to the Notch
                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Type I membrane protein (Probable). ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Contains 1 DSL domain.
SIMILARITY: Contains 6 EGF-like domains.
                               381 CRAGFAGPRCEHDLDDCAGRACANGGTCV 409
        CR--IXNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=O88516-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                               Development 124:3065-3076(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Neural tube;
                                                                                                                                                                                                                                                                                                                                                  the mouse embryo."
                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Probable)
                                                                                                                                                                             3).
Name=D113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -
                                                                                                 g
      ò
```

```
and for commercial
                                      (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ۲;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                          R EMBL; AF066865; AAC40170.1; -.
R EMBL; AF066865; AAC40169.1; -.
R EMBL; AF066865; AAC40169.1; -.
R EMBL; AL013440; BAA33716.1; -.
R EMBL; AB013440; BAA33716.1; -.
R EMBL; AB013440; BEDM.
R GO; GO:0005102; F:Notch binding; NAS.
GO; GO:0007386; P:cell fate determination; IMP.
GO; GO:0007386; P:cempartment specification; IMP.
R GO; GO:0007389; P:nourcogeneeis; NAS.
GO; GO:0007219; P:Notch signaling pathway; NAS.
GO; GO:0007219; P:Notch signaling pathway; NAS.
R GO; GO:0001501; P:Skeletal development; IMP.
R InterPro; IPR00143; EGF_1:
R InterPro; IPR001438; EGF_1:
R InterPro; IPR001438; EGF_1:
R DF4mr. PF00ANDA: ABCF_1:
R DF4mr. PF0ANDA: ABCF_1:
R DF4mr. PF0ANDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; Differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00022; EGF 1; 6.
PROSITE; PS01186; EGF 2; 6.
PROSITE; PS50026; EGF 3; 6.
Alternative splicing; Developmental protein; Differentiat:
EGF-like domain; Notch signaling pathway; Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DWLIGVLF -> A (in isoform 1).
/FTIG4VSP 001376.
E -> K (in Ref. 3).
G -> A (in Ref. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Potential.
Delta-like protein 3.
Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1A84F8022E7E7DCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 377 CRAGFAGPRCEHDLDDCAGRACANGGTCV 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 55; DE
Pred. No. 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGF-like 1.
EGF-like 2.
EGF-like 3.
EGF-like 4.
EGF-like 5.
EGF-like 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CR -- IXNOKCFQHLDDCCSRKCNRFNKCV 27
```

```
CHAIN
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                           EMBL;
                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
                                                                                                   MIM;
**REDLINE=22388257; PubMed=12477912; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins E.S., Wagner L., Shemmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A stapleton M., Soares M.B., Bonaldo M.F., Casvant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunstane P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse CDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Inhibits primary neurogenesis. May be required to divert
neurons along a specific differentiation pathway. Play a role in
the formation of somite boundaries during segmentation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISEASE: Defects in DLL3 are the cause of autosomal recessive spondylocostal dysostosis type 1 (SCDO1) [MIM:277300]. SCDO1 is characterized by multiple hemivertebrae, rib fusions and deletions
                                                                                                                                                                                                  SEQUENCE FROM N.A., AND VARIANT SCDOI ASP-385.
MEDLINE-20206573; PubMed=10742114; DOI=10.1038/74307;
Bulman M.P., Kusumi K., Frayling T.M., McKeown C., Garrett C.,
Lander E.S., Krumlauf R., Hattersley A.T., Ellard S., Turnpenny P.D.;
"Muteations in the human delta homologue, DLi3, cause axial skeletal
defects in spondylocostal dysostosis.";
Nat. Genet. 24:438-441(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          paraxial mesoderm (89 similarity).
--- SUBUNIT: Can bind and activate Notch-1 or another Notch receptor (By similarity).
--- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
--- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Delta-like protein 3 precursor (Drosophila Delta homolog 3).
Name=DLi3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            with a non-progressive kyphosocliosis.
SIMILARITY: Contains 1 DSL domain.
SIMILARITY: Contains 6 EGF-like domains.
                           618 AA.
                          PRT;
                           STANDARD;
                                                                                                                               Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor.
                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain;
                           DLL3 HUMAN
         DLL3 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>:</u>
```

```
Gaps
                                                                                                                                                                                           R GO; GO:0016021; C:integral to membrane; NAS.
R GO; GO:0016021; F:Notch binding; NAS.
R GO; GO:000710; P:cell fate determination; ISS.
R GO; GO:0001701; P:cell fate determination; ISS.
R GO; GO:0001701; P:embryonic development (sensu Mammalia); ISS.
R GO; GO:0007219; P:Notch signaling pathway; ISS.
R GO; GO:0007219; P:Notch signaling pathway; ISS.
R GO; GO:0001201; P:Notch signaling pathway; ISS.
R InterPro; IPR000742; EGF_I:
R InterPro; IPR0006209; EGF_I:
R InterPro; IPR000639; EGF_I:
R PRINTS; PR00006; EGF_I:
R PRINTS; PR00006; EGF_I:
R PROSITE; PS00025; EGF_I:
R PROSITE; PS00186; EGF_2:
R PROSITE; PS0026; EGF_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Developmental protein; Differentiation, Disease mutation, EGF-like domain; Notch signaling pathway; Polymorphism; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.2%; Score 55; DB 1; Length 618; 37.9%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 By similarity.
FridevAR_005952.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Delta-like protein 3.
Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58A9BCOA7DEAD1A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytoplasmic (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CR--IXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGF-like 3.
EGF-like 4.
EGF-like 5.
EGF-like 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Potential
JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              618 AA; 64617 MW;
AF241371; AAF62542.1;
AF241372; AAF62542.1;
BC000218; AAH00218.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11, Conservative
                                                                     HSSP; P00740; IEDM.
Genew; HGNC:2909; DLL3.
H-InvDB; HIX0015121; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal; Transmembrane, SIGNAL 1 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
```

EMBL, AF241373; AAF62542.1; -EMBL, AF241367; AAF62542.1; JOINED.
EMBL, AF241369; AAF62542.1; JOINED.
EMBL, AF241369; AAF62542.1; JOINED.

1;

```
SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CXOA CON
P05484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CXOA CONMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 60
                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ij
                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=2225708; PubMed=12368867; DCI=10.1038/nature01095; AM Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D., Mungall N., Bowman S., Atkin R., Baker S., Barron A., Brooks K., Buckee C.O., Burrows C., Cherevach I., Chillingworth C., Corton C., Cherevach I., Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C., Croin A., Davis B., Dear P., Dearden F., Doggett J., Feltwell T., Goble A., Goodhed I., Gwilliam R., Hamlin N., Hance Z., Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P., Angels K., James K.D., Johnson D., Kerhornou A., Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N., Line A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L., Angels K., Smith R.S., Guares R., Summonds M., Seeger K., Sharp S., Smith R., Squares S., Stevens K., Sulston J.E., Craig A., Nowbold C., Barrell B.G, Sulston J.E., Craig A., Nowbold C., Barrell B.G, Seguence of Plasmodium falciparum chromosomes 1, 3-9 and 13."; Denter M. Denter M. Stevens K., Denter M., Stevens K., Denter M., Stevens K., Denter M., Stevens K., Denter M., Stevens K., Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carlton J.M., Angluoli S.V., Suh B.B., Kooji T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cho J.K., Cuackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., Harris M.A., Van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                               Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium yoelii yoelii.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=73239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 55; DB 2; Length 162
Pred. No. 2.4e+02;
5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191996 MW; 31A7292B814ACE0F CRC64;
                                                                                                01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hyporbetical protein PF0170c.
Name=PFA0170c; Synonyms=MAL1P1.74b;
Plasmodium falciparum (isolate 3D7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0004182; F:carboxypeptidase A activity; IEA. GO; GO:0006508; P:proteolysis and peptidolysis; IEA. InterPro; IPR000834; Peptidase M14. Fam: Proptidase M14. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2004 (TrEMBLrel. 26, Created)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein (Fragment).
Name=PY00634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 5309 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 XNOKCFQHLDDCCSRKCNRF-----NKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=12368865; DOI=10.1038/nature01099;
                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AL031745; CAD48994.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch
1 Similarity 37.9%;
11; Conservative
                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                          Q812A6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q7RRT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
OB 1246
OB 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCOCO OCTO DE LA PACA COCO OC
```

```
EMBL/GenBank/DDBJ whole genome shotgun (MGS) entry which is preliminary data.

EMBL/GenBank/DDBJ whole genome shotgun (MGS) entry which is preliminary data.

EMBL, AABLO1000111; EAA17439.1; -

GO; GO:000160; P:two-component signal transduction system (p. .; IEA. InterPro; IPR001612; Pannine.S.

InterPro; IPR002078; Sig54 interact.

PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN.1.

PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN.1.
"Genome sequence and comparative analysis of the model rodent malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lewis R.J., Nielsen K.J., Craik D.J., Loughnan M.L., Adams D.A., Sharpe I.A., Luchian T., Adams D.J., Bond T., Thomas L., Jones A., Matheson J.-L., Drinkwater R., Andrews P.R., Alewood P.F., "Novel omega-conotoxins from Conus catus discriminate among neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chung D., Gaur S., Bell J.R., Ramachandran J., Nadasdi L., "Determination of disulfide bridge pattern in omega-conopeptides."; Int. J. Pept. Protein Res. 46:320-325(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Olivera B.M., Cruz L.J., de Santós V., Lecheminant G.W., Griffin
Zeikus R.D., McIntosh J.M., Galyean R., Varga J., Gray W.R.,
Rivier J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  channel subtypes using omega-conotoxin from Conus magus venom."; Biochemistry 26:2086-2090(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; hurgan comer; Apogastropoda; Orthogastropoda; Apogastropoda; Apogastropoda; Cannogastropoda; Sorbeoconcha; Hypsogastropoda; Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 46-70.

MEDLINE=86070213; PubMed=4071055;

Olivera B.M., Gray W.R., Zeikus R.D., McIntosh J.M., Varga J.,
Rivier J.E., de Santos V., Cruz L.J.;

"Peptide neurotoxins from fish-hunting cone snails.";
Science 230:1338-1343(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUB=Venom duct;
MEDLINE=20519630; PubMed=10938268; DOI=10.1074/jbc.M002255200;
MEDLINE=20519630; PubMed=10938268; DOI=10.1074/jbc.M002255200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neuronal calcium channel antagonists. Discrimination between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.2%; Score 55; DB 2; Length 5309; 32.4%; Pred. No. 6.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.4%; Pred. No. 6.05702,
tive 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5309 AA; 628397 MW; 2406AC52CF2F5A93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1988 (Rel. 09, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Omega-conotconin MVIIa precursor (SNX-111) (Ziconotide).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CR-IXNOKCFQH-----LDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 AA.
                                  parasite Plasmodium yoelii yoelii.";
Nature 419:512-519(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              calcium channel subtypes.";
J. Biol. Chem. 275:35335-35344(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 46-70.
MEDLINE=87299637; PubMed=2441741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96122182; PubMed=8537186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 32.4
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          5309
                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
NON_TER 5309 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONMA
```

5

```
Presynaptic neurotoxin; Signal; Toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.9%;
                                                                                                                                           58
7587 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 AA; 7942 MW;
                                                                                                                                                                                      33.9%;
                                                                                                                                                                                                   38.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                 Local Similarity 38.5
es 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Conservative
                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel.
                   Phytoxin-like SCR74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                         71 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4787;
 Pharmaceutical;
                             23
46
53
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phytophthora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-OCT-2004
25-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kamoun S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kamoun S.;
                            PROPEP
PEPTIDE
DISULFID
DISULFID
DISULFID
                                                                                                                                            MUTAGEN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                MOD_RES
                                                                                                                             MUTAGEN
                                                                                                                                                                                                                                                                                                                                                              Q646V4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q646V5;
                IGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q646V5
                                                                                                                                                                                                                                                                                                                                              0646V4
                                                                                                                                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                                                                                RESULT 61
Q646V4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STTTTTTTTT
                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein Sci. 10:538-550(2001).
-!- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind and block voltage-sensitive calcium channels (VSCC). This toxin blocks N-type calcium channels.
-!- SUBCELDIARE LOCATION: Secreted.
-!- SUBCELDIARE LOCATION: Secreted.
-!- PHARMACEUTICAL: Is under clinical trial by Neurex. It blocks acute pain in patients who no longer obtain relief from opiate drugs. It is 100 to 1000 times more potent than morphine. By blocking calcium channels it disable nerves that transmit pain signals.
-!- SIMILARITY: Belongs to the conotoxin O-superfamily. Omega-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRUCTURE BY NMR.
MEDLINE=20213238; PubMed=10747778; DOI=10.1021/bi992651h;
Atkinson R.A., Kieffer B., Dejaegere A., Sirockin F., Lefevre J.-F.;
"Structural and dynamic characterization of omega-conotoxin MVIIA: the binding loop exhibite slow conformational exchange.";
Biochemistry 39:3908-3919(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                  STRUCTURE BY NMR.
MEDLINE=99303703; PubMed=10373375; DOI=10.1006/jmbi.1999.2817;
Nielsen K.J., Adams D., Thomas L., Bond T., Alewood P.F., Craik D.J.,
                                                                                                                                                                                                             MEDLINE-95385787; PubMed-7656969; DOI=10.1016/0014-5793(95)00819-U; Basus V.J., Nadasdi L., Ramachandran J., Miljanich G.P.; "Solution structure of omega-conotoxin WVIIA using 2D NMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Structure-activity relationships of omega-conotoxins MVIIA, MVIIC 14 loop splice hybrids at N and P/Q-type calcium channels."; J. Mol. Biol. 289:1405-1421(1999).
                         Kim J.I., Takahashi M., Ohtake A., Wakamiya A., Sato K.; Tayatl she essential for the activity of omega-conotoxin MVIIA and GVIA, specific N-type calcium channel blockers."; Biochem. Biophys. Res. Commun. 206:449-454(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DATABASE: NAME=Ziconotide Source; NOTE=Web site on ziconotide
                                                                                                                          Kohno T., Kim J.-I., Kobayashi K., Kodera Y., Maeda T., Sato K., "Three-dimensional structure in solution of the calcium channel blocker omega-conotcaxin MVIIA,"; Biochemistry 34:10256-10265 (1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21243158; PubMed=11344322; DOI=10.1110/ps.30701;
Goldenberg D.P., Koehn R.E., Gilbert D.E., Wagner G.;
"Solution structure and backbone dynamics of an omega-conotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR004214; Conotoxin.
Pfam; PF02350; Conotoxin; 1.
3D-structure; Amidation; Calcium channel inhibitor; Neurotoxin;
Direct protein sequencing; Ionic channel inhibitor; Neurotoxin;
                                                                                                                                                                                                                                                                                                  STRUCTURE BY NMR.
MEDLINE=97070382; PubMed=8913308; DOI=10.1006/jmbi.1996.0576;
Mielsen K.J., Thomas L., Lewis R.J., Alewood P.F., Craik D.J.;
"A consensus structure for omega-conotoxins with different selectivities for voltage-sensitive calcium channel subtypes: comparison of MVIIA, SVIB and SNX-202.";
J. Mol. Biol. 263:297-310(1996).
SYNTHESIS, ÂND MUTAGENESIS OF LYS-47 AND TYR-58.
MEDLINE=95126938; PubMed=7826361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WWW="http://docmd.com/ziconotide/".
JH0700; JH0700.
                                                                                                      STRUCTURE BY NMR.
MEDLINE=95367555; PubMed=7640281;
                                                                                                                                                                                                                                                          spectroscopy.";
FEBS Lett. 370:163-169(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DW4; NMR; A=1-25.
1 DW5; NWR; A=1-25.
1 FFO; NMR; A=1-25.
1 MVI; NWR; @=1-25.
1 OMG; NMR; @=1-25.
                                                                                                                                                                                                 STRUCTURE BY NMR.
                                                                                                 STRUCTURE BY NMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRUCTURE BY NMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRUCTURE BY NMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lewis R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eamilv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -
```

```
"Patterns of Diversifying Selection in the Phytotoxin-like scr74 Gene Family of Phytophthora infestans."; Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases. EMBL, AY723713; AAU21454.1.
                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Parterns of Diversifying Selection in the Phytotoxin-like scr74 Gene Family of Phytophthora infestans.";
                                                                                                                                                 Cysteine amide (G-71 provides amide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                group).
K-As: Little decrease in activity.
Y-As: Strong decrease in activity.
E2A32725C81AF31D CRC64;
                                                                                                                                                                                                                                                                                                    Score 54.5; DB 1; Length 71;
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phytoxin-like SCR74.
Phytophthora infestans (Potato late blight fungus).
Eukaryota, stramenopiles, Oomycetes, Pythiales, Pythiaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phytophthora infestans (Potato late blight fungus).
Eukaryota, stramenopiles, Oomycetes, Pythiales, Pythiaceae,
                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CE020986B607E796 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                               Omega-conotoxin MVIIa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 AA
                                                                                                                                                                                                                                                                                                                                                         5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 54.5; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 KCFQHLD-----DCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Potential
                                                                                                                                                                                                                                                                                                                                                                                                         1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                              group)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT:
```

ï

Page 30

```
Hypothetical protein.
SEQUENCE 247 AA; 27954 MW; 26FAB589C121FBEB CRC64;
                                    T06G6.6; CE13343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clostridium,
                                    WormPep;
                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                   Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  097GL5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          097GL5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        018720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 66
018720
AC 01872
AC 01872
AC 01972
DT 01-JA
DT 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q97GL5
                                    SKB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Patterns of Diversifying Selection in the Phytotoxin-like scr74 Gene Family of Phytophthora infestans "; Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL: AY723705; AAUZ1446.1; -
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
                                                                                                                                                                                                                                                            7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
                                                                                                                                                                              DB 2; Length 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phytoxin-like SCR74.

Phytophthora infestans (Potato late blight fungus).

Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                        Indels
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kershaw J.K.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; Z81587; CAB04705.2; -.
WormBase; WBGene00011548; T06G6.6.
                                                        -.
537318ANFF612545 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7885 MW; 98D110005D613927 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein T06G6.6.
                                                                                                                                                                                                                                                        .,
                                                                                                                                                                  ; Score 54.5; DE; Pred. No. 18; 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.9%; Score 54.5; I
                                                                                                                                                                                                                                                                                                                 7 KCFQHLD-----DCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                  45 KCCQAINADPIAFHDCCSKSCNTGSPC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 KCFQHLD-----DCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45 KCCQAINPDPIAFHDCCSKSCNTGSPC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                  33.9%;
                                        EMBL; AY723711; AAU21452.1;
SEQUENCE 74 AA; 7825 MW;
                                                                                                                                                  Query Match 33.99
Best Local Similarity 37.09
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    investigating biology.";
Science 282:2012-2018(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 37.0 Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kamoun S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q646W1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0646W1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      018052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 63
Q646W1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 64
018052
AC 01805
AC 01805
DT 01-JA
DT 01-JA
DT 01-JA
DT 01-JA
DE HYPOT
CO CREAD
OC READ
OC RE
                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                              쉽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCOC ON THE STANTANT OF THE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

```
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=SAW760; PubMed=9233678; DOI=10.1016/S0166-6851(97)00047-9; MEDLINE=977376907; PubMed=9233678; DOI=10.1016/S0166-6851(97)00047-9; Pillai D.R., Britten D., Ackers J.P., Ravdin J.I., Kain K.C.; "A gene homologous to hgl2 of Entamoeba histolytica is present and expressed in Entamoeba dispar.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-21359325; PubMed=11466286; DOI=10.1128/JB.183.16.4823-4838.2001; DOI=10.1128/JB.183.16.4823-4838.2001; DOI=10.1128/JB.183.16.4823-4838.2001; Moelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Hitti J., Wolf Y.I., Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P., Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.; Glenome sequence and comparative analysis of the solvent-producing bacterium clostridium acetobutylicum."; J. Bacteriol. 183:4823-4838(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                   Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                       7;
            DB 2; Length 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 252;
                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0016740; F:transferase activity; IEA.
InterPro; IPR001173; Glyco trans 2.
Complete proteome; Transferase.
SEQUENCE 252 AA; 29892 MW; C7A45BA39F534DE9 CRC64;
                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     018720;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JANR-2004 (TrEMBLrel. 26, Last annotation update)
Gal/GalNAc-inhibitable adherence lectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
       Score 54.5; DE Pred. No. 52; 5; Mismatches
                                                                                                                                                                                                                                                                       252 AA
                                                                                                                                  Score 54.5; DE Fred. No. 53; 5; Mismatches
                                                                                               3 IXNOKCFOHLD-----DCCSRKCNRFNK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1282 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 LAEDACF--IEDCCKQGIKIYSCNRFN 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 IXNOKCFOHLDDCCSR----KCNRFN 24
                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Entamoebidae; Entamoeba.
NCBI_TaxID=46681;
Jacal Similarity 33.3%;
Local Similarity 33.3%;
                                                                                                                                                                                                                                                                                                             01-0CT-2001 (TrEMBLrel. 18, 01-0CT-2001 (TrEMBLrel. 18, 01-JUN-2003 (TrEMBLrel. 24, Glycosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 33.9%;
Best Local Similarity 37.0%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               OrderedLocusNames=CAC2351;
                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; H97189; H97189.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=dhgl2;
Entamoeba dispar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1488;
```

247 AA.

PRELIMINARY;

```
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
Adoxophyes hommai nucleopolyhedrovirus.
Viruses: dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                    Nucleopolyhedrovirus
                                                                                                                                                                                                                                                                            NCBI_TaxID=224399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  090476;
                                                   Q80LT7
RESULT 68
Q80LT7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LHX1_BRARE
                                                                             ACCOCCOS SELECT 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                    7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                they bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE-20519630; PubMed-10938268; DOI=10.1074/jbc.M002252200; Lewis R.J., Nielsen K.J., Craik D.J., Loughnan M.L., Adams D.A., Sharpe I.A., Luchlan T., Adams D.J., Bond T., Thomas L., Jones A., Matheson J.-L., Drinkwater R., Andrews P.R., Alewood P.F.; "Novel omega-conoccains from Conus catus discriminate among neuronal calcium channel subtypes.";
J. Biol. Chem. 275:35335-35344 (2000).
-!- FUNCTION: Omega-conotcains act at presynaptic membranes, they bin and block voltage-sensitive calcium channels (VSCC) (By similarity). This toxin blocks N-type calcium channels.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom duct.
-!- SIMILARITY: Belongs to the conotoxin O-superfamily. Omega-type
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR004214; Conotoxin.
Pfam; PF02950; Connotoxin; 1.
Amidation; Calcium channel inhibitor; Direct protein sequencing;
Ionic channel inhibitor; Neurotoxin; Presynaptic neurotoxin; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., SEQUENCE OF 46-72, SYNTHESIS, AND STRUCTURE BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cysteine amide (G-73 provides amide
                                                                                                                                                                                                                                                  э
Э
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conús catus (Cat cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conúae; Conús.
                                                                                                                                                                                              Length 1282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 54; DB 1; Length 73;
Pred. No. 20;
5; Mismatches 8; Indels
                                                                                                                                                                                                                                                    11; Indels
                                                                                                                                                1282 AA; 143481 MW; 48BD2FA64140C33E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     group).
C4CEBD30C77DAEC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Omega-conotoxin CVID.
                                                                                                                                                                                                 Score 54.5; DB 2;
Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
0mega-conotoxin CVID precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          By similarity.
                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     By similarity.
Mol. Biocham. Parasitol. 87:101-105(1997).
EMBL; U73710; AAC47580.1; -.
                                                                                                                                                                                                                                                                                                                                               708 CSMGTDNVISYCEDCASRKSQCGNFNGKC 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 By similarity
                                                                                                                                                                                                                                                                                                1 CRIXNQKCFQHLDDCCSRK--CNRFN-KC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Potential.
                         EMBL, U73710; AAC47580.1; -.
GO; GO:0005529; F:susgar binding; IEA.
InterPro; IPR006209; EGF like.
PROSITE; PS00022; EGF_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                 33.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.5%;
38.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7748 MW;
                                                                                                                                                                                                                                                  11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22
445
72
72
72
72
                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=101291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P05484; 1DW4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
wes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CXOD CONCT
P58920;
                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
DISULFID
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP;
                                                                                                                                                                                                                                                    Matches
  g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            There are no restrictions on
SEQUENCE FROM N.A. STRANDOL; MARCHARD STRANDS 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Nov-1997 (Rel. 35, Last sequence update)
Name=lhxla; Synonyms=lhxl, Homeobox protein LIM-1).
Name=lhxla; Synonyms=lhxl, liml;
Brachydanio rerio (Zebrafish) (Danio rerio).
Butaxyota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                         Length 247;
                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                               247 AA; 28773 MW; 9E53E54D3E022C25 CRC64;
                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         405 AA.
                                                                                                                                                                                                                                                                                                                                      33.5%; Score 54; DB 40.7%; Pred. No. 60; tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168 CEKKCFTAPRLHLDGLVCDKCNGYNFC 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 XNQKCFQ----HLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                               EMBL; AP006270; BAC67260.1; -. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 40.7 tes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BRARE
                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                               Query Match
```

ö

Gaps

ö

1 CRIXNOKCFOHLDDCCSRKCN 21 | : : | | : | | : 46 CKSKGAKCSKLMYDCCSGSCS 66

Conservative

Matches

ઠે

```
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=99457719; PubMed=10528412; DOI=10.1016/S0965-1748(99)00068-5;
Vogtli M., Imhof M.O., Brown N.E., Rauch P., Spindler-Barth M.,
Lezzi M., Henrich V.C.;
"Functional characterization of two Ultraspiracle forms (CtUSP-1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4;
                                                                                                                                                               EMBL: Li37802; AAA32157.1;

R HSSP; P06601; 1FJL.

R ZFIN; ZDB-GRNE-980526-347; lbx1a.

R InterPro; IPR001556; Homeobox:

InterPro; IPR001567; Homeobox:

R InterPro; IPR001781; LIM.

R InterPro; IPR001781; LIM.

R Pfam; PF004412; LIM, 2.

R PRINTS; PR00024; HOMEOBOX; 1.

R PRODOM; PD0000124; HOMEOBOX; 1.

R PROSITE; PS000127; HOMEOBOX; 1.

R PROSITE; PS000127; HOMEOBOX 2; 1.

R RPGSITE; PS000127; HOMEOBOX 2; 1.

R PROSITE; PS00013; LIM_DOMAIN 1; 2.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chironomus tentans (Midge).
Bukaryota, Metazoa, Arthropoda; Hexapoda, Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Chironomoidea;
Chironomidae; Chironominae; Chironomus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.5%; Score 54; DB 1; Length 405; 44.0%; Pred. No. 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 238 Homeobox.
405 AA; 45153 MW; 186EEBEB59C88123 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CtUSP-2) from Chironomus tentans.";
Insect Blochem. Mol. Biol. 29:931-942(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               552 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 RAWHIKCVQ----CCECKCNLTEKC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 RIXNOKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
tes 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=7153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ultraspiracle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA BIND
SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              045117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        045117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 70
005117
AC 045117
DT 01-JUID DT 01-JUID DT 01-JUID DE 01-SEQUE RA VOGE1 RA VOGEN RA VO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

```
;
                  R InterPro; IPR001233; Stdhrmn.__ereptor.

R InterPro; IPR001946; Str_ncl_receptor.

R InterPro; IPR001046; Str_ncl_receptor.

R InterPro; IPR001045; Arc.ncl_receptor.

R Pfam; PP00104; Hormone_recep; 1.

R PRINTS; PR00145; RETINOIDAR.

R PRINTS; PR000345; STRDHORMONER.

R PRINTS; PR000347; STROHORMONER.

R SMART; SM00430; HOLI; 1.

SMART; SM00399; ZnF C4; 1.

R SMART; SM00399; ZnF C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Barrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Thomas J.T., Weih K.A., Prakash D., Moos M. Jr.;
"Vgl and CDMP-1/GDF5 Have Specific Processing Requirements That
Restrict their Sites of Action to Body Axis and Joint Patterning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T Centers."

Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.

R EMBL; Ave68229; AAP9305.1;

R GO; GO:0008239; F:peptidase activity; IEA.

R InterPro; IPR006212; Furin repeat.

R InterPro; IPR00920; Grow Fac_recept.

R InterPro; IPR00920; Grow Fac_recept.

R InterPro; IPR00920; Prot in propept.

R Fam; Pr00082; Peptidase S8; 1.

R Ffam; Pr00082; Peptidase S8; 1.

R FAM; PR00113; ProtonconvertsP; 1.

R RAMRT; SM00111; FU; 5.

DR SWART; SM00181; FU; 5.

DR PROSITE; PS00136; SUBTILIASE ASP; 1.

R PROSITE; PS00138; SUBTILIASE HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 33.5%; Score.54; DB 2; Length 911; Local Similarity 38.1%; Pred. No. 1.9e+02; es 8; Conservative 4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 33.5%; Score 54; DB 2; Length 552
Best Local Similarity 40.0%; Pred. No. 1.2e+02;
Matches 10; Conservative 6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           911 AA; 101427 MW; E75C63CB60D3B82F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Subtilisin-like procease SPC6A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        911 AA.
InterPro; IPR000003; RtnoidX_receptor.
InterPro; IPR001723; Stdhrmn_receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             345 CAMVNKQVFQHMDFC--RRLPHFTK 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CRIXNOKCFQHLDDCCSRKCNRFNK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 683 KKCFQHCDICVGSRIDOCIAC 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 OKCFOHLDDCCSRKCNRFNKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopodinae; Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=spc6A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q68KF8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 71
Q68KF8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loca
Matches
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DE REAL PROPERTY OF THE PROPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
```

Gaps

ö

Indels

10;

7; Mismatches

7; Conservative

```
Q9DE37
                                                                                               RESULT 73
Q9DE37
Matches
                           ò
                                                        g
                                                                                                                           Hypothetical protein W02C12.1.
Name=W02C12.1; ORFNames=W02C12.1;
Caenorhabditis elegans.
Elwaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                             investigating biology. The C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.5%; Score 54; DB 2; Length 1372; 29.2%; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
A: 150561 MW; 0537FA79BA0576C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Bristol N2;
Murray J., Wohldmann P.;
"The sequence of C. elegans cosmid W02C12.";
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Waterston R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, 100015; ABA31995.1; -.
PIR; T25933; T25933.
HSSP, Q12780; 1HAE.
                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wormbase; WaGene0020228; W02C12.1.
Wormpep; W02C12.1; CE14412.
GG; GG; O005509; F:calcium ion binding; IEA.
InterPro; IPR00152; Asx hydroxyl S.
InterPro; IPR00152; Asx hydroxyl S.
InterPro; IPR001895; Cona like_lec_gl.
InterPro; IPR001891; EGF_Ca.
InterPro; IPR001891; EGF_TI.
InterPro; IPR001803; EGF_II.
InterPro; IPR0019030; Grow_fac_recept.
InterPro; IPR0019030; Grow_fac_recept.
InterPro; IPR001759; Pentaxin.
                                                        PRT; 1372 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #RINIS,
Probom; PD00212...
Probom; P00032; CCP, 1.
SWART; SW00179; EGF CA; 4.
PROSITE; PS00010; ASX HYDROXYL; 5.
PROSITE; PS00022; EGF 1; 11.
PROSITE; PS01186; EGF 2; 12.
                                                                                     Created)
                                                                                                                                                                                                                                                STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PROODIO; EGFBLOOD.
Prodom; PBOGDS13; Pentaxin; 1.
SWART; SMO032; CCP; 1.
SWART; SM00179; EGF_CA; 4.
                                                                                               (TrEMBLrel. 03, (TrEMBLrel. 26,
                                                                                   01-MAY-1997 (TrEMBLrel. 03,
                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=Bristol N2;
WormBase Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1372 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGF-like domain;
SEQUENCE 1372 A
                                                                                                 01-MAY-1997
01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                      P91526
P91526;
                         RESULT 72
                                          P91526
```

Best Local Similarity

```
Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostarlophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                extension of
                                                                                                                                                                                                                                                                                                     MEDLINE=21098742; PubMed=11161558; DOI=10.1006/dbio.2000.0105; Yeo S.Y., Little M.H., Yamada T., Miyashita T., Halloran M.C., Kuwada J.Y., Huh T.L., Okamoto H.; Okarexpression of a slit homologue impairs convergent extensithe mesoderm and causes cyclopia in embryonic zebrafish.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1515 AA; 166871 MW; 12FD111277D18D5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 ZFIN; ZDB-GENE-010306-4; slit3.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                             PRT; 1515 AA
              GO; GO:0007155; P:cell adhesion; IEA.
4 XNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000152; Asx hydroxyl S. InterPro; IPR008985; Con like lec_g InterPro; IPR008095; Con like lec_g InterPro; IPR0000742; Cyg Knot C. InterPro; IPR000742; EGF 2. InterPro; IPR0006209; EGF 1ike. InterPro; IPR0016209; EGF 1ike. InterPro; IPR001619; Laminin G. InterPro; IPR001611; Laminin G. InterPro; IPR0016483; LRR.Cterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS01187; EGF_CA; 2.
PS50025; LAM_G_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00369; LRR TYP; 9.
PROSITE; PS00010; ASX HYDROXYL;
                                                                                                                                                                                                                                                                                                                                                                          Dev. Biol. 230:1-17(2001).
EMBL; AF210320; AAG36772.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRR Nterm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF02210; Laminin G_2; 1.
Pfam; PF01463; LRRCT; 4.
Pfam; PF01462; LRRNT; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRR_typ.
TSP_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEURICHRPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CT; 1.
EGF CA; 1
                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FOLN; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'fam; PF00008; EGF; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nterPro; IPR00372;
nterPro; IPR003591;
nterPro; IPR003129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00560; LRR
PRINTS; PROO019; LE
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=Michigan;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00041; C
SMART; SM00179; E
SMART; SM00274; F
SMART; SM00282; L
SMART; SM00082; L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00013;
SMART; SM00369;
                                                                                                                                                                            Name=slit3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
EGF-like
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ROSITE;
                                                                                                             2
```

```
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T 76
CAEEL
                        RP RT RT RT RT DR DR DR DR DR DR DR DR SQ SQ SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gimenaz-Bonafe P., Ribes E., Sautiere P., Gonzalez A., Kasinsky H.E., Kouach M., Sautiere P.-E., Ausio J., Chiva M.;

"Chromatin condensation, cysteine-rich protamine, and establishment of disulphide interprotamine bonds during spermiogenesis of Bledone cirrhosa (Cephalopoda).",

Bur. J. Cell Biol. 81:341-349(2002).

-I-FUNCTION: Protamines substitute for histones in the chromatin of sperm DNA into a highly condensed, stable and inactive compact sperm DNA into a highly condensed, stable and inactive complex. This protamine condenses spermiogenic chromatin in a pattern which comprises fibres with a progressively larger diameter and lamellae that finally undergo definitive coalescence.

-I-SUBUNIT: Cross-linked by, interchain disulfide bonds around the
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    Elegone cirrhosa (Curled octopus) (Ozaena cirrosa).
Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
Octopodiformes; Octopoda; Incirrata; Octopodidae; Eledone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interchain (with C-12) (By similarity)
Interchain (with C-63) (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Taxaceae; Taxus.
NCBI_TaxID=85957;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY
                                                                ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3,
Query Match 33.5%; Score 54; DB 2; Length 1515; Best Local Similarity 37.5%; Pred. No. 38+02; Matches 9; Conservative 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 53.5; DB 1; Length 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
3-hydroxy-3-methylglutaryl-CoA synthase (EC 2.3.3.10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70932DAC3C71837E CRC64;
                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                            84 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               476 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 27; 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bimilarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CRIXNOKCFQHLDDCCSRK---CNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 CRRCHRRCSRIVKKCCRRRSKCCRRRRRC 52
                                                                                                                                   1059 VGQCCEQDYNDCLENKCQHGAECV 1082
                                                                                                     4 XNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA-helix (By similarity).
SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Sperm;
MEDLINE=22108191; PubMed=12113475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10612 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 33.2%;
Similarity 31.0%;
9; Conservative
                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                            Cysteine-rich protamine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Taxus x media.
                                                                                                                                                                                                                   JT 74

SELECI

HSPC ELECI

P83183;

-FSB-20'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q693N8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RECULT 75
069308
AC 06930
DT 25-0C
DT 2
                                                                                                     à
                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
A Kai G., Miao Z., Tang K.;

A Kai G., Miao Z., Tang K.;

T. "Cloning and expression analyses of a new gene encoding 3-hydroxy-3-
"T. "Cloning and expression analyses of a new gene encoding 3-hydroxy-3-
"T. "Cloning and expression analyses of a new gene encoding 3-hydroxy-3-
"T. "Cloning and expression analyses of a new gene encoding 3-hydroxy-3-
"S. Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

R. GO; GO:0008441; F. RayLransferase activity; IEA.

R. GO; GO:0016740; F. transferase activity; IEA.

R. InterPro; IPR008260; HMG CoA Synth.

DR. TherPro; IPR010122; HMG CoA Synth.

DR. Pfam; PP01154; HMG CoA Synth.

R. TGREAMS; TIGRRAMS; HMG-CoA-S_euk; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftz-fl, is required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The C. elegans sequencing consortium;
"Genome sequence of the nematode C. elegans: a platform for
"Investigating biology.";
Science 282:2012-2018(1998).
-!- FUNCTION: Orphan nuclear receptor. Seems to be required during
development. Disruption of nhr-25 function leads to embryonic
arrest due to failure of the epidermally mediated process of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISOId=019345-2; Sequence=VSP 003723;
-!- TISSUE SPECIFICITY: Expressed in the epidermis, the developing somatic gonad, and a subset of other epithelial cells.
-!- SIMILARITY: Belongs to the nuclear hormone receptor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND CHARACTERIZATION STRAIN-Bristol N2; MEDLINE-20237592; Pubmed=10772806; DOI=10.1006/dbio.2000.9679;
                                                                                                                                                                                                                                                                                                                                                                                                               Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                         52863 MW; 973883623142EE0D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                     / Match 33.2%; Score 53.5; DB 2; Local Similarity 43.5%; Pred. No. 1.2e+02; les 10; Conservative 5; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gissendanner C.R., Sluder A.E., "nhr-25, the Caenorhabditis elegans ortholog of for epidermal and somatic gonad development."; Dev. Biol. 221:259-272(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NH25_CABEL
O19345; QSNU395; QSNU396; QSNU397;
O19345; QSNU395; QSNU396; QSNU397;
O-MAY-2000 (Rel. 39, Last sequence update)
O-MAY-2000 (Rel. 39, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Nuclear hormone receptor family member nhr-25.
Name=nhr-25; ORFNAmes=FllCl.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     embryo elongation.
SUBCELLULAR LOCATION: Nuclear (Potential).
ALTERNATIVE, PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=Q19345-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 LSQTCYLKALDSCYKRFCNKFEK 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 XNOKCF-QHLDDCCSRKCNRFNK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                           Acyltransferase, Transferase.
SEQUENCE 476 AA; 52863 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhabditidae, Pel
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=Alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name≃Beta;
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
```

1,

```
release channel of skeletal and cardiac muscle.";
                                                                                            FUNCTION ON RYR1 AND RYR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           · PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clostridium.
                                                                                                                                                                                                                                                                                                                                                                           Garcia J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28XKK8
              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Venom;
MEDLINE=97561909; PubMed=9108323; DOI=10.1016/S0014-5793(97)00227-5;
Zamudio F.Z., Gurrola G.B., Arevalo C., Sreekumar R., Walker J.W.,
Valdivia H.H., Possani L.D.;
"Primary structure and synthesis of Imperatoxin A (IpTx(a)), a peptide activator of Ca2+ release channels/ryanodine receptors.";
PEBS Lett. 405:385-389(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDINE=93101692; Pubmed=1334561; Valdivia H.H., Kirby M.S., Lederer W.J., Coronado R.; Sacorpion toxins targeted against the sarcoplasmic reticulum Ca(2+)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pandinus imperator (Emperor scorpion).
Eukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Scorpiones,
Ilurida, Scorpionoidea, Scorpionidae, Scorpioninae, Pandinus.
NCBI_TaxID=55084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO039; STRDHOKMONER.
PRINTS; PRO0309; STROIDFINGER.
PRINTS; PRO0301; STROIDFINGER.
PRODOM; PRO0303; Znf C48teroid; 1.
SMART; SM00399; ZnF C4; 1.
SMART; SM00399; ZnF C4; 1.
SMART; SM00399; ZnF C4; 1.
Alternative splicing; Developmental protein; DNA-binding;
Nuclear protein; Receptor; Transcription regulation; Zinc-finger.
DNA_BIND
DNA_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.2%; Score 53.5; DB 1; Length 572; 32.4%; Pred. No. 1.40+02; tive 8; Mismatches 6; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 C4-type.

80 Missing (in isoform Beta).

/FTd=VSP 003723.

100 F -> L (in Ref. 2; AAF67039).

540 R -> Q (in Ref. 2; AAF67039).

64772 MW, D3092AE533092D7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 IXNQKCFQ------HLDDCCSRKCN--RFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46 VQNKKQYQCSAEANCHVDRTCRKRCPSCRFQKCL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
Imperatoxin A (IpTxa) (Imperatoxin activator)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 AA
                                                                                                                                        C4-type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00104; Hormone recep; 1. Pfam; PF00105; zf-C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 540 5
572 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DENTIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ITXA PANIM
P59868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZN_FING
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA BIND
ZN FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 77
ITXA_PANIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THE SET AND SET OF SET 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
```

```
ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fully and a control of the control o
                                                                                                                       MEDIJINE-98233523; PubMed-9565405; Tripathy A., Resch W., Xu L., Valdivia H.H., Meissner G.; Inderdorate subconductance states in Ca2+ release channels (ryanodine receptors) of cardiac and skeletal muscle."; Gardiac and skeletal muscle.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Imperatoxin A enhances Ca(2+) release in developing skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=13;
MEDUINE=21664373; PubMed=11792842; DOI=10.1073/pnas.022493799;
Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
Shiba T., Ogaaawara N., Hattori M., Kuhara S., Hayashi H.;
"Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION ON RYR3.
MEDLINE=21855993; PubMed=11867448;
Nabhani T., Zhu X., Simeoni I., Sorrentino V., Valdivia H.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 53; DB 1; Length 33;
Pred. No. 13;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 53; DB 2; Length 85;
Pred. No. 31;
5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID 3 17 By similarity.
DISULFID 10 21 By similarity.
DISULFID 16 32 By similarity.
SEOUENCE 33 AA, 3764 MW; DODFBEFFFE294537 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          flesh-eater.";

Proc. Natl. Acad. Sci. U.S.A. 99:996-1001 (2002).

EMBL. AP001319; BAB81092.1; -..

FRINTS; PRO0003; 4DISULPHCORE.

Complete proteome; Hypothetical protein.

SEQUENCE 85 AA; 9440 MW; 90EA03381B8DB681 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
11-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein CPE1386.
OrderedLocusNames=CPE1386;
Proc. Natl. Acad. Sci. U.S.A. 89:12185-12189(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 CFQHL-----DDCCSRKCNR 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 CLPHLKRCKADNDCCGKKCKR 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , 32.9%;
y 42.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 32.9%;
Best Local Similarity 37.5%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Beet Local Similarity 42.53,
Beet Local Similarity 62.53,
Conservative
```

36

CRIXNQ-KCFQHLDDCCSRK----CNRFNKC 26

RESULT 79

g ò

```
MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847; Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzar M., Rosenthal A., Noegel A.A.; "Sequence and analysis of chromosome 2 of Dictyostelium discoideum."; Nature 418:79-85(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bevan M., Stiekema W., Murphy G., Wambutt R., Pohl T., Terryn N., Kreis M., Kavanagh T., Entian K.D., Rieger M., James R., Pujdomenech P., Harzopoulos P., Obermaier B., Duesterhoft A., Jones J., Palme K., Ansorge W., Delseny M., Bancroft I., Mewes H.W., Schueller C., Chalwatzis N.; Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thailana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids; eurosids II, Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
95-JUL-2004 (TrEMBLrel. 127, Last annotation update)
14-Ypochetical protein d13245w (Hypochetical protein AT4g14410)
Name=d13245w; Synonyms=AT4g14410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.9%; Score 53; DB 2; Length 234; 40.0%; Pred. No. 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bungart C.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AC116305, AA052288.1; -.
Hypothetical protein.
SEQUENCE 234 AA; 27944 MW; BB426ECDAF9B3032 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EU Arabidopsis sequencing project;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                 Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.
NCBL_TaxID=44689;
                                                                                                                                                                                  01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
                                                                                                            234 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       277 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:|: | :|: | :|| 36 ITNENIFNKNYLKCCNCKINNYNK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 IXNOKCF--OHLDDCCSRKCNRFNK 25
                                                                                                                                                            (TrEMBLrel. 24, Created)
                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 40.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3702;
                                                                                                                                                            -JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=AX4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=AX4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                              086152;
                                                                                                Q86152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           023297
                                          RESULT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23297

2023297

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

20
                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=S2 / LL;
Hendrickson E.L., Kaul R., Zhou Y., Bovee D., Chapman P., Chung J.,
Conway de Macario E., Dodsworth J., Gillett W., Graham D.E.,
Haydock A.K., Kang A., Land M.L., Levy R., Lie T.J., Major T.,
Moore B., Porat I., Overbeek R., Palmeiri A., Rouse G.,
Saenphimmachak C., Soll D., Whitman W.B., Larimer F.W., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Notch-like protein la (Fragment).
Griffithsia japonica (Red alga).
Bukaryota; Rhodophyta; Florideophyceae; Ceramiales; Ceramiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genome sequence of the mesophilic hydrogenotrophic methanogen Methanococous maripaludis.";
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, BX557220; CARF30170.1;
InterPro; IPR05025; FMN red.
Pfam, PF03588; FMN red.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.9%; Score 53; DB 2; Length 191; 38.1%; Pred. No. 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanococcaceae; Methanococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu C.L., Lee Y.K., Lee H.K.;
Submitted (JUN-2202) to the EMBL/GenBank/DDBJ databases.
EMBL; AY123122; AAM93994.1; -...
NON TER
SEQUENCE 225 AA; 25897 MW; 1D93A3AA1531D058 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          191 AA; 21019 MW; BCF6A6F18BDF7163 CRC64;
                                                                                                                                                                                                                                                             05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Related to iron-sulfur flavoprotein of Methanosarcina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           225 AA; 25897 MW; 1D93A3AA1531D058 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 32.9%; Score 53; DB 2; Local Similarity '41.4%; Pred. No. 73; es 12; "Conservative 4; Mismatches
191 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ECPPKKDDCETCSKDKDCKSGDCRYNKCI 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 KCFOHLDDC--CS--RKCN----RFNKCV 27
                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last seq
05-JUL-2004 (TrEMBLrel. 27, Last ann
                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 KCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |||:|:|:| :| ||:
KCFETLNNKCIIECDIINNCI 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 38.18;
                                                                                                                                                                                                                                                                                                                                                                    OrderedLocusNames=MMP0614;
                                                                                                                                                                                                                                                                                                                                                                                                  Methanococcus maripaludis
                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=39152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome
SEQUENCE 191 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=83288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                Q6LZL1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q7XZ30
```

RESULT 80

SPR RAPIN SOC SET THE SOC SET THE SOC SET THE SET THE

ð 셤 Best Loca Matches

ઠે q

ä

Gaps

;; 73

```
Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUN-2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wilson R.;
Submitted (AUG-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6239
                                                                                                                                                                                                  Aypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1998
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waterston R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilson R.;
                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                044635;
                                                                                                                                                                                                                                                                                                                                                                        RESULT 84
                                                                                                                                                                                                                                                                                                                                                                                     044635
  à
                                                                                                                                                                                                                                                                                                                            요
                                                                                                                                                                                                                                                                                                                                                                                                                                ö
              MEDLINE=22598051; PubMed=12679534; DOI=10.1093/molbev/msg088; Heim M.A., Jakoby M., Werber M., Martin C., Weisshaar B., Bailey P.C.; "The basic helix-loop-helix transcription factor family in plants: a genome-wide study of protein structure and functional diversity."; Mol. Biol. Evol. 20:735-747(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q81467 PRELIMINARY; PRT; 283 AA.
Q81467;
Q81467;
Q81467;
Q81-677-2002 (TrEMBLrel. 22, Created)
O1-OCT-2002 (TrEMBLrel. 22, Last sequence update)
O5-JUL-2004 (TrEMBLrel. 27, Last annotation update)
A74g14410/d1345w (Hypothetical protein).
A74g14410/d1345w (Hypothetical protein).
Eukaryota; Viridiplantea; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Satou M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SLIND P., Chenk R., Kim C.J., Meyers M.C., Banh J.,
Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.
Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Shinn P., Chen H., Cheuk R., Kim C.J., Banh J., Bowser L.,
Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
                                                                                                               TISSUE-Whole plant;
Jakoby M.J., Heim M.A., Bailey P., Martin C., Weisshaar B.;
Jakoby M.J., Heim M.A., Bailey P., Martin C., Weisshaar B.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Conteains 1 basic helix-loop-helix (bHLH) domain.
EMBL; 2973136; CAB10220.1; -.
                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22088475; PubMed=12093376; Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov Feldmann K.A., Flavell R.B., White O., Salzberg S.L.; "Full-length messenger RNA sequences greatly improve genome
                                                                                                                                                                                                                                                                                                                            32.9%; Score 53; DB 2; Length 277; 58.8%; Pred. No. 88; ive 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brower V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell Feldmann K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                       SMART; SM0035; HLH; 1.
PROSITE; PS50888; HLH; 1.
HYPOCHELICAI protein.
SEQUENCE 277 AA; 31190 MW; 17D79957B8B77B48 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       annotation.";
Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002)
                                                                                                                                                                                  EMBL; AL161538; CAB78483.1; -. EMBL; AF488628; AAM10963.1; -. PIR; B71406; B71406; B71406. InterPro; IPR001092; HLH basic. Pfam; PF00010; HLH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                 106 EHLDDDCSRKRARTGSC 122
                                                                                                                                                                                                                                                                                                                                                                                       10 QHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                           10; Conservative
TISSUE=Whole plant;
                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ecker J.R.;
                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A. Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S. Shinozaki K., Davis R.W., Theologis A., Ecker J.R., Yu G., Yu S. Submitted (JUL-2002) to the Embl/Genbank/DDBJ database.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRALM-BAILSOL N2;
MEDILINE-99069613; PubMed-9851916;
WormBase Consortium;
"Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 53; DB 2; Length 283;
Pred. No. 89;
1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wilson R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Davidson S., Wohldmann P., Bauer C., O'Neal D.;
"The sequence of C. elegans cosmid F16B4.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                AB758D25A07E12BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
U-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein P1684.9.
Name-F1684.9, ORFNames=F1684.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                  EMBL; AY133565; AAM91395.1; -
InterPro; IPR001092; HLH_basic.
                                                                                                                                                                                                        EMBL; AY102106; AAM26676.1; -. EMBL; AY088053; AAM65599.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 EHLDDDCSRKRARTGSC 128
                                                                                                                                                                                                                                                                                                                                                                                                                    l protein.
283 AA; 31995 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 06,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 QHLDDCCSRKCNRFNKC
                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50888; HLH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.9
Best Local Similarity 58.8
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                         Pfam; PF00010; HLH; 1.
SMART; SM00353; HLH; 1.
```

REPRESENTATION OF THE PROPERTY OF THE PROPERTY

```
.
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  insights into vegetal plate regionalization and Notch receptor regulation.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match
Local Similarity 33.3%; Score 53; DB 2; Length 1286;
Local Similarity 33.3%; Pred. No. 3.4e+02;
es 8; Conservative 4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 1286 AA; 144156 MW; EE919D876B21BB3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Development 124:3363-3374(1997).
| Remb., AF000634; AAB82088.1; -. |
| PIR; 731070; 731070.
| R HSCP; POLI132; 1BGF.
| GO; GO:0016020; C:membrane; IEA.
| GO; GO:0016020; C:membrane; IEA.
| GO; GO:0016509; F:cell differentiation; IEA.
| GO; GO:0010154; P:cell differentiation; IEA.
| GO; GO:0010154; P:cell differentiation; IEA.
| R GO; GO:0050793; P:regulation of development; IEA.
| R GO; GO:0050793; P:regulation of development; IEA.
| R GO; GO:0050793; P:regulation of development; IEA.
| R InterPro; IPR001801; EGF_1.
| R InterPro; IPR001801; RGF_2.
| R InterPro; IPR001801; RGF_1.
| R INTS; PR00115; ANKYRIN.
| R INTS; PR00110; EGFBLOOD.
| R INTS; PR01145; NOTCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 2531 AA
                                                                                                                                                                                                                                                                 PROSITE; PS00022; EGF 1; 7.
PROSITE; PS00186; EGF 2; 4.
PROSITE: PS50126; EGF 3; 7.
PROSITE; PS01187; EGF 3; 7.
PROSITE; PS01187; EGF CA; 2.
PROSITE; PS00119; EGF CA; 2.
EGF -1ike domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  801 TGSRCEVNIDDCVGHKCQNNGTCV 824
                                IPR001211; PhospholipaseA2
                                                  Pfam; PF00008; EGF; 7.

Pfam; PF01463; LRRCT; 3.

Pfam; PF01463; LRRCT; 3.

Pfam; PF001463; LRRUT; 3.

Pfam; PF000160; EGFBLOOD.

PRINTS; PR00019; EGFBLOOD.

PROSITE; PS00110; ASX HYDROXL; 3.

PROSITE; PS01186; CTCK 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 XNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lytechinus.
NCBI_TaxID=7654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Notch homolog.
                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           016004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     016004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 86
016004
                              DR DR DR KW KW SQ CS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RP SEQUENCE FROM N.A.

RC STRAINBAISTOOLNA.

RC STRAINBAISTOOLNA.

RC STRAINBAISTOOLNA.

RU WormBase Consortium,

Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.

CC -1- SUBELLULAR LOCATION: Nuclear (By similarity).

-1- SINLIARITY: Belongs to the nuclear hormone receptor family.

BRBL; AF039048; AAB94240.2; -..

BR GO; GO:0003700; FISBA-9.

BR InterPro; IPR00936; Str ncl. receptor.

BR InterPro; IPR00946; Str ncl. receptor.

BR InterPro; IPR00946; Str ncl. receptor.

BR InterPro; IPR009846; Str ncl. receptor.

BR InterPro; IPR009836; Str ncl. receptor.

BR PRINTS; PR000035; Znf C48teroid, 1.

BR PRINTS; PR00039; Znf C48teroid, 1.

BR SWART; SW00399; ZnF C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anopheles gambiae str. PEST.
Waldaryota, Metazoa, Arthropoda, Haxapoda, Insecta, Prerygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Anopheles.
NGBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A Anopheles Genome Sequencing Consortium;
A Anopheles Genome Sequencing Consortium;
L Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL; AAABA1008889; EAA07783.1; -...

R EMSP; P00740; IEDM.

R GO; GO:0005509; F:calcium ion binding; IEA.

R InterPro; IPR000421; ASX hydroxyl S.

R InterPro; IPR000425; ASX hydroxyl S.

R InterPro; IPR000421; EGF 2.

R InterPro; IPR001438; EGF 2.

R InterPro; IPR001438; EGF II.

R InterPro; IPR001438; EGF II.

R InterPro; IPR001439; EGF II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.9%; Score 53; DB 2; Length 421; 40.7%; Pred. No. 1.3e+02; Live 4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07QCT2;
01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AgCP1804 (Fragment).
Name=agCG51928; ORFNames=ENSANGG0000014325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1286 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CRIXNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 CRGGMAKCIVNTNDRYQCRLCRFNKCV 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LRR_Cterm.
LRR_Nterm.
LRR_typ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 40.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR001611, LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR000483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=PEST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               070CT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 85
Q7QCT2
```

ò g 

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lytechinus variegatus (Sea urchin).
Eukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
Echinoidea, Euechinoidea, Echinacea, Temnopleuroida, Toxopneustidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=97454256; PubMed=9310331;
Sherwood D.R., McClay D.R.;
"Identification and localization of a sea urchin Notch homologue:
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-98250176; PubMed-9590294;

MEDLINE-98250176; PubMed-9590294;

MEDLINE-98250176; PubMed-9590294;

MEDLINE-98250176; PubMed-9590294;

A MEDLINE-98250176; PubMed-9590294;

Ordentlich P., Kadesch T., Attavanie-Teakonas S.;

"Human deltex is a conserved regulator of Notch signalling.";

I. Nat. Genet. 19:74-78(1998).

I. Nat. Genet. 19:74-78(198).

I. Nat. Genet. 19:74-78(1988).

I. Nat. Genet. 19:74-78(1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L., Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.; "Human ligands of the Notch receptor."; Am. J. Pathol. 154:785-794 (1999).
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-2444 FROM N.A.
MEDILINE-91347367; PubMed=1831692; DOI=10.1016/0092-8674(91)90111-B;
MEDILINE-91347367; PubMed=1831692; DOI=10.1016/0092-8674(91)90111-B;
Ellisen L.W., Bird J., West D.C., Soreng A.L., Reynolds T.C.,
Smith S.D., Sklar J.;
"TAN. I, the human homolog of the Drosophila notch gene, is broken by
chromosomal translocations in T lymphoblastic neoplasms.";
cell 66:649-661(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FCB-2003 (Rel. 46, Last annotation update)
Neurogenic locus notch homolog protein 1 precursor (Notch 1) (hNI)
(Translocation-associated notch protein TAN-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                       32.9%; Score 53; DB 2; Length 2531; 45.0%; Pred. No. 6.2e+02;
                                                                                                                                                                                                                 2531 AA; 273982 MW; 5BF42BEC627CA303 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mann R.S., Blaumueller C.M., Zagouras P.; "Complete human notch 1 (hN1) cDNA sequence."; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                            3; Mismatches
                                                          PROSITE; PSS0088, ANK REPEAT; 5.
PROSITE; PSS0297; ANK REP REGION; 1.
PROSITE; PS00010; ASX—HVDROXYL; 21.
PROSITE; PS00022; EGF 1; 33.
PROSITE; PS01166; EGF 2; 25.
PROSITE; PS01167; EGF 7; 35.
PROSITE; PS01187; EGF CA; 20.
ANK repeat; EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99180765; PubMed=10079256;
                                                                                                                                                                                                                                                                                                                                                       CEEDIDDCESRPCHNGGTCV 681
                                                                                                                                                                                                                                                                                                                                 8 CFQHLDDCCSRKCNRFNKCV 27
SMART; SMO0248; ANK; 6.
SMART; SMO0179; EGF_CA; 23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=NOTCH1; Synonyms=TAN1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTIFICATION OF LIGANDS
                                                                                                                                                                                                                                                                        Local Similarity 45.0 es 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NTC1_HUMAN
                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 87
NTC1 HUMAN
                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                   셤
           ò
```

```
-i-TISSUE SPECIFICITY: In fetal tissues most abundant in spleen, brain stem and lung. Also present in most adult tissues where it is found mainly in lymphoid tissues.

-i- PTM: Synthesized in the endoplasmic reticulum as an inactive form which is proteclytically cleaved by a furin-like convertase in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C-terminal fragment N(TM) and a N-terminal fragment N(EC). Following ligand binding, it is cleaved by TNP-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notch extracellular truncation (NEXT). This fragment is then cleaved by presentlin dependent gamma-secretase to release a notch-derived peptide containing the intracellular domain (NICD) from the membrane (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensee@ibb-sib.ch).
                          SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EC) which are probably linked by disulfide bonds (By similarity). Interacts with DTX1 and DTX2.
SUBCELLULAR LOCATION: Type I membrane protein. Following proteolytical processing NICD is translocated to the nucleus (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTM: Phosphorylated (By similarity).
DISEASE: NOTCH1 truncation is associated with T-cell acute
both CD4+ and CD8+ cells in the thymus (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3D-structure; Activator; ANK repeat; Developmental protein; Differentiation; EGF-like domain; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0016021; C:integral to membrane; NAS. GO; GO:00160215; P:immune response; NAS. InterPro; IPR00110; ANK. InterPro; IPR0001210; ANK. hydroxyl_S. InterPro; IPR000142; BGF_Z. InterPro; IPR00143; BGF_T. InterPro; IPR001438; BGF_TI. InterPro; IPR001438; BGF_TI. InterPro; IPR001438; BGF_TI. InterPro; IPR001660; NOD. InterPro; IPR008097; Notch. InterPro; IPR008097; Notch. InterPro; IPR008000; Notch_region. Pfam; PF000213; Ank; 6. Pfam; PF000213; Ank; 6. Pfam; PF000018; BGF; 35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PSS0088; ANK REPEAT; 4.
PROSITE; PSS0297; ANK REP REGION; 1
PROSITE; PS00010; ASX HYDROXYL; 20
PROSITE; PS00022; EGF_1; 34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF308602; AAG33848.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; 34.
2; 26.
3; 36.
CA; 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M73980; AAA60614.1; -. PDB; 1PBS; NMR; A=1447-1481.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIRSF; PIRSF002279; Notch; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00248; ANK; 6.
SMART; SM00179; EGF_CA; 23.
SMART; SM00004; NL; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genew; HGNC:7881; NOTCH1.
MIM; 190198; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO1415; ANKYRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00066; Notch; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS01187; EGF
                                                                                                                                                                                                                      similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS;
```

```
EGF-11Ke 29.
EGF-11Ke 29.
EGF-11Ke 29.
EGF-11Ke 31.
EGF-11Ke 31.
EGF-11Ke 32.
EGF-11Ke 33.
EGF-11Ke 34.
EGF-11Ke 35.
EGF-11Ke 36.
EGF-11Ke 36.
EGF-11Ke 36.
EGF-11Ke 37.
EGF-11Ke 37.
EGF-11Ke 38.
EGF-1
                                                                                                                                                                                                                                                                                                                                                                                             EGF-like 15, carcium-binding (Potential).
EGF-like 16, calcium-binding (Potential).
EGF-like 17, calcium-binding (Potential).
EGF-like 19, calcium-binding (Potential).
EGF-like 20.
EGF-like 20.
EGF-like 21, calcium-binding (Potential).
EGF-like 22.
EGF-like 23.
EGF-like 24.
EGF-like 24.
EGF-like 24.
EGF-like 25.
EGF-like 26.
EGF-like 27.
                                                                                                                                                                                                                                                                              (Potential). (Potential). (Potential).
                                                                                                                                                                                                                                                                                                                                           (Potential)
                                                                                                                                                                                                                                                                                                                                                                         (Potential)
                                                                                                                                                                                                                                                                                                                                                                                        (Potential)
                                                                         protein
                                                                                                                                                                                                                                                calcium-binding (Potential)
Notch signaling pathway; Phosphorylation; Receptor; Repeat; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cleavage (by furin-like protease)
                                                   Potential.
Neurogenic locus notch homolog
Notch extracellular truncation
                                                                                                           Notch intracellular domain (By
                                                                                                                                                                                                                                                                                                                                   calcium-binding (
                                                                                                                                                                                                                                                                            calcium-binding (calcium-binding (calcium-binding)
                                                                                                                             similarity).
Extracellular (Potential).
                                                                                                                                                                        Cytoplasmic (Potential)
EGF-like 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            By similarity.
                                                                                                                                                                                                   EGF-like 2.
EGF-like 3.
EGF-like 4.
EGF-like 5.
EGF-like 7.
EGF-like 7.
EGF-like 9.
                                                                                                  similarity)
                                                                                                                                                            Potential.
                                                                                                                                                                                                                                                                                                                                                   EGF-like 1
EGF-like 1
EGF-like 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Poly-Pro.
Poly-Ser.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Poly-Glu.
Poly-Gly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Poly-Val.
Poly-Arg.
Poly-Pro.
Poly-Ala.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -Gln.
                                                                 2556
2556
                                                                                                             2556
                                                                                                                                                                                                                 139
179
179
179
133
133
137
137
1410
4450
4450
4450
601
639
                                                                                                                                                                                                                                                                                                                                                                                                                                          714
751
789
827
868
906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1347
1385
1427
1481
1523
1563
1957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1020
1058
1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2024
2057
2090
1579
                                                                 19
                                                                                                             1755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1482
1524
1928
1961
1995
2061
1576
1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1268
1308
1349
1388
                                                                                                                                                         'RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                         DOMAIN
                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
DOMAIN
                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
REPEAT
REPEAT
                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                    OMAIN
                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
REPEAT
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SITE
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vol. Phylogenet. Evol. 22:333-341(2002).
-!- FUNCTION: Protamines substitute for histones in the chromatin of sperm during the haploid phase of spermatogenesis. They compact sperm DNA into a highly condensed, stable and inactive complex (By
                                                                                                                                                                                                                                                                                                                                                                                                                                            [1] -
SEQUENCE FROM N.A.
MEDLINE=21881971; PubMed=11884158; DOI=10.1006/mpev.2001.1051;
Wan Den Bussche R.A., Hoofer S.R., Hansen E.W.;
"Characterization and phylogenetic utility of the mammalian protamine
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF435940; AALJS574.1; -.

EMBL; AF435940; AALJS574.1; -.

Plan; PF00260; Protamine P1; 1.

PROSITE; PS00048; PROTAMINE P1; 1.

Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein; Nucleosome core; Spermatogenesis; Testis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                          Plecotus townsendii (Townsend's big-eared bat).
Eukaryots, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Chiroptera; Microchiroptera; Vespertilionidae;
Corynorhinus.
                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2
                                                                                           Score 53; DB 1; Length 2556;
Pred. No. 6.3e+02;
4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLIAR LOCATION: Nuclear (By similarity).
-!- TISSUE SPECIFICITY: Testis.
-!- SIMILARITY: Belongs to the protamine Pl family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0 0 By similarity.
47 AA; 6530 MW; B4670EBB86CEDB19 CRC64;
                                                                                                                                                                                                                                                                                     25-OCT-2004 (Rel. 45, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
   / similarity.
/ similarity.
/ similarity.
/ similarity.
/ similarity.
                                                                                                                                                                                                                                                                Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 52.5; DE Pred. No. 21; 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRIXNOKCFOHLDDCCSRK----CNRFNK 25
                                                                                                                                                                                                                                                                47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRRRRRCYRRRRCCRRRRRRRVCCRRYTR
                                                                                                                                                                      250 TGQNCEENIDDCPGNNCKNGGACV 273
                                                                                                                                                     4 XNOKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                           32.9%;
ilarity 33.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.6%;
Similarity 26.7%;
8; Conservative 8
                                                                                                                                                                                                                                                             STANDARD;
 127
138
155
164
175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                     Similarity
8; Conserva
                                                                                                                                                                                                                                                                                                                                       Sperm protamine P1.
Name=PRM1;
                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI TaxID=124745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity)
                                                                                                                                                                                                                                                          HSP1 PLETO
Q8WNZ0;
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P1 gene."
                                                                                         Query Match
                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INIT MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                         Best Loc
Matches
                                                                                                                                                                                                                               RESULT 88
HSP1 PLETO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q646U5
ID Q646US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 89
                                                                                                                                                                                                                                                          g
                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
```

ï

Gaps

ä

Indels

9

92,

χ. ..

```
TISSUE=Needles;
MEDLINE=97214637; PubMed=9061017; DOI=10.1016/S0005-2760(96)00161-0;
MEDLINE=97214637; Werner T., Hani J., Ernst D., Sandermann H.;
Megener A., Gimbel W., Werner T., Hani J., Ernst D., Sandermann H.;
"Molecular cloning of coron-inducible protein from Pinus sylvertris L.
with high sequence similarity to vertbrate 3-hydroxy-3-methylglutaryl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0004421; F:hydroxymethylglutaryl-CoA synthase activity; IEA. GO; GO:0006084; P:acetyl-CoA metabolism; IEA. InterPro; IPR000886; ER target_S. InterPro; IPR000860; ER target_S. InterPro; IPR0008260; HMG COA synth. InterPro; IPR010122; HMG COA synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Coniferopsida, Coniferales, Pinaceae, Pinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (japonica cultivar-group).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                    Yu C., Zhang F., Mihoko K., Masahiro I., Zhu Y., Hirayama Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY570752; AAS68257.1; - . SEQUENCE 92 AA: 10345 MW; 052F01BS3D379F5F CRC64;
                                                                                                                                                                                                                                DB 2; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam: PF01154; HMG CoA Bynt; 1.
TIGRFAMS; TIGR01833; HMG-CoA-S euk; 1.
PROSITE; PS00014; ER TARGET; UNKNOWN 1.
SECHENCE 474 AA; 52998 MW; 3ECB48ESF23D37BA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1997 (TrEMBLrel. 03, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annocation update) 1-Mydroxy-3-methylglutaryl-CoA-synthase.
Pinus sylvestris (Scots pine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004. (TrEMBLrel. 27, Created) 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Schistosomatoidea; Schistosomatidae; Schistosoma
NCBI_TaxID=6182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32.6%; Score 52.5; DB 2; 43.5%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          474 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Z
                                                                                                                                                                                                                                                                                      5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochim. Biophys. Acta 1350:247-252(1997).
EMBL; X96386; CAA65250.1; -.
PIR; T09688; T09688.
                                                                                                                                                                                                                                   Score 52.5;
Pred. No. 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       764
                                                                                                                                                                                                                                                                                                                                          1 CRIXNOKCFQHLDDCCSRKCNRFN 24
                                                                                                                                                                                                                                                                                                                                                                        66 CLPDKQQCRRN-KDCCSKSCYRGN 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211 LSÓTCYLMALDSCYKRFCNKFEK 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 03, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 XNOKCF-QHLDDCCSRKCNRFNK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Putative wall-associated kinase.
Name=P0016F11.13;
                                                                                                                                                                                                                                   32.6%;
                                                                                                                                                                                                                                                         Local Similarity 41.7 tes 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 10; Conserv
                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1997
                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q6K5W7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q6K5W7
                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q6K5W7
  SOREBES
                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OCC OS GENTLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä
                                                                                                                                                                                                                                                                                                                                  Kamoun S.;
Patterns of Diversifying Selection in the Phytotoxin-like scr74 Gene
"maily of Phytophthora infestans.";
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY723722; AAU21463.1;
EMBL; AY723721; AAU21462.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kamoun S.;
"Patterns of Diversifying Selection in the Phytotoxin-like scr74 Gene Family of Phytophthora infestans.";
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AY723720; AMU214G1.1;
SEQUENCE 74 AA; 7802 MW; 57A8231D29AB5F8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                    Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phytophthora infestans (Potato late blight fungus).
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.6%; Score 52.5; DB 2; Length 74; 34.6%; Pred. No. 32;
                                                                                                                                            Bukaryota, stramenopiles; Oomycetes; Pythiales; Pythiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Indels
                           25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Phytoxin-like SCR74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                 Phytoxin-like SCR74.
Phytophthora infestans (Potato late blight fungus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 92 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.6%; Score 52.5; D
34.6%; Pred. No. 32;
Live 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | : : | : : | | : | CKAINAEPVA-FNDCCSKSCNTGSPC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | : : | : : | | : | | : | CKAINAEPVA-FNDCCSKSCNTGSPC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CRIXNOKCFOHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          japonicum (Blood fluke).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ilarity 34.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 34.6
nes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Egg protein CP422.
Name=CP422;
Schistosoma japoni
                                                                                                                                                                                                           NCBI_TaxID=4787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phytophthora.
NCBI_TaxID=4787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q6PYV0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q646U7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0646U7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O6PYV0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 90
064607
AC 06460
DT 25-0C
DT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 91
Q6PYV0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRECTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
```

ä

Gaps

1,

Indels

Length 474;

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-aib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                   Direct protein sequencing; Glycoprotein; Lectin; Phosphorylation; Repeat; Signal; Transmembrane. SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1285;
                                                                                                                                                                                                                                                                                                                                                                     X approximate tandem repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence of the nematode C.elegans: A platform for investigating biology.";
Science 282:2012-2018(1998).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     > G (in Ref. 3).
64BB2DFD2AD8ECBA CRC64;
                                                                                                                                                                                                                                                                                                    Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                   Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                170 kDa surface lectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GlcNAc. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
1-NAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein F46B3.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlcNAc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 52.5; DB 1;
Pred. No. 3.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GlcNAc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GlcNAc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GlcNAc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GlcNAc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        354 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CRIXNOKCFQHLDDCCSRK--CNRFN-KC 26
                                                                                                                                                                                                                                                                                                                   Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .N-linked
N-linked
                                                                                                                                                                                                                                                                                                                                                      Cys-rich.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-linked
N-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ٠
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144410 MW;
                                                                                                                                                                                       EMBL; M60498; AAA29106.1; -.
EMBL; X61003; CAA43321.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 41.4%;
12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1285 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
              transduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                              CHAIN
DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9XV21
Q9XV21;
                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09XV21
              7
                                            Lasaki T., Matsumoto T., Katayose Y.;
Sasaki T., Matsumoto T., Katayose Y.;
Submitted (MAY-2002) to the EMBL/GenEank/DDBJ databases.

R GO; GO:0005224; FATP binding; IEA.

GO; GO:0004713; FATP binding; IEA.

GO; GO:0004713; Fiprotein serine/threonine kinase activity; IEA.

GO; GO:0004714; Fiprotein serine/threonine kinase activity; IEA.

GO; GO:0004714; Fiprotein amino acid phosphorylation; IEA.

R GO; GO:0004719; Fiprotein amino acid phosphorylation; IEA.

R GO; GO:0006468; Piprotein amino acid phosphorylation; IEA.

R GO; GO:0006468; Piprotein amino acid phosphorylation; IEA.

R InterPro; IPR00129; Kinase like.

R InterPro; IPR00129; For thr pkinase.

R InterPro; IPR00129; For thr pkinase.

R InterPro; IPR00129; For thr pkinase.

R Fam; PF07645; EGF CA; I.

R SWART; SM00219; TYrK; I.

R SWART; SM00219; TYrK; I.

R SWART; SM00219; TYRC; I.

R SWART; SM00219; TYRC; I.

R PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN I.

R PROSITE; PS00118; PROTEIN KINASE ST; UNKNOWN I.

R PROSITE; PS00118; PROTEIN KINASE ST; UNKNOWN I.

R PROSITE; PS00118; PROTEIN KINASE ST; UNKNOWN I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Subunit structure of the galactose and N-acetyl-D-galactosamine-inhibitable adherence lectin of Entamoeba histolytica.";
J. BAD1. Chem. 264:3007-3012(1989).
-1- FUNCTION: Mediates adherence of E.histolytica to colonic mucins, an essential step for pathogenic tissue invasion.
-1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- PIM: Phosphorylated regions may have a role in signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 16-30.
MEDLINE-89123408; PubMed=2536/31;
Perri W.A. Jr., Chapman M.D., Snodgrass T., Mann B.J., Broman J.
Ravdin J.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91156704; PubMed=2000392;
Tannich E., Ebert F., Horstmann R.D.;
"Primary structure of the 170-kDa surface lectin of pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.6%; Score 52.5; DB 2; Length 7
26.2%; Pred. No. 2.5e+02;
Live 6; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 280 CRSTNSECFDTIDGGGYRCNCCQGYEGNPYLDGGCTDINECL 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVISIONS TO N-TERMINUS.
Tannich E., Nickel R., Ebert F.; Horstmann R.D.;
Submitted (AUG-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         764 AA; 85266 MW; SECAB51B666C88C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CRIXNQKCFQHLD-----DCC-----SRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Entamoeba histolytica.";
Proc. Natl. Acad. Sci. U.S.A. 88:1849-1853(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1285 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF 16-33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Entamoebidae; Entamoeba.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1991 (Rel. 20, Created)
01-JUL-1993 (Rel. 26, Last sequer
05-JUL-2004 (Rel. 44, Last annota
170 kDa surface lectin precursor.
Name=CEL-170/4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 26.29
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Entamoeba histolytica.
                               SEQUENCE FROM N.A.
NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=5759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SL17 ENTHI P23502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 94
SL17_ENTHI
```

ò 셤 7

```
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                        EGF-like domain.
SEQUENCE 487 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DROME .
                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DROME
          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RC Staninger From N.A.

Stapleton M., Broketein P., Hong L., Agbayani A., Carlson J.,

Stapleton M., Broketein P., Hong L., Agbayani A., Carlson J.,

Change M., Chavez C., Dorsett V., Dresnek D., Farian D., Fariae E.,

RA Gaoralez M., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,

Miradda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,

RA Garge R., Gonzalez M., Wannin H., Yu C., Lewis S.E., Rubin G.M.,

RA Galiker S.,

RA Calliker S.,

Ca
                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                  .,
,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                             32.3%; Score 52; DB 2; Length 354; 35.7%; Pred. No. 1.4e+02; ive 5; Mismatches 11; Indels
                                                                               Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                               354 AA; 37229 MW; 5769BF095E8E03F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       487 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 CKLVNGSPKCVPELDQCSHIKCSIGSHC 185
                                                                                                                                                                                                                                                                                                                                                                                                                              1 CRIXN--QKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly)
                                                                                                   EMBL; Z81540; CAB04398.1; -. PIR; T22274; T22274. WormBase; WBGene00009762; F46B3.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                        MormPep; F46B3.9; CE18691.
InterPro; IPR003645; F01_N.
SMART, SM00274; F01L; 8.
Hypothetical protein.
SEQUENCE 354 AA; 37229 My
                                                                                                                                                                                                                                                                                                                                                    Local Similarity 35.7 ies 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                 STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
FROM N.A.
                                                          Ainscough R.;
                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=crb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8MSX5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8MSX5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 96

ORMSXS

ORMSXS

AC QBMSXX

AC QBMSXX

DD 1-OC OC

DT 01-OC OC

DT 01-OC

DT 01-OC OC

DT 01-OC

DT 01-OC OC

DT 01-OC

DT 01-
                                                                                                                                                                                                                                                                                                                                                                                Matches
       a
                                                                                                                                                                                                                                                                                                                                                                                                                                 8
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Holt P.W., Hookins R.A., Galle R.F., A Amanatides P.G., Scheres S.E., Li P.W., Hookins R.A., Galle R.F., Strong E.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutron G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Barton G.G., Mortman J.R., Yandell M.D., Change M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., Baxendale J., Bayraktaroglu L., Beasley E.M., Ballew R.M., Banos P.V., Berman B.P., Bhandari D., Bolshakov S., Berkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burkova D., Botchan M.R., Buller H., Cadieu E., Center A., Chandra I., A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., A Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21966.109; PubMed=11970894; DOI=10.1016/S1534-5807(02)00142-9; Cohen B.D., Mariol M.-C., Wallace R.M.H., Weyers J., Kamberov Y.G., Pradel J., Wilder E.L.; "DWnt4 regulates cell movement and focal adhesion kinase during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 151-539 FROM N.A.

MEDLINES-5511909; PubMed-7867502;

Graba Y., Gieseler K., Aragnol D., Laurenti P., Mariol M.-C.,

Berenger H., Sagnier T., Pradel J.;

Berenger H., Sanier T., Pradel J.;

Cubmt-4, a novel Drosophila Wnt gene acts downstream of homeotic complex genes in the visceral mesoderm.";

Development 121:209-218(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P40589; QBMPQ1, QBSWT3; Q9VM29; D1-FEB-1995 (Rel. 31, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Mnt-4 protein precursor (dWnt-4).
Name-Wht4; Synonyms-Wht 4; ORPNames-CG4698;
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.3%; Score 52; DB 2; Length 487; 30.4%; Pred. No. 1.9e+02; ive 6; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            487 AA; 52498 MW; C69E5B14E36B3D22 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             539 AA.
Pfam; PF00008; EGF; 8.

PRANTS; PR001010; EGFBLGOD.
SWART; SW00110; EGFBLGOD.
SWART; SW00110; EGF CA; 3.

PROSITE; PS000210; AGX_HYDROXYL; 4.

PROSITE; PS01022; EGF 1; 7.

PROSITE; PS01186; EGF 2; 6.

PROSITE; PS01187; EGF 2; 8.

PROSITE; PS01187; EGF 2; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 XNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila ovarian morphogenesis.";
Dev. Cell 2:437-448(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 30.43
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEOUENCE FROM N.A.
```

```
SEQUENCE FROM N.A.
MEDLINE=20245325; PubMed=10781962; DOI=10.1016/S0925-4773(00)00280-X;
Kuriyama S., Miyatani S., Kinoshita T.;
"Xerl; a novel secretory protein expressed in eye and brain of Xenopus
PRINTS; PRO1844; WNT4PROTEIN.
PRINTS; PRO1349; WNTPROTEIN.
SMART; SM00097; WNT1; 1
PROSITE; PS00246; WNT1; 1.
Developmental protein; Glycoprotein; Lipoprotein; Palmitate; Signal;
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                           F-palmicoyl cysteine (By similarity) F -> L (in Ref. 1). G -> R (in Ref. 1). F -> L (in Ref. 1). R -> L (in Ref. 5). R -> A (in Ref. 1). L -> V (in Ref. 1). L -> V (in Ref. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                   Wnt-4 protein.
N-linked (GlcNAc. .) (Potential).
N-linked (GlcNAc. .) (Potential).
N-linked (GlcNAc. .) (Potential).
                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                   32.3%; Score 52; DB 1; Length 539; 39.1%; Pred. No. 2.1e+02; ive 5; Mismatches 9; Indels
                                                                                                                                                                                                                             6682C8B3D729D067 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR00995; Asx hydroxyl interPro; IPR00996; Cond like lec_gl.
InterPro; IPR00996; Cond like lec_gl.
InterPro; IPR001891; EGF Za.
InterPro; IPR001891; EGF Za.
InterPro; IPR001438; EGF II.
InterPro; IPR001438; EGF II.
InterPro; IPR009030; Grow fac recept.
InterPro; IPR001791; Laminin G.
InterPro; IPR001791; Laminin G.
InterPro; IPR001791; Laminin G.
InterPro; IPR001791; EGF Za.
InterPro; IPR001791; ISP N.
Pfam; PF00210; Laminin G Z; I.
PRINTS; PR00010; EGF Za. G.
SWART; SM00179; EGF CA, G.
SWART; SM00179; EGF CA, G.
                                                                                                                                                                                                                                                                                                                       514 CRFNNGRCCQLICDYCQRLENKY 536
                                                                                                                                                                                                                                                                                                      1 CRIXNOKCFOHLDDCCSRKCNRF 23
                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sec
                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00010; ASX HYDROXYL; 7. PROSITE; PS00022; EGF 1; 10. PROSITE; PS01186; EGF 2; 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN, 1
                                                                                                                                                                                                                           58685 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mech. Dev. 93:233-237(2000).
EMBL; AB027453; BAA95001.1; -.
HSSP; Q12780; 1HAE.
                                                                                                                                                                                                                                    Query Match
Best Local Similarity 39.10,
Conservative
                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS01187; EGF_CA
PS50025; LAM_G_
                                                                 Wnt signaling pathway SIGNAL
                                                                                                                                                                                                              532 :
539 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=8355;
                                                                                           CHAIN
CARBOHYD
                                                                                                                    CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         embryo.";
                                                                                                                                                          CONFLICT
                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                 Q91BG4
  ò
                                                                                                                                                                                                                                                                                                                            g
```

```
ERRATUM.
               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
Pneumocystis.
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Pneumocystis carinii f. sp. carinii;
Murphy L., Quail M., Harris D., Hall N., Wakefield A., Smulian A.G.,
Cushion M.T., Stringer J.R., Keely S.P., Barrell B.G.;
Submitted (MAX-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL592382; CAC43459.1; -.
InterPro; IPR003330; NSG.
Pfem; PP02149; MSG; 7.
SEQUENCE 1069 AA; 120586 MW; 791A8C514D3BFB0B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Crumbs encodes an EGF-like protein expressed on apical membranes of Drosophila epithelial cells and required for organization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-DEGOON-R; TISSUE-Embryo;
MEDLINE-920263104; Pubmed-2344615; DOI=10.1016/0092-8674(90)90189-L;
Tepass U., Theres C., Knust E.;
                                                                                                                                                                                            ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1069;
                                                                                                                        Score 52; DB 2; Length 778;
Pred, No. 2.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha
Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                 . 2.9e+02;
tches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.3%; Score 52; DB 2; Length 106
40.6%; Pred. No. 3.8e+02;
ive 4; Mismatches 9; Indels
                                                                   462D2C84AE435CF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAX-1989 (Rel. 10, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CRIXNQKC--FQHLDD----CCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1069 AA.
                                                                                                                                                                                      6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2139 AA
                                           Potential
                                                                                                                                                                                                                                                                               285 DGELCQQDIDECQSQPCQNGGRCV 308
                                                                                                                                                                                                                                                 4 XNQKCFQHLDDCCSRKCNRFNKCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probable major surface glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Embryo;
MEDLINE=87218537; PubMed=3107986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Crumbs protein precursor (95F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1663-1955 FROM N.A.
                                           SIGNAL 1 27 P
SEQUENCE 778 AA; 85516 MW;
                                                                                                                           Query Match
Best Local Similarity 33.3%;
Matches 8; Conservative
EGF-like domain; Signal. SIGNAL 1 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell 61:787-799(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pneumocystis carinii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=PCCW03G5.13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 epithelia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRB_DROME
P10040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=crb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                            096VI2
                                                                                                                                                                                                                                                                                                                                                                                               RESULT 99
100501
AC 096VI
DT 01-DE
DT 01-DE
DT 01-OC
DE Proba
GN Nemen
OC Eukar
OC NCBI
RR SEQUE
RR SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
            SHE
                                                                                                                                                                                                                                                                                                        유
                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THE SECOND CONTRACT OF THE SECOND CONTRACT OF
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             photoreceptor morphogenesis in Drosophila.";
Development 130:4363-4373(2003).
-!- FUNCTION: Plays a central role in cell polarity establishment.
Participates in the assembly, positioning and maintenance of adherens junctions via its interaction with the SAC complex.
Controls the coalescence of the spots of zonula adherens (2A) into a adhesive ring around the cells. It may act as a signal. Involved in morphogenesis of the photoreceptor rhabdomere, for positioning and growth of rhabdomere and AJ during the crucial period of photoreceptor extension along the proximodistal axis of the
                                                                                                                                                                                                                                                                                                MEDLINE=99200394; PubMed=10102271; DOI=10.1016/S0092-8674(00)80593-0; Bhat M.A., Izaddoost S., Lu Y., Cho K.-O., Choi K.-W., Bellen H.J.; "Discs Lost, a novel multi-PDZ domain protein, establishes and maintains epithelial polarity."; cell 96:833-845(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBDINIT: Component of the SAC complex, a complex composed of crb, Patj and sdt. May interact with the par-6 complex, which is composed of par-6, baz and aPKC, via its interaction with Patj. Interacts with other proteins with Patj and sdt via its short cytoplasmic tail.
-!- SUBCELLUIAR LOCATION: Type I membrane protein. Specifically localized to the apical membrane.
-!- PTM: Phosphorylated in the cytoplasmic domain (Potential).
-!- SIMILARITY: Contains 3 laminin G-like domains.
Knust E., Dietrich U., Tepass U., Bremer K.A., Weigel D., Vaessin H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bhat M.A., Izaddoost S., Lu Y., Cho K.-O., Choi K.-W., Bellen H.J.; Cell 115:765-766(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=11076972; DOI=10.1083/jcb.151.4.891; Tanentzapf G., Smith C., McGlade J., Tapass U.; "Apical, lateral, and basal polarization cues contribute to the development of the follicular epithelium during Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDENTIFICATION IN A SAC COMPLEX WITH PATJ AND SDT.
MEDLINE=21603015; PubMed=11740560; DOI=10.1038/414638a;
Bachmann A., Schneider M. Theilenberg E., Grawe F., Knust E.;
"Drosophila Stardust is a partner of Crumbs in the control of
                                     Campos-Ortega J.A.;
"EGF homologous sequences encoded in the genome of Drosophila melanogaster, and their relation to neurogenic genes.";
EMBO J. 6:761-766(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nam S.-C., Choi K.-W.; Interaction of Par-6 and Crumbs complexes is essential for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION, AND INTERACTION WITH PATJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A35672; A35672.
PIR; B26637; B26637.
HSSP; P00740; 1EDM.
F; PBase; F8gn0000368; crb.
GO; GO:0016324; C:apical plasma membrane; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERACTION WITH THE PAR-6 COMPLEX.
PubMed=12900452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M33753; AAA28428.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell Biol. 151:891-904(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  epithelial cell polarity.";
Nature 414:638-643(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X05144; CAA28793.1;
                                                                                                                                                                                                                                                                             INTERACTION WITH PATJ.
```

```
Search completed: April 18, 2005, 20:37:49
Job time : 120 secs
                           DISULPID
                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Crumbs protein.

Extracellular (Potential).

Cytoplasmic (Potential).

Cytoplasmic (Potential).

EGF-like 1.

EGF-like 2.

EGF-like 3.

EGF-like 6.

EGF-like 10.

EGF-like 10.

EGF-like 10.

EGF-like 11.

EGF-like 11.

EGF-like 12.

EGF-like 13.

EGF-like 13.

EGF-like 14.

EGF-like 13.

EGF-like 14.

EGF-like 14.

EGF-like 15.

EGF-like 16.

EGF-like 17.

EGF-like 17.

EGF-like 18.

EGF-like 19.

EGF-like 19.

EGF-like 10.

EGF-like 10.

EGF-like 10.

EGF-like 10.

EGF-like 10.

EGF-like 20.

Laminin G-like 2.

EGF-like 21.

Laminin G-like 2.

EGF-like 22.

EGF-like 23.

EGF-like 24.

EGF-like 25.

EGF-like 26.

EGF-like 27.

EGF-like 27.

EGF-like 28.

EGF-like 29.

EGF-like 20.

EGF-like 20
DR GO; GO:0016327; C:apicolateral plasma membrane; IDA.
DR GO; GO:0016332; P:establishment and/or maintenance of cell po. .;
GO; GO:0016332; P:establishment and/or maintenance of polarit. .;
DR GO; GO:0016332; P:establishment and/or maintenance of polarit. .;
DR GO; GO:0016332; P:morphogenesis of an epithelium; NAS.
DR GO; GO:004206; P:morphogenesis of an epithelium; NAS.
DR GO; GO:004206; P:photoreceptor maintenance; IMP.
DR GO; GO:004206; P:rabdomere development; NAS.
DR GO; GO:004206; P:rabdomere development; NAS.
DR GO; GO:004206; P:rabdomere development; NAS.
DR InterPro; IPR001042; RGF Z.
DR InterPro; IPR001042; RGF Z.
DR InterPro; IPR001042; RGF Z.
DR InterPro; IPR001043; RGF Z.
DR RINTS; RM00179; Laminin G; 3.
DR Pfam; PR00006; RGF; Z.
DR RINTS; PR00101; RGFBLOD.
DR RANT; SM001079; RGF Z.; 17.
DR ROSITE; PS00106; RGF Z; 17.
DR RAMEN Z012; RGF CA; 12.
DR ROSITE; PS00106; RGF Z; 17.
DR ROMAIN Z012 Z139 Cytoplasmic (Potential).
TRANSMEM Z018 Z33 BGF-1ike Z.
TRANSMEM Z018 Z33 BGF-1ike Z.
DR ROMAIN Z017 Z018 BGF-1ike Z.
TRANSMEM Z018 Z33 BGF-1ike Z.
TRANSMEM Z018 Z311 POPALIN Z017 BGF-1ike Z.
TRANSMEM Z018 Z311 POPALIN Z017 BGF-1ike Z.
TRANSMEM Z018 Z311 RD RGF-1ike Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 52; DB 1; Length 213
Pred. No. 7.1e+02;
; Mismatches 10; Indels
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : | | | ::|:| | 1828 EGQHCEQNIDECADQPCHNGGNC 1850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 XNQKCFQHLDDCCSRKCNRFNKC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 32.3%;
Best Local Similarity 30.4%;
Matches 7; Conservative
```